

Table 42: Comparative Sequences relating to SAG 0764

## SEQ ID NO. 4201: 2603 V/R STRAIN

ATGGTAAATAGTATTCGCACGCCACGGTGAATCTGAGTGGAAATAAGCTAACCTTTTC  
 ACTGGATGGGCTGACGTAGATCTTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGG  
 AAATTAATTCAGCAGCAGGTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGT  
 GCCATCAAAACAACCTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAA  
 AAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAATAAGCAGAA  
 GCAGCTGAACAATTTGGTGATGAGCAAGTTTCAATTTGGCGTCGTTTATATGATGATTG  
 CTTCCAGATATGGCTAAAGATGATGAACATTTCAGCACATACTGATCGTCGCTATGCTTCA  
 CTAGATGATTCTGTTATTCAGATGCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCTT  
 CCTTTCTGGGAAGATAAAATTTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTGTTGGT  
 GCACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATCAACAATTTGTCAGATGATGAA  
 ATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTTCGAATTTGATGAAAAATTA  
 AACCTTGTTTCAGAAATATTACTTAGGTAAA

## SEQ ID NO. 4202: 090 STRAIN

GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTG  
 GAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAA  
 AAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAGCAGCAGGT  
 ATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAAC  
 AACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAA  
 AATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAAT  
 AAAGCAGAGCAGCTGAACAATTTGGTGATGAGCAAGTTTCAATTTGGCG  
 TCGTTTATATGATGATTGCTTCCAGATATGGCTTAAAGATGATGAACATT  
 CAGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTCCA  
 GATGCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCTTCTTTCTGGGA  
 AGATAAAATTTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTGTTGGTG  
 CACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATCAACAATTTGTCAG  
 GATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTT  
 CGAATTTGATGAAAAATTAACCTTGTTTCAGAAATATTACTTAGGTAAA

## SEQ ID NO. 4203: A909 STRAIN

GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTGG  
 AATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAA  
 AAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAGCAGCAGGT  
 TTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAACA  
 ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAAA  
 ATCATGGCGCTTAAACGAACGTCATTACGGTGGATTGACAGGAAAAATA  
 AAGCAGAGCAGCTGAACAATTTGGTGATGAGCAAGTTTCAATTTGGCGT  
 CGTTTATATGATGATTGCTTCCAGATATGGCTTAAAGATGATGAACATT  
 AGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTCCAG  
 ATGCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCTTCTTTCTGGGA  
 GATAAAATTTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTGTTGGTG  
 ACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATCAACAATTTGTCAG  
 ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTT  
 GAATTTGATGAAAAATTAACCTTGTTTCAGAAATATTACTTAGGTAAA

## SEQ ID NO. 4204: H36B STRAIN

GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAG  
 TGGAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAA  
 AAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAGCAGCAG  
 GTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAA  
 ACAAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAA  
 AAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAATA  
 ATAAAGCAGAGCAGCTGAACAATTTGGTGATGAGCAAGTTTCAATTTGG  
 CGTCTTATATGATGATTGCTTCCAGATATGGCTTAAAGATGATGAACA  
 TTCAGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTTC  
 CAGATGCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCTTCTTTCTGG  
 GAAGATAAAATTTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTGTTGG  
 TGACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATCAACAATTTGTCAG  
 ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTT  
 TTCGAATTTGATGAAAAATTAACCTTGTTTCAGAAATATTACTTAGGTAA  
 A

## SEQ ID NO. 4205: 18RS21 STRAIN

GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTGG  
 AATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAA  
 AAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAGCAGCAGGT  
 TTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAACA  
 ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAA  
 ATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAATA  
 AAGCAGAGCAGCTGAACAATTTGGTGATGAGCAAGTTTCAATTTGGCGT  
 CGTTTATATGATGATTGCTTCCAGATATGGCTTAAAGATGATGAACATT  
 AGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTCCAG  
 ATGCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCTTCTTTCTGGGA  
 GATAAAATTTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTGTTGGTG  
 ACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATCAACAATTTGTCAG  
 ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTT  
 GAATTTGATGAAAAATTAACCTTGTTTCAGAAATATTACTTAGGTAAA

## SEQ ID NO. 4206: M732 STRAIN

GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTGG  
 AATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAA  
 AAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAGCAGCAGGT

Table 42: Comparative Sequences relating to SAG 0764

TTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAACA  
 ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACAGTTGAAAA  
 ATCATGGCGCTTGAACGACGTCATTACGGTGGATTGACAGGAAAAATA  
 AAGCAGAGCAGCTGAACCAATTGGTGATGAGCAAGTTCATATTTGGCGT  
 CGTTTCATATGATGATTGCTCCAGATATGGCTAAAGATGATGAACATTC  
 AGCACAATCTGATCGTTCGCTATGCTTCACTAGATGATTCTGTTATTCCAG  
 ATGCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCTTCCCTTCTGGGAA  
 GATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTGTGGTGC  
 ACACGGTAACTCAATCCGTGCTCTTGTAAACATATCAACCAATTGTGAG  
 ATGATGAAATCATGGACGTTGAATTCCTAACCTCCACCACTTGTTTTC  
 GAATTTGATGAAAAATTAAACCTTGTTTCAGAAATATTACTTAGGTAAA

**SEQ ID NO. 4207: COH1 STRAIN**

GTAAAAATTAGTATTCGCACGCCACGG  
 TGAATCTGAGTGGAAATAAGCTAACCTTTTCACTGGATGGGCTGACGTAG  
 ATCTTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATT  
 CAAGCAGCAGGTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACG  
 TGCCATCAAAACAATAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGG  
 TACCAGTTGAAAAATCATGGCGCTTGAACGAACTGATTACGGTGGATTG  
 ACAGGAAAAATAAGCAGAGCAGCTGAACAATTGGTGATGAGCAAGT  
 TCATATTTGGCGTCGTTTCATATGATGATTGCTCCAGATATGGCTAAAG  
 ATGATGAACATTGAGCACAATACTGATCGTCGCTATGCTTCACTAGATGAT  
 TCTGTTATTCCAGATGTCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCT  
 TCCCTTCTGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATG  
 TGTGTTGTGGTGACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATC  
 AAACAATTGTCAGATGATGAAATCATGGACGTTGAAATTCTTAACCTCCC  
 ACCACTTGTTTTCGAATTTGATGAAAAATTAAACCTTGTTTCAGAAATATT  
 ACTTAGGTAAA

**SEQ ID NO. 4208: CJB110 STRAIN**

GTAAAAATTAGTATTCGCACGCCACGG  
 TGAATCTGAGTGGAAATAAGCTAACCTTTTCACTGGATGGGCTGACGTAG  
 ATCTTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATT  
 CAAGCAGCAGGTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACG  
 TGCCATCAAAACAATAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGG  
 TACCAGTTGAAAAATCATGGCGCTTGAACGAACTGATTACGGTGGATTG  
 ACAGGAAAAATAAGCAGAGCAGCTGAACAATTGGTGATGAGCAAGT  
 TCATATTTGGCGTCGTTTCATATGATGATTGCTCCAGATATGGCTAAAG  
 ATGATGAACATTGAGCACAATACTGATCGTCGCTATGCTTCACTAGATGAT  
 TCTGTTATTCCAGATGTCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCT  
 TCCCTTCTGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATG  
 TGTGTTGTGGTGACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATC  
 AAACAATTGTCAGATGATGAAATCATGGACGTTGAAATTCTTAACCTCCC  
 ACCACTTGTTTTCGAATTTGATGAAAAATTAAACCTTGTTTCAGAAATATT  
 ACTTAGGTAAA

**SEQ ID NO. 4209: 1169NT STRAIN**

AGTATTCGCACGCCACGGTGAATCTGAGTGGAAATAAGCTAACCTTTTCA  
 CTGGATGGGCTGACGTAGATCTTTTCAGAAAAAGGTACACAACAAGCTATT  
 GATGCTGGGAAATTAATTCAAGCAGCAGGTATTGAGTTTCGACCTTGCTTT  
 TACATCAGTTCTTAAACGTGCCATCAAAACAATAACCTTGCCCTTGAAG  
 CAGCTGATCAACTTTGGGTACAGTTGAAAAATCATGGCGCTTGAACGAA  
 CGTCAATTCGGTGGATTGACAGGAAAAATAAGCAGAGCAGCTGAACA  
 ATTTGGTGATGAGCAAGTTTCATATTTGGCGTCGTTTCATATGATGATTGCT  
 CTCAGATATGGCTAAAGATGATGAACATTGAGCACAATACTGATCGTCGC  
 TATGCTTCACTAGATGATTCTGTTATTCCAGATGTCAGAAAACTTAAAGT  
 TACTTTAGAGCGTGCTCTTCCCTTCTGGGAAGATAAAATTGCTCCTGCTC  
 TTAAGATGCTTAAATGTGTTGTTGGTGACACGGTAACTCAATCCGT  
 GCTCTTGTAAAAACATATCAACAATTGTCAGATGATGAAATCATGGACG  
 TGAAATTCCTAACCTCCACCACTTGTTTTCGAATTTGATGAAAAATTAA  
 ACCTTGTTTCAGAAATATTACTTAGGTAAA

**SEQ ID NO. 4210: M781 STRAIN**

GTAAAAATTAGTATTCGCACGCCACGGT  
 GAATCTGAGTGGAAATAAGCTAACCTTTTCACTGGATGGGCTGACGTAGA  
 TCTTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATT  
 AAGCAGCAGGTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACG  
 GCCATCAAAACAATAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGT  
 ACCAGTTGAAAAATCATGGCGCTTGAACGAACTGATTACGGTGGATTGA  
 CAGGAAAAATAAGCAGAGCAGCTGAACAATTGGTGATGAGCAAGTT  
 CATATTTGGCGTCGTTTCATATGATGATTGCTCCAGATATGGCTAAAGA  
 TGATGAACATTGAGCACAATACTGATCGTCGCTATGCTTCACTAGATGATT  
 GTGTTATTCCAGATGTCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCT  
 CCTTTCTGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATG  
 GTTGTGTTGGTGACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATCA  
 AACAAATTGTCAGATGATGAAATCATGGACGTTGAAATTCCTAACCTCCA  
 CCACCTTGTTTTCGAATTTGATGAAAAATTAAACCTTGTTTCAGAAATATT  
 CTTAGGTAAA

**SEQ ID NO. 4211: JM930013 STRAIN**

GTAAAAATTAGTATTCGCACGCCACGGTGAATCT  
 GAGTGGAAATAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTC  
 AGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAG

Table 42: Comparative Sequences relating to SAG 0764

CAGGTATTGAGTTGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATC  
 AAAACAACCTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCACT  
 TGA AAAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAA  
 AAAATAAAGCAGAAGCAGCTGAACAAATTTGGTGATGAGCAAGTTTCATATT  
 TGGCGTGGTTTCATATGATGATTTGCTCCAGATATGGCTAAAGATGATGA  
 ACATTGAGCAGCATACTGATCGTGGCTATGCTTCACTAGATGATTCTGTTA  
 TTCCAGATGCAGAAAACCTAAAGATTACTTTAGAGCGTGCTCTTCCITTC  
 TGGGAAGATAAAATTTGCTCTGCTCTTAAAGATGGTAAAAATGTGTTGT  
 TGGTGACACCGGTAACCTCAATCCGTGCTCTTGTAAACATATCAAACAAT  
 TGTGATGATGAAATCATGGACGTTGAAATTCCTAACCTTCCCAACCACTT  
 GTTTTCGAATTTGATGAAAAATTAACCTTGTTTCAGAAATATTACTTAGG  
 TAAA

PRETTY of: /biotmp/msa63264.2{\*} March 10, 2003 09:30 ..

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      1
msa63264.2{110_090} ---gtaaaat tAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_1169NT} ----- -AGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_18RS21} ---gtaaaat tAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_2603} atggtaaaaat tAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_CJB110} ---gtaaaat tAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_COH1} ---gtaaaat tAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_H36B} ---gtaaaat tAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_JM9130013} ---gtaaaat tAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_M732} ---gtaaaat tAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_M781} ---gtaaaat tAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
msa63264.2{110_A909} ---gtaaaat tAGTATTGCG ACGCCACGGT GAATCTGAGT GGAATAAAGC
      Consensus *****
      51
msa63264.2{110_090} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_1169NT} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_18RS21} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_2603} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_CJB110} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_COH1} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_H36B} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_JM9130013} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_M732} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_M781} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
msa63264.2{110_A909} TAACCTTTTC ACTGGATGGG CTGACGTAGA TCTTTCAGAA AAAGGTACAC
      Consensus *****
      101
msa63264.2{110_090} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_1169NT} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_18RS21} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_2603} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_CJB110} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_COH1} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_H36B} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_JM9130013} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_M732} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_M781} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
msa63264.2{110_A909} AACCAAGCTAT TGATGCTGGG AAATTAATTC AAGCAGCAGG TATTGAGTTC
      Consensus *****
      151
msa63264.2{110_090} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_1169NT} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_18RS21} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_2603} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_CJB110} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_COH1} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_H36B} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_JM9130013} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_M732} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_M781} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
msa63264.2{110_A909} GACCTTGCTT TTACATCAGT TCTTAAACGT GCCATCAAAA CAACTAACCT
      Consensus *****
      201
msa63264.2{110_090} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
msa63264.2{110_1169NT} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
msa63264.2{110_18RS21} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
msa63264.2{110_2603} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
msa63264.2{110_CJB110} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
msa63264.2{110_COH1} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
msa63264.2{110_H36B} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
msa63264.2{110_JM9130013} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
msa63264.2{110_M732} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
msa63264.2{110_M781} TGCCCTTGAA GCAGCTGATC AACTTTGGGT ACCAGTTGAA AAATCATGGC
      Consensus *****

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Table 42: Comparative Sequences relating to SAG 0764

msa63264.2{110_A909}	TGCCCCITGAA	GCAGCTGATC	AACITTTGGGT	ACCAGTTGAA	AAATCATGGC
Consensus	*****	*****	*****	*****	*****
251					
msa63264.2{110_090}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_1169NT}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_18RS21}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_2603}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_CJB110}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_COH1}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_H36B}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_JM9130013}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_M732}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_M781}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_A909}	GCTTaAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
Consensus	*****	*****	*****	*****	*****
301					
msa63264.2{110_090}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_1169NT}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_18RS21}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_2603}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_CJB110}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_COH1}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_H36B}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_JM9130013}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_M732}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_M781}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_A909}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
Consensus	*****	*****	*****	*****	*****
351					
msa63264.2{110_090}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_1169NT}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_18RS21}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_2603}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_CJB110}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_COH1}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_H36B}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_JM9130013}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_M732}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_M781}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_A909}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
Consensus	*****	*****	*****	*****	*****
401					
msa63264.2{110_090}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_1169NT}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_18RS21}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_2603}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_CJB110}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_COH1}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_H36B}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_JM9130013}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_M732}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_M781}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_A909}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
Consensus	*****	*****	*****	*****	*****
451					
msa63264.2{110_090}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_1169NT}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_18RS21}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_2603}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_CJB110}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_COH1}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_H36B}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_JM9130013}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_M732}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_M781}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_A909}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
Consensus	*****	*****	*****	*****	*****
501					
msa63264.2{110_090}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_1169NT}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_18RS21}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_2603}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_CJB110}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_COH1}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_H36B}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_JM9130013}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_M732}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA



Table 42: Comparative Sequences relating to SAG 0764

msa63264.2{110_M781}	TGCTCCTGCT	CTTAAAGATG	GTAAAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_A909}	TGCTCCTGCT	CTTAAAGATG	GTAAAAATGT	GTTTGTGGT	GCACACGGTA
Consensus	*****	*****	*****	*****	*****
msa63264.2{110_090}	551				600
msa63264.2{110_1169NT}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_18RS21}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_2603}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_CJB110}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_COH1}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_H36B}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_JM9130013}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_M732}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_M781}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
msa63264.2{110_A909}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATTGTC	AGATGATGAA
Consensus	*****	*****	*****	*****	*****
msa63264.2{110_090}	601				650
msa63264.2{110_1169NT}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
msa63264.2{110_18RS21}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
msa63264.2{110_2603}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
msa63264.2{110_CJB110}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
msa63264.2{110_COH1}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
msa63264.2{110_H36B}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
msa63264.2{110_JM9130013}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
msa63264.2{110_M732}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
msa63264.2{110_M781}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
msa63264.2{110_A909}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTIT	TCGAATTGTA
Consensus	*****	*****	*****	*****	*****
msa63264.2{110_090}	651				690
msa63264.2{110_1169NT}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_18RS21}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_2603}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_CJB110}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_COH1}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_H36B}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_JM9130013}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_M732}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_M781}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_A909}	TGAAAAATTA	AACCTTGTIT	CAGAATATTA	CTTAGGTAAA	
Consensus	*****	*****	*****	*****	

## SEQ ID NO. 4212: 2603 V/R STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA  
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV  
 PDMKDDHSAHTDRRYASLDDSVI PDAENLKVTLEALPFWEDKIAPALDKGKNVFGA  
 HGNSIRALVKHIKQLSDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

## SEQ ID NO. 4213: 090 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA  
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV  
 PDMKDDHSAHTDRRYASLDDSVI PDAENLKVTLEALPFWEDKIAPALDKGKNVFGA  
 HGNSIRALVKHIKQLSDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

## SEQ ID NO. 4214: A909 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA  
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV  
 PDMKDDHSAHTDRRYASLDDSVI PDAENLKVTLEALPFWEDKIAPALDKGKNVFGA  
 HGNSIRALVKHIKQLSDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

## SEQ ID NO. 4215: H36B STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA  
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV  
 PDMKDDHSAHTDRRYASLDDSVI PDAENLKVTLEALPFWEDKIAPALDKGKNVFGA  
 HGNSIRALVKHIKQLSDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

## SEQ ID NO. 4216: 18RS21 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA  
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV  
 PDMKDDHSAHTDRRYASLDDSVI PDAENLKVTLEALPFWEDKIAPALDKGKNVFGA  
 HGNSIRALVKHIKQLSDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

## SEQ ID NO. 4217: M732 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA  
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV  
 PDMKDDHSAHTDRRYASLDDSVI PDAENLKVTLEALPFWEDKIAPALDKGKNVFGA  
 HGNSIRALVKHIKQLSDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

## SEQ ID NO. 4218: COH1 STRAIN

Table 42: Comparative Sequences relating to SAG 0764

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA IKITNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV PDMADDEHSAHTDRRYASLDDSVIPDAENLKVTILERALPFWEDKIAPALKDGNVVFVGA HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK									
SEQ ID NO. 4219: CJB110 STRAIN VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA IKITNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV PDMADDEHSAHTDRRYASLDDSVIPDAENLKVTILERALPFWEDKIAPALKDGNVVFVGA HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK									
SEQ ID NO. 4220: 1169NT STRAIN VFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA IKITNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV PDMADDEHSAHTDRRYASLDDSVIPDAENLKVTILERALPFWEDKIAPALKDGNVVFVGA HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK									
SEQ ID NO. 4221: M781 STRAIN VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA IKITNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV PDMADDEHSAHTDRRYASLDDSVIPDAENLKVTILERALPFWEDKIAPALKDGNVVFVGA HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK									
SEQ ID NO. 4222: JM9130013 STRAIN VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA IKITNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV PDMADDEHSAHTDRRYASLDDSVIPDAENLKVTILERALPFWEDKIAPALKDGNVVFVGA HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK									
PRETTY of: /biotmp/msa70722.2{*} March 10, 2003 09:33 ..									
msa70722.2{110_090}	1	50							
msa70722.2{110_18RS21}	vk1VFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD								
msa70722.2{110_2603}	vk1VFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD								
msa70722.2{110_A909}	vk1VFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD								
msa70722.2{110_CJB110}	vk1VFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD								
msa70722.2{110_COH1}	vk1VFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD								
msa70722.2{110_H36B}	vk1VFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD								
msa70722.2{110_JM9130013}	vk1VFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD								
msa70722.2{110_M732}	vk1VFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD								
msa70722.2{110_M781}	vk1VFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD								
msa70722.2{110_1169NT}	---VFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD								
Consensus	-----*****								
msa70722.2{110_090}	51	100							
msa70722.2{110_18RS21}	LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE								
msa70722.2{110_2603}	LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE								
msa70722.2{110_A909}	LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE								
msa70722.2{110_CJB110}	LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE								
msa70722.2{110_COH1}	LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE								
msa70722.2{110_H36B}	LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE								
msa70722.2{110_JM9130013}	LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE								
msa70722.2{110_M732}	LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE								
msa70722.2{110_M781}	LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE								
msa70722.2{110_1169NT}	LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE								
Consensus	*****								
msa70722.2{110_090}	101	150							
msa70722.2{110_18RS21}	AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN								
msa70722.2{110_2603}	AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN								
msa70722.2{110_A909}	AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN								
msa70722.2{110_CJB110}	AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN								
msa70722.2{110_COH1}	AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN								
msa70722.2{110_H36B}	AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN								
msa70722.2{110_JM9130013}	AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN								
msa70722.2{110_M732}	AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN								
msa70722.2{110_M781}	AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN								
msa70722.2{110_1169NT}	AEQFGDEQVH IWRRSYDVLV PDMADDEHS AHTDRRYASL DDSVIPDAEN								
Consensus	*****								
msa70722.2{110_090}	151	200							
msa70722.2{110_18RS21}	LKVTILERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI								
msa70722.2{110_2603}	LKVTILERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI								
msa70722.2{110_A909}	LKVTILERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI								
msa70722.2{110_CJB110}	LKVTILERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI								
msa70722.2{110_COH1}	LKVTILERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI								
msa70722.2{110_H36B}	LKVTILERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI								
msa70722.2{110_JM9130013}	LKVTILERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI								
msa70722.2{110_M732}	LKVTILERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI								

Table 42: Comparative Sequences relating to SAG 0764

msa70722.2{110_M781}	LKVTLERALP	FWEDKIAPAL	KDGKNVFGA	HGNSIRALVK	HIKQLSDDEI
msa70722.2{110_1169NT}	LKVTLERALP	FWEDKIAPAL	KDGKNVFGA	HGNSIRALVK	HIKQLSDDEI
Consensus	*****	*****	*****	*****	*****
	201		229		
msa70722.2{110_090}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_18RS21}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_2603}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_A909}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_CJB110}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_COH1}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_H36B}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_JM9130013}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_M732}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_M781}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_1169NT}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
Consensus	*****	*****	*****		

Table 43: Comparative Sequences relating to SAG0079

## SEQ ID NO. 4301: 2603 V/R STRAIN

ATGAATCTTTTAATTATGGGTTTGCCCTGGTGTGCTGGTAAAGGTACTCAAGCAGCTAAGATC  
 GTTGAAGAATTTGGTGTGCTCAGATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCT  
 AATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCT  
 GATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAA  
 GGTTTTTTACTTTGATGGATATCCACGTACTATTGAACAAGCACACGCCCTTAGATGCTACG  
 CTTGAAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGT  
 CTTATAGAGCGTTTGGTGTGCTATATCAATCGTAAAACTGGTGAACTTTCCACAAA  
 GTGTTCAACCCACAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAG  
 CCTGAACTGTCAACCGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAA  
 CACTATCGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTT  
 TTTGCAGATGTTGAAAAAGCGTTGCTAGAACTCAA

## SEQ ID NO. 4302: 090 STRAIN (reverse complement)

AATCTTTTAATTATGGGTTTGCCCTGGTGTGCTGGTAAAGGTACTCA  
 AGCAGCTAAGATCGTTGAAGAATTTGGTGTGCTCAGATCTCAACAGGGGATATGTTCCG  
 CGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGG  
 TGAATTTGGTTCCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGA  
 TATCGCAGAAAAAGGTTTCTTACTTTGATGGATATCCACGTACTATTGAACAAGCACACGC  
 CTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGT  
 GGATCCATCATGTCTTATAGAGCGTTTGGTGTGCTATTATCAATCGTAAAACTGGTGA  
 AACTTTCCACAAAGTGTTCACCCACAGTAGATTATAAAGAAGAAGATTACTATCAACG  
 TGAAGATGATAAGCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGA  
 ACCATTTCTTGAACTACTATCGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGA  
 AATAACAGAAGTTTTTGCAGATGTTGAAAAAGCGTTG

## SEQ ID NO. 4303: 1169NT STRAIN (REVERSE COMPLEMENT)

TGGTAAAGGGACTCAAGCAGCTAAGATTGTTGAAGAATTTGGTGTGCGCACATCTCAAC  
 AGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAG  
 TTATATTGATAAAGGTGAATTGGTTCCTGATCAAGTAACAAACGGGATTGTAAAAGAGCG  
 CTTAGCTGAGGATGATATCGCAGAAAAAGGTTTTTACTTTGATGGGTATCCACGTACTAT  
 TGAACAAGCACACGCGCTTAGATGCTACGCTTGAAGAAGTACGCTTAGATGGTGT  
 TATTAAATATTAAAGTGGATCCATCATGTCTTATAGAGCGTTTGGTGGTGTATTATCAA  
 TCGTAAACTGGTGAAGCTTTCCACAAAGTGTCAAACCCACAGTAGATTATAAAGAAGA  
 AGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTGCTTGGACGTTCA  
 TATTGCTCAAGGAGAACCTATTCTTGAACTACTATAGTAAGCTTGGCTTGTACAGATAT  
 TGAAGGTAATCAAGAAATAA

## SEQ ID NO. 4304: 18RS21 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAACACCGGGTTTCGCTGGTGTGCTGGTAAAGGTACTCAAGCAGCTAAGATCG  
 TTGAAGAATTTGGTGTGCTCAGATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTA  
 ATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTG  
 ATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAG  
 GTTTTTTACTTTGATGGATATCCACGTACTATTGAACAAGCACACGCTTAGATGCTACGC  
 TTGAAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGTG  
 TTTATAGAGCGTTTGGTGTGCTATTATCAATCGTAAAACTGGTGAAGCTTTCCACAAAG  
 TGTTCACCCACAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGC  
 CTGAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAAC  
 ACTATCGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTT  
 TTTGCAGATGTTGAAAAAGCGTTG

## SEQ ID NO. 4305: A909 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAATTATGGGTTTGCCCTGGTGTGCTGGTAAAGGTACTCAAGCAG  
 CTAAGATCGTTGAAGAATTTGGTGTGCTCAGATCTCAACAGGGGATATGTTCCGCGCCG  
 CAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAAT  
 TGGTTCCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCG  
 CAGAAAAAGGTTTTTACTTTGATGGATATCCACGTACTATTGAACAAGCACACGCTTAG  
 ATGCTACGCTTGAAGAAGTACGCTTAGATGGTGTATTAAATATTAAAGTGGATC  
 CATCATGTCTTATAGAGCGTTTGGTGTGCTATTATCAATCGTAAAACTGGTGAAGCTT  
 TCCACAAAGTGTTCACCCACAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAG  
 ATGATAAGCCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGAACCTA  
 TCTTGAACACTATCGAAAGCTTGGTCTTGTACAGATATTGAAGGTAA

## SEQ ID NO. 4306: CJB110 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAACCAACGGGTTTGCTTGGTGTGCTGGTAAAGGTACTCAAGCAGCTAA  
 GATCGTTGAAGAATTTGGTGTGCTCAGATCTCAACAGGGGATATGTTCCGCGCCGCAAT  
 GGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGT  
 TCCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGA  
 AAAAGGTTTTTACTTTGATGGATATCCACGTACTATTGAACAAGCACACGCTTAGATGC  
 TACGCTTGAAGAAGTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATC  
 ATGCTTATAGAGCGTTTGGTGTGCTATTATCAATCGTAAAACTGGTGAAGCTTTCCA  
 CAAAGTGTTCACCCACAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGA  
 TAAGCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCT  
 TGAACACTATAG

## SEQ ID NO. 4307: COH1 STRAIN (REVERSE COMPLEMENT)

ATCTTTTAATTATGGGTTTGCCCTGGTGTGCTGGTAAAGGTACTCAAGCAGCTAAGATGTTG  
 AAGAATTTGGTGTGCTCAGATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAATC  
 AAACCAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGATG  
 AAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGTT  
 TTTTACTTTGATGGATATCCACGTACTATTGAGCAAGCACACGCTTAGATGCTACGCTTG  
 AAGAAGTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCACATGCTTTA  
 TAGAGCGTTTGGTGGCCGTATTATCAATCGTAAAACTGGTGAAGCTTTCCACAAAGTGT

Table 43: Comparative Sequences relating to SAG0079

TCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTG  
AAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCTATCTTTGAACACT  
ATCGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTTG  
CAGATGTTGAAAAAGCGTTG

SEQ ID NO. 4308: H36B STRAIN (REVERSE COMPLEMENT)

CAGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAA  
GTTATATTGATAAAGGTGAATGGTTCCTGATGAAGTAACAAACGGGATTTGTAAGAGAGC  
GCTTAGCTGAGGATGATATCGCAGAAAAAGGTTTTTACTTGTGATGATATCCACGTACTA  
TTGAACAAGCACACGCCCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTG  
TTATTAATATTAAAGTGGATCCATCATGTCTTATAGAGCGTTTGGTGGTTCGATTATCA  
ATCGTAAAACTCGGAGAAAACTTTCCACAAAGTGTCAACCCACAGTAGATTATAAAGAAG  
AAGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTGCGTTGGAGCTTA  
ATATTGCTCAAGGAGAATCTATTCTTGAACACTATCGTAAGCTTGGTCTTGTACAGATA  
TTAAGGTAATCAAGAAATAACAGAAGTTTTTGCAGATGTTGAAAAAGCGTTG

SEQ ID NO. 4309: JM9130013 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAATTATGGGTTTGCCTGGTGTGCTGTTAAAGGT  
ACTCAAGCAGCTAAGATCGTTGAAGAATTTGGTGTGCTCACATCTCAACAGGGGATATG  
TTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAAGTTATATTGAT  
AAAGGTGAATTTGGTTCCTGATGAAGTAACAAACGGGATTTGTAAGAGAGCGCTTAGCTGAG  
GATGATATCGCAGAAAAAGGTTTTTACTTGTGATGATATCCACGTACTATTGAACAAGCA  
CACGCCCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTATTAATATT  
AAAGTGGATCCATCATGTCTTATAGAGCGTTTGGTGGTTCGATTATCAATCGTAAAACT  
GGTGAACCTTTCCACAAAGTGTTCACCCACAGTAGATTATAAAGAAGAAGATTACTAT  
CAACGTGAAGATGATAAGCCTGAAACTGTAAACGTGCGTTGGAGCTTAATATTGCTCAA  
GGAGAACCTATTCTTGAACACTATAAAAAAGCTTGGTCTTGTACAGATATTGAAGGTAAT  
CA

SEQ ID NO. 4310: M732 STRAIN (REVERSE COMPLEMENT)

CTTTAATTATGGGTTTGCCTGGTGTGCTGTTAAAGGTACTCAAGCAGCTAAGATTTGTGAA  
GAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAATCAA  
ACCCAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTTGGTTCCTGATGAA  
GTAACAAACGGGATTTGTAAGAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGTTTT  
TTACTTGTATGGATATCCACGTACTATTGAGCAAGCACACGCCCTTAGATGCTACGCTTGAA  
GAACTAGGACTACGCTTAGATGGTGTATTATTAATTTAAAGTGGATCCAACATGCCCTTATA  
GAGCGTTTGAAGTGGCGCTTATTATCAATCGTAAACTGGTGAACCTTTCCACAAAGTGTTC  
AACCCACAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTGAA  
ACTGTCAAACGTGCGTTGGAGCTTAATATTGCTCAAGGAGAACCTATTCTTGAACACTAT  
CGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTGCA  
GATGTTGAAAAAGCGTTG

SEQ ID NO. 4311: M781 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAATTACGGGTTTGCCTGGTGTGCTGTTAAAGGTACTCAA  
GCAGCTAAGATTGTTGAAGAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCG  
GCCGCAATGGCTAATCAAACCCAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGT  
GAATTTGGTTCCTGATGAAGTAACAAACGGGATTTGTAAGAGAGCGCTTAGCTGAGGATGAT  
ATCGCAGAAAAAGGTTTTTACTTGTATGGATATCCACGTACTATTGAGCAAGCACACGCC  
TTAGATGCTACGCTTGAAGAAGTAGGACTACGCTTAGATGGTGTATTATTAATTTAAAGT  
GATCCACATGCCCTTATAGAGCGTTTGGTGGCGGCTATTATCAATCGTAAAACTGGTGAA  
ACTTTCCACAAAGTGTTCACCCACAGTAGATTATAAAGAAGAAGATTACTATCAACGT  
GAAGATGATAAGCCTGAAACTGTCAAACGTGCGTTGGAGCTTAATATTGCTCAA

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa25038.2{\*} April 17, 2002 08:53 ..  
PRETTY of: /biotmp/msa252229.2{\*} January 31, 2003 03:05 ..

	1		50
msa252229.2{114_COH1}	----atcttt taattatggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_M732}	-----cttt taattatggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_M781}	---Aatcttt taattacggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_A909}	---Aatcttt taattatggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_JM9130013}	---Aatcttt taattatggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_CJB110}	---Aatcttt taaccacggg tttgcttggg gctggtaaag gtactcaagc		
msa252229.2{114_090}	---Aatcttt taattatggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_2603}	atgAatcttt taattatggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_H36B}	-----		
msa252229.2{114_18RS21}	---Aatcttt taaccacggg ttcgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_1169NT}	-----		
Consensus	*****		
	51		100
msa252229.2{114_COH1}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_M732}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_M781}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_A909}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_JM9130013}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_CJB110}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_090}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_2603}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_H36B}	-----		
msa252229.2{114_18RS21}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_1169NT}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		

Table 43: Comparative Sequences relating to SAG0079

Consensus	-----	-----	-----	-----	-----	*****
	101					150
msa252229.2{114_COH1}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_M732}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_M781}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_A909}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_JM9130013}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_CJB110}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_090}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_2603}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_H36B}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_18RS21}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_1169NT}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
Consensus	*****	*****	*****	*****	*****	*****
	151					200
msa252229.2{114_COH1}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_M732}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_M781}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_A909}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_JM9130013}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_CJB110}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_090}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_2603}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_H36B}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_18RS21}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_1169NT}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
Consensus	*****	*****	*****	*****	*****	*****
	201					250
msa252229.2{114_COH1}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_M732}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_M781}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_A909}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_JM9130013}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_CJB110}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_090}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_2603}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_H36B}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_18RS21}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
msa252229.2{114_1169NT}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTTTTAC	
Consensus	*****	*****	*****	*****	*****	*****
	251					300
msa252229.2{114_COH1}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_M732}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_M781}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_A909}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_JM9130013}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_CJB110}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_090}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_2603}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_H36B}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_18RS21}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_1169NT}	TTGATGGgTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
Consensus	*****	*****	*****	*****	*****	*****
	301					350
msa252229.2{114_COH1}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_M732}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_M781}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_A909}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_JM9130013}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_CJB110}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_090}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_2603}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_H36B}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_18RS21}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_1169NT}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
Consensus	*****	*****	*****	*****	*****	*****
	351					400
msa252229.2{114_COH1}	TCCAaCATGc	CTTATAGAGC	GTTTGAGTGg	cCGTATTATC	AATCGTAAAA	
msa252229.2{114_M732}	TCCAaCATGc	CTTATAGAGC	GTTTGAGTGg	cCGTATTATC	AATCGTAAAA	
msa252229.2{114_M781}	TCCAaCATGc	CTTATAGAGC	GTTTGAGTGg	cCGTATTATC	AATCGTAAAA	
msa252229.2{114_A909}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	
msa252229.2{114_JM9130013}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	
msa252229.2{114_CJB110}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	
msa252229.2{114_090}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	
msa252229.2{114_2603}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGk	tCGTATTATC	AATCGTAAAA	
msa252229.2{114_H36B}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	
msa252229.2{114_18RS21}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	

Table 43: Comparative Sequences relating to SAG0079

msa252229.2{114_1169NT}	TCCATCATGt	CTTATAGAGC	GTTTGAGTg	tCGTATTATC	AATCGTAAAA
Consensus	****-****	*****	*****	-*****	*****
	401				450
msa252229.2{114_COH1}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_M732}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_M781}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_A909}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_JM9130013}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_CJB110}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_090}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_2603}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_H36B}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_18RS21}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_1169NT}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
Consensus	*****	*****	*****	*****	*****
	451				500
msa252229.2{114_COH1}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_M732}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_M781}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_A909}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_JM9130013}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_CJB110}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_090}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_2603}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_H36B}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_18RS21}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_1169NT}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
Consensus	*****	*****	*****	*****	*-*****
	501				550
msa252229.2{114_COH1}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_M732}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_M781}	CTTGGACGTT	aATATTGCTC	AA-----	-----	-----
msa252229.2{114_A909}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgaa
msa252229.2{114_JM9130013}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactataaaa
msa252229.2{114_CJB110}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatag--
msa252229.2{114_090}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_2603}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_H36B}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_18RS21}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_1169NT}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatagta
Consensus	*****	*****	*****	-----	-----
	551				600
msa252229.2{114_COH1}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_M732}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_M781}	-----	-----	-----	-----	-----
msa252229.2{114_A909}	agcttggtct	tggtacagat	attgaaggta	a-----	-----
msa252229.2{114_JM9130013}	agcttggtct	tggtacagat	attgaaggta	atca-----	-----
msa252229.2{114_CJB110}	-----	-----	-----	-----	-----
msa252229.2{114_090}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_2603}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_H36B}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_18RS21}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_1169NT}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aa-----
Consensus	-----	-----	-----	-----	-----
	601				636
msa252229.2{114_COH1}	tttgccagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_M732}	tttgccagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_M781}	-----	-----	-----	-----	-----
msa252229.2{114_A909}	-----	-----	-----	-----	-----
msa252229.2{114_JM9130013}	-----	-----	-----	-----	-----
msa252229.2{114_CJB110}	-----	-----	-----	-----	-----
msa252229.2{114_090}	tttgccagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_2603}	tttgccagatg	ttgaaaaagc	gttgctagaa	ctcaaa	-----
msa252229.2{114_H36B}	tttgccagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_18RS21}	tttgccagatg	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_1169NT}	tttgccagatg	ttgaaaaagc	gttg-----	-----	-----
Consensus	-----	-----	-----	*****	*****
SEQ ID NO. 4312: 2603 V/R STRAIN					
MNLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRILAKSYIDKGELVP					
DEVINGIVKERLAEDDIAEKGFLLDGYPTIEQAHALDLEELGLRLDGVINIKVDPSC					
LIERLSKRIINRKTGETFHKVFNPFPVYKEDDYQREDDKPETVKRRLDVNIAQGEPILE					
HYRKLGLVTDIEGNQETIEVFADVEKALLELK					
SEQ ID NO. 4313: 090 STRAIN					
NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRILAKSYIDKGELVP					
EVINGIVKERLAEDDIAEKGFLLDGYPTIEQAHALDLEELGLRLDGVINIKVDPSC					
LIERLSGRIINRKTGETFHKVFNPFPVYKEDDYQREDDKPETVKRRLDVNIAQGEPILE					

Table 43: Comparative Sequences relating to SAG0079

YRKLGLVTDIEGNQEITEVFADVEKALLELK

SEQ ID NO. 4314: 1169NT STRAIN

GKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRKLSYIDKGELVPDQVTNGIVKER  
LAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPSCLIERLSGRI IN  
RKTGETFHKVFNPVDYKEEDYYQREDDKPKETVKRRLDVHIAQGEPILEHYSKLGVLTDI  
EGNQEI

SEQ ID NO. 4315: 18RS21 STRAIN

NLLITGSPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRKLSYIDKGELVPD  
EVTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPSCLI  
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPKETVKRRLDVHIAQGEPILEH  
YRKLGLVTDIEGNQEITEVFADVEKALLE

SEQ ID NO. 4316: A909 STRAIN

NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRKLSYIDKGELVPD  
EVTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPSCLI  
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPKETVKRRLDVHIAQGESILEH  
YRKLGLVTDIEG

SEQ ID NO. 4317: A909 STRAIN

NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRKLSYIDKGELVPD  
EVTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPSCLI  
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPKETVKRRLDVHIAQGESILEH  
YRKLGLVTDIEG

SEQ ID NO. 4318: CJB110 STRAIN

NLLITGGLGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRKLSYIDKGELVPD  
EVTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPSCLI  
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPKETVKRRLDVHIAQGEPILEH  
Y

SEQ ID NO. 4319: COH1 STRAIN

LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRKLSYIDKGELVPDE  
VTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPTCLI  
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPKETVKRRLDVHIAQGEPILEH  
RKLGLVTDIEGNQEITEVFADVEKALL

SEQ ID NO. 4320: H36B STRAIN

GDMFRAAMANQTEMGRKLSYIDKGELVPDEVNTNGIVKERLAEDDIAEKGFLLDGYPRITIE  
QAHALDATLEELGLRLDGVINIKVDPSCLIERLSGRI INRKTGETFHKVFNPVDYKEE  
DYQREDDKPKETVKRRLDVHIAQGESILEHYRKLGLVTDIEGNQEITEVFADVEKAL

SEQ ID NO. 4321: JM9130013 STRAIN

NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRKLSYIDKGELVPD  
EVTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPSCLI  
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPKETVKRRLDVHIAQGEPILEH  
YKLGVLTDIEGN

SEQ ID NO. 4322: M732 STRAIN

LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRKLSYIDKGELVPDE  
VTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPTCLI  
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPKETVKRRLDVHIAQGEPILEH  
RKLGLVTDIEGNQEITEVFADVEKALLELK

SEQ ID NO. 4323: M781 STRAIN

NLLITGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRKLSYIDKGELVPD  
EVTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPTCL  
IERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPKETVKRRLDVHIAQ

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa32357.2{\*} April 17, 2002 09:17 ..

	1				50
msa252352.2{114_18RS21}	~nllttgspg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGRlak
msa252352.2{114_M781}	~nllitglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTqMGRlak
msa252352.2{114_CJB110}	~nllttgllg	agkgtqaaki	veefgvahis	tGDMFRAAMA	tGDMFRAAMA
msa252352.2{114_090}	~nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGRlak
msa252352.2{114_JM9130013}	~nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	tGDMFRAAMA
msa252352.2{114_A909}	~nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGRlak
msa252352.2{114_1169NT}	~nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGRlak
msa252352.2{114_2603}	~nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGRlak
msa252352.2{114_COH1}	~nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTqMGRlak
msa252352.2{114_M732}	~nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGRlak
msa252352.2{114_H36B}	~nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGRlak
Consensus	*****	*****	*****	*****	*****
	51				100
msa252352.2{114_18RS21}	SYIDKGELVP	DeVINGIVKE	RLAEDDIAEK	GFLLDGYPRT	IEQAHALDAT
msa252352.2{114_M781}	SYIDKGELVP	DeVINGIVKE	RLAEDDIAEK	GFLLDGYPRT	IEQAHALDAT
msa252352.2{114_CJB110}	SYIDKGELVP	DeVINGIVKE	RLAEDDIAEK	GFLLDGYPRT	IEQAHALDAT



Table 43: Comparative Sequences relating to SAG0079

msa252352.2{114_090}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_JM9130013}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_A909}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_1169NT}	SYIDKGELVP	DqVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_2603}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_COH1}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_M732}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_H36B}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
Consensus	*****	*-*****	*****	*****	*****
101					
msa252352.2{114_18RS21}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_M781}	LEELGLRLDG	VINIKVDPtC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_CJB110}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_090}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_JM9130013}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_A909}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_1169NT}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_2603}	LEELGLRLDG	VINIKVDPsC	LIERLSxRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_COH1}	LEELGLRLDG	VINIKVDPtC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_M732}	LEELGLRLDG	VINIKVDPtC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_H36B}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
Consensus	*****	*****	*****	*****	*****
151					
msa252352.2{114_18RS21}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_M781}	EDYYQREDDK	PETVKRRLDV	nIAQ-----	-----	-----
msa252352.2{114_CJB110}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hy-----	-----
msa252352.2{114_090}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_JM9130013}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hykklglvtd	iegn-----
msa252352.2{114_A909}	EDYYQREDDK	PETVKRRLDV	nIAQgesile	hyrklglvtd	ieg-----
msa252352.2{114_1169NT}	EDYYQREDDK	PETVKRRLDV	hIAQgepile	hysklglvtd	iegnqe---
msa252352.2{114_2603}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_COH1}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_M732}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_H36B}	EDYYQREDDK	PETVKRRLDV	nIAQgesile	hyrklglvtd	iegnqeitev
Consensus	*****	*****	-----	-----	-----
201					
msa252352.2{114_18RS21}	fadvekalle	--			
msa252352.2{114_M781}	-----	--			
msa252352.2{114_CJB110}	-----	--			
msa252352.2{114_090}	fadvekalle	LK			
msa252352.2{114_JM9130013}	-----	--			
msa252352.2{114_A909}	-----	--			
msa252352.2{114_1169NT}	-----	--			
msa252352.2{114_2603}	fadvekalle	LK			
msa252352.2{114_COH1}	fadvekal--	--			
msa252352.2{114_M732}	fadvekalle	LK			
msa252352.2{114_H36B}	fadvekal--	--			
Consensus	-----	**			
212					

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

SEQ ID NO. 4401  
**STRAIN 2603**  
 GTGGATAAACATCACTCAAAAAAGGCTATTTTAAAGTTAACA  
 CTTATAACAACCTAGTATTTTATTAATGTCATAGCAATCAAGTGAATGCAGAGGAGCAAGAA  
 TTAATAAACCAAGAGCAATCACCTGTAATTGCTAATGTTGCTCAACAGCCATCGCCATCG  
 GTAACCTACTAATCTGTTGAAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGCG  
 AAAGAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATATTAGAAAGAG  
 TTATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTGAAGAAAGATATCCCTCT  
 AAACCAGAGACAACCAACAATAAAGAAAGCAATGTAGTAACAAATGCTTCACTGCAATA  
 GCACAGAAAGTTCCTCAGCATATGAAGAGGTGAAGCCAGAAAGCAAGTCATCGCTTGCT  
 GTTCTTGATACATCTAAAAATAACAAATTAACAAGCCATAACCAAGAGGAAAGGGAAAT  
 GTAGTAGCTATTATGATACCTGGCTTTGATATTAACCATGATATTTTCGTTTAGATAGC  
 CCAAAAGATGATAAGCACAGCTTTAAAACTAAGACAGAAATTTGAGGAATTAAGCAAAAA  
 CATAATATCACTTATGGGAAATGGGTAAACGATAAGATTGTTTTGACATAACTACGCC  
 AACAAATACAGAAACGGTGGCTGATATTGCAGCAGCTATGAAGATGGTTATGGTTAGAA  
 GCAAGAAATATTTCCCATGGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAACAGT  
 CCAGCAATCAATGGTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTTATTAAATG  
 CGTATTCAGATGATAAATGATTGCGACAAATTTGGTGAAGCATATGCTAAAGCAATCACA  
 GACGCTGTTAATCTAGGAGCAAAAAAGCATTAATATGAGTATTTGAAAAACAGCTGATCT  
 TTAATGCTCTCAATGATAAAGTTAAATTAGCACTTAAATTAGCTTCTGAGAAAGGCGTT  
 GCAGTTGTTGGCTGCCGAAATGAAGCGCATTTGGTATGGATTATAGCAAAACATT  
 TCAACTAATCCTGACTACGGTAAATAGTCCAGCTATTTCTGAAGATACCTTTGAGT  
 GTTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTGCTGAACAACTATTGAAGGT  
 AAGTTAGTTAAGTTGCCGATTTGTGACTTCTAAACCTTTTGACAAAGGTAAAGGCTACGAT  
 TGGTTTATGCCAATTTATGGTGCAAAAAAGACTTTGAAGGTAAGGACTTTAAAGGTAAG  
 ATTGCATTAATGAGCGTGGTGGGACTTGATTTATGACTAAATCACTCATGTCTACA  
 AATGCAGGTGTTGTTGATCGTTATTTTAAACGATCAAGAAAAACGTTGAAATTTTCTA  
 ATTCTTACCGTGAATCACCTGTTGGGATTTATAGTAAAGTAGATGGCGAGCGTATAAAA  
 AATACTTCAAGTCAGTTAAACATTTAACCAGAGTTTGAAGTAGTTGATAGCCAAAGTGGT  
 AATCGTATGCTGGAACAAATCAAGTTGGGGCGTGACAGCTGAAGGAGCAATCAAGCTGAT  
 GTAACAGCTTCTGGCTTTGAAATTTATCTTCAACCTATAATAATCAATACCAAAACATG  
 TCTGGTACAAGTATGGCTTACCACATGTTGCAGGATTAATGACAATGCTTCAAAGTCAT  
 TTGGCTGAGAAATATAAGGGATGAATTTAGATTCTAAAAAATGCTAGAAATGTCTAAA  
 AACATCCTCATGAGCTCAGCAACAGCATTTATAGTGAAGAGGATAAGGCGTTTATTCA  
 CCACGTCAGCAAGGTGCAGGTGATGTTGATGCTGAAAAAGCTATCAAGCTCAATATTAT  
 ATTACTGGAACCATGGCAAGCTAAAAATTAATCTCAACCAAGTGGGAGATAAATTTGAT  
 ATCAGATTACAATTATAAACTTTGTAAGAGGTGTCAAAGAAATGTATTTATCAAGCTAAT  
 GTAGCAACAGAAACAGTAAATAAAGGTAAATTTGCCCTTAAACCAAGCCCTTGCTAGAT  
 ACTAATTGGCAGAAAGTAATCTTCTGTGATAAAGAAACACAAGTTTCGATTTACTATTGAT  
 GCTAGTCAATTTAGTCAAGAAATTAAGAAACAGATGGCAATGGTTATTTCTAGAAGGT  
 TTTGTACGTTTAAAGAGGCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGT  
 GAAAGAGATGCAGGCAATTAATCCATATTTGCCATTTCTCCAAATAAAGATGGAATAGG  
 GACGAAATCACTCCCGAGGCACTTTCTTAAGAAATGTTAAGGATATTTCTGCTCAAGTT  
 CTAGATCAAAATGGAATGTTATTTGGCAAGTAAGGTTTACCCTCTTATCGTAAAAAT  
 TTCCATTAATTAATCCAAAGCAAGTGTGCTCATTATCGTATGATGCTCTTCAGTGGAGT  
 GGTTTAGATAAGGATGGCAAGTTGTAGCAGATGGTTTATATCTTATCGCTTACGTTTAC  
 ACACAGTAGCAGGAAGGAGCAATAGTCAGGAGTCAGACTTTAAAGTACAAGTAAGTACT  
 AAGTCACCAATCTTCTTACAGAGCTCAGTTTGTATGAACTAATCGAACATTAAAGCTTA  
 GCCATGCTAAGCAAGTAGTTATGTTTCTACATATCGTTTACAAATAGTTTATCTCAT  
 GTTGTAAAAGATGAAGAAATATGGGATGAGACTTCTTACCATTATTTCCATATAGATCAA  
 GAAGTTAAGTGAACCTTCTTAAACCGTTAAGATAGGAGAGAGTGAAGTTGCGGTAGAC  
 CCTAAGGCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTGCAACCGTAAATTTG  
 TCTGATCTCTTGAATAGGCAAGTAGTATCAGAGAAAGAAACGCTATAGTAATTTCTAAC  
 AGTTTCAAAATATTTGATACTTGAAGAAAGAACCTATGTTTATTTCTAAAAAGAAAAA  
 GTAGTAAACAGAAATCTAGAAGAAATTAATATTAGTTAAGCCGCAAACTACAGTTACTACT  
 CAATCATTTGTCTAAAGAAATAACTAAATCAGGAAATGAGAAAGTCTCACTTCTACAAAC  
 AATAATAGTAGCAGAGTAGCTAAGATCATATCACTAAACATAACGGGGATTTCTGTTAAC  
 CATACCTTACCTAGTACATCAGATAGAGCAACGAATGGTCTATTTGTTGGTACTTTGGCA  
 TTGTTATCTAGTTTACTTCTTTATTTGAAACCCAAAGACTAAAAATAATAGTAAA

SEQ ID NO. 4402  
**STRAIN 090**  
 GAGGAGCAAGAAATTAATAAACCAAGAGCAATCACCTGTAATTGCT  
 AATGTTGCTCAACAGCCATCGCCATCGGTAACCTACTAATATGTTGAAAA  
 AACATCTGTAACAGCTGCTTCTGCTAGTAATACAGTGAAGAAATGGGTG  
 ATACATCTGTAATAAATGACAAAAACAGAAGATGAATATTAGAAAGATT  
 TCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTTGAAGAAATA  
 TCCCTCTAAACAGAGACAACCAACAATAAAGAAAGCAATGTAGTAACAA  
 ATGCTTCAACTGCAATAGCACAGAAAGTTCCTCAGCGTATGAAGAGGT  
 AAGCCAGAAAGCAAGTCATCGCTTGCTGTTTGTATACATCTAAATAAC  
 AAAATTGCAAGCCATAACCCAAAGAGGAAAGGGAATGTAGTAGCTATTA  
 TTGATACTGGCTTTGATATTAACCATGATATTTTCGTTTAGATAGCCCA  
 AAAGATGATAAGCACAGCTTTAAACTAAAGCAGAAATCGAGGAATTA  
 AGCAAAACATAATACCTTATGGGAAATGGGTAAACGATAAGATTGTTT  
 TTGCACATAACTACGCCAACATAACAGAAACGGTGGCTGATATTGCAGAC  
 GCTATGAAAGATGGTTATGGGTGAGAGCAAGAAATATTTCCCATGGTAC  
 ACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGCTCCAGCAATCAATG  
 GTCTTCTTTAGAAAGGTGCAGCGCCAAATGCTCAAGTCTTATTAAATGCGT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

ATTCCAGATAAAATTGATTTCGGACAAATTTGGAGAAGCATATGCTAAAGC  
 AATCAGACAGCGCTGtTAATCTAGGAGCAAAaCGATTAAATATGAGCCITG  
 GAAAAACAGCAGATTCTTTAAAttGCaCTCAATGATAAAGTTAAATTAGCA  
 CTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGGCTGCCGGA  
 TGAAGGTGCAATTGGTATGGATTATAGCAAACCATATCAACTAAATcCTG  
 ACTACGGTACGGTTAAATAGTCCAGCTATTTCTGAAGATACTtTGAGTGT  
 GCTAGCTATGAATCACTTAAACCTATCAGTGAGGTCGTTGAAACAACAT  
 TGaaGGTAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAACCTTTtGACA  
 AAGGTAAGGCCCTACGATGTGGTTTATGCCAATTATGGTGCAaaaaAAGAC  
 TTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAAAtGAGCGTGGtGG  
 TGGACTTGATTTTATGACTAAaatCACTcATGCTACAAATGCAGGTGTTG  
 tTGGTATCGTtATTTtTAACgATCAAGAAaAACGtGGAATTTTtTAATT  
 CCTTACCCTGAATTACCTGTGGGGTTATTAGTAAAGTAGATGGCGAGCG  
 TATAAAAAATACTTCAAGTCAGTTAACATTTAACAGAGTTTtGAAGTAG  
 TTGATAGCCAAAGTTGGCAATCGTATGCTGGAAACAAATCAAGTTGGGGCGTG  
 ACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTTTGAAAT  
 TTATTCTTCAACCTATAATAATCAATACCAACCAATGTCTGGTACAAGTA  
 TGGCTTCACCACATGTTGCAGGATTAAAGACAATGCTTCAAAGTCATTG  
 GCTGAGAAATATAAAGGGATGAATTTAgATTCTTAAAAATTTGCTAGAATT  
 GTCTAAaACATCCTCATGAGCTCAGCAaCAGCATTATATAGTgAAGAgG  
 ATAAAGCGTtTtATTcACCAAGTCAGCAAGGtGCAGGtGTAGTTGATGCT  
 GAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAAACGATGGCAAGC  
 TAAAAATTAACTCTCAAAACGAGTGGGAGATAAAATTTGATATCACAGTTACA  
 TTTCAAACTTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCTAATGTA  
 GCAACAGAAcAAGTAATAAAGGTAATTTGCCCTTAAACCAACAGCctT  
 GCTAGATACTAATTGGCAGAAAGTAATTCTTcGTGATAAAGAAACACAAG  
 TTcGATTTACTATTGATGCTAGTCAATTTAGTCAGAAATTTAAAGAACAG  
 ATGGCAAAATGGTTATTCTTAgAAGGTTTGTACGTTTAAAGAAAGCCAA  
 GGATAGTAATCAGGAGTTAaTGAGTATTCCTTtTGTAAGATtTAATGGTG  
 ATTTTGGCAACTTACAAGCACTTGAAACACCGATTATAAGACGCTTTCT  
 AAAGGTAGTTTCTACTATAAACCAAAATGATACAACTCATAAAGCCAATT  
 GGAGTACAATGAATCAGCTCCTTTTGAAGCAACAACCTATAGTGCCTTGT  
 TAACCAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAATGGTGGG  
 GAGTTAGAATTAGCACCGGAGAGTcCAAAAGAATTTATTTAGGAACCTT  
 TGAGAATAAGGTTGAGGATAAAACAATTCACTCTTTTGGAAAGAGATGCA  
 GcAATAATCCATATTTCCTCAATTTCAAAATTAAGATGGAATAGGGAAT  
 GAATCACTCCCAGGCACTTCTTAAGAAATGTTAAGGATATTCTGTC  
 TCAAGTTCTAGATCAAAATGGAATGTTATTGGCAAGTAAGGTTTAC  
 CATCTTATCGTAAAAATTTCCATAAATCTCAAAGCAAGTGATGGTCAT  
 TATCGTATGGATGCCCTTTCAGTGGAGTGGTTAGATAAGGATGGCAAGT  
 TGTAAGCAGATGGTTTATATCTTATCGCCTACGTTACACACAGTAGCAG  
 AAGGAGCAAAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAAGTACTAAG  
 TCACCAATCTTCTTACTAGCTCAGTTTGATGAACTAATCGAACATT  
 AAGCTTAGCCATGCCCTAAGGAAAGTAGTTATGTTCTTACATATCGTTTAC  
 AATTAGTTTATCTCATGTTGTAAGAGATGAAGAATATGGGGATGAGACT  
 TCTTACCATTATTTCATATAGATCAAGAAAGTAAAGTGACACTTCCTAA  
 AACGGTTAAGATAGGAGAGAGTGGGTTGCAAGTAGACCTAAGGCTTGA  
 CACTTGTGTGGAAGATAAAGCTGGTAATTTTGAACGGTAAATTTGTCT  
 GACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAACGCTATAGTAAT  
 TTCTAACAGTTTCAAATATTTTGATACTTGAaaaaAGAACTATGTTTA  
 TTTCTAAAGAAAGAAAGTAGTAAACAGAATCTAGAAGAAATAACATTA  
 GTTAAGCCGCAAACTACAGTTACTACTCAATCATTTGCTAAAGAAATAAC  
 TAAATCAGGAAATGAGAAAGTCTCACTTCTACAAACAATAATAGTAGCA  
 GAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTAACCAT  
 ACC

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STRAIN A909

GAGGAGCAAGAATTAAAAAACCAAGAGCAAT  
 CACCTGTAATTGCTAAATGTTGCTCAACAGCCATCGCCATCGGTAACACT  
 AATACTGTTGAAAAACATCTGTAAACATCTGCTTCTGCTAGTAATACAGC  
 GAAAGAAATGGGTGATACATCTGTAAAAATGACAAAACAGAAGATGAAT  
 TATTAGAAGAGTTATCTAAAAACCTTGATACGCTCAATTTGGGGCTGAT  
 CTTGAAGAAGAAATATCCCTCTAAACAGAGACAACCAACAATAAAGAAAG  
 CAATGTAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCTCAG  
 CATATGAAGAGGTGAAGCCAGAAAGCAAGTCATCACTTGCTGTTCTTGAT  
 ACATCTAAATAACAAATTTGCAAGCCATAACCCAAAGAGGAAAGGGAAA  
 TGTAGTAGCTATTATTGATATCTGGCTTTGATATTAAACCATGATATTTTT  
 GTTTAGATAGCCCAAAAGATgaTAAGCACAGCTTTAAaACTAAGGCAGAA  
 TTTGAGGAATTAAAGCAAAACATAATATCACTTATGGGAATGGGTTAA  
 CGATAAGATTGt:TTTGCACATAACTACGCCaCAATACAGAAACGGTGG  
 CTGATATTGCAGCAGCTATGAAAGATGGTTATGGGTGAGAAGCAAGAAT  
 ATTTCCGATGGTACACAGCTTGCTGGTATTTTGTAGGTAATAGTAAAGC  
 TCCAGCAATCAATGGTCTTCTTTAGAAGGTGCAGCGCCAAATGCTCAAG  
 TCTTATTAAATGCGTATTCAGATAAAATTTGATTCGGACAAATTTGGTGAA  
 GCATATGCTAAAGCAATCACAGACGCTGTTAATCTAGGAGCAAAACGAT  
 TAATATGAGCCTTGGAAAAACAGCAGATTCTTTAATTGCTCTCAATGATA  
 AAGTTAAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTT  
 GTGGCTGCCGAAATGAAGGTGCATTGGTATGGATTATAGCAAAACCAT  
 ATCAACTAATCCTGACTACGGTACGGTTAAATAGTCCAGCTATTCTGAAG  
 ATACTTTGAGTGTGCTAGCTATGAATCACTTAAAACTATCAGTGAGGTC  
 GTTGAAACAATATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTC  
 TAAACCTTTTGACAAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATG

**Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)**

GTGCAAAAAAGACTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATT  
 AATTGAGCGTGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTA  
 CAAATGCGGTGTTGTTGGTATCGTTAATTTTAAACGATCAAGAAAAACGT  
 GGAATTTTCTAATTCCTTACCGTGAATACCTGTGGGGTTATAGTAA  
 AGTAGATGGCGAGCGTATAAAAAATACCTCAAGTCAGTTAACATTTAAC  
 AGAGTTTGAAGTAGTTGATAGCCAGGTGGCAATCGTATGCTGGAACAA  
 TCAAGTTGGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAAACAGC  
 TTCTGGCTTTGAAATTTATTTCTCAACCTATAATAATCAATACCAACAA  
 TGCTGGTACAGATATGGCTTACCACATGTGTCAGGATTAAATGACAAATG  
 CTTCAAGTCATTTGGCTGAGAAATATAAAGGATGAATTTAGATTCTAA  
 AAAATTGCTAGaATTGTCTAAAAACATcCTCATGAGCTCAGCAACAGCAT  
 TATATAGTGAAGAGGATAAGGCGTTTATTTACCACGTCAGCAAGGTGCA  
 GGTGTAGTTGATGCTGAAAAAGCTATCCAGCTCAATATTATGTTTACG  
 AAACGATGGCAAAGCTAAATTAATCTCAAACGAGTGGGAGATAAATTTG  
 ATATCACAGTTACAATTCATAAATTTAGAGGTTGTCAAAGAAATTTGAT  
 TATCAAGCTAATGTAGCAACAGAACTAAATAAAGGTAATTTGCCTT  
 TAAACCaCAAGCCTTGCTAGATACTAATTGGCAGAAAGTAATTTCTGCTG  
 ATAAAGAAACACAAGTTCCGATTACTATGATTCTAGTCAATTTAGTCAG  
 AAATTAAGAAACAGATGGCAATGTTATTTCTAGAAGGTTTGTACG  
 TTTTAAAGAAAGCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTG  
 TAGGATTTAATGGTATTTTGGCACTTACAAGCACTTGAACACCGATT  
 TATAAGACGCTTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAAC  
 TCATAAAGACCAATTTGAGTACAATGAATCAGCTCCTTTTGAAAGCAACA  
 ACTATACCTCTGTGTAACACAAATCAGCGTCTTGGGGCTATGTTGATTAT  
 GTCAAAAATGGTGGGAGTTAGAAATAGCACCGGAGAGTCCAAAAAGAAAT  
 TATTTTAGGAACCTTTGAGAATAAGGTTGAGGATAAAACAAATTCATCTTT  
 TGGAAGAGATGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAA  
 GATGAAATAGGAGTGAATCACTCCCCAGGCAACTTTCTAAGAAATGT  
 TAAGGATATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGC  
 AAAGTAAGGTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAG  
 CAAAGTGATGGTCATTCGTATGGATGCCCTTCAGTGGAGTGGTTAGA  
 TAAGGATGGCAAAGTTGTAGCAGATGGTTTATACCTATCGTTTACGTT  
 ACACACCGTAGCAGAGGAGCAATAGTCAGGAGTCAGACTTTAAAGTT  
 CAAGTAAGTACTAAGTCACCAAACTCTTCTTACGAGCTCAGTTTGTATGA  
 AACTAATCGAACATTAAGCTTAGCCATGCCCTAAGGAAAGTAGTTATGTTT  
 CTACATATCGCTACAAATAGTTTATCTCATGTTGTAAAAGATGAAGAA  
 TATGAGATGAGAGCTTCTTACCATTAATTTCCATATAGATCGAGAAGGTAA  
 AGTGACACTTCTTAAACAGTTAAGATAGGAGAGAGTGGGTTGAGTAG  
 ACCCTAAGACCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTGCGA  
 ACGGTAAAATTTGCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGA  
 AAACGCTATAGTAATTTCTAACAATTTCAAATATTTGATAACTTGAAAA  
 AAGAACCTATGTTTATTTCTAAAGAAAGGAAAGTAGTAAACAGAACTA  
 GAAGAAATAGCATTAGTTAAGCCGCAAACTACAGTTACTACTCAATCAT  
 GTCTAAGAAATAACTCAATCAGGAAATGAGAAAGTCTCACTTCTACAA  
 ACAATAATAGTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGG  
 GATTCTGTTAACCATACC

SEQ ID NO. 4404

STRAIN H3B

GAGGAGCAAGAATTAAAAACCAAGAGCAATCACCTGTAATTGC  
 TAATGTTGCTCAACAGCCATCGCCATCGGTAACTACTAATACTGTTGAAA  
 AAACATCTGTAAACATCTGCTTCTGCTAGTAATACAGCGAAAGAAATGGGT  
 GATACATCTGTAAAAATGACAAACAGAAAGATGAATTTATAGAAGATT  
 ATCTAAAAACCTTGATACGCTCAATTTGGGGCTGATCTTGAAGAAGAAAT  
 ATCCCTCTAAACAGAGACAAACCAATAAAGAAAGCAATGTAGTAACA  
 AATGCTTCAACTGCAATAGCACAGAAaGTTCCTCAGCATATGAAGAGGT  
 GAAGCCAGAAAGCAAGTCATCACTTGCTGTTCTTGATACATCTAAATAA  
 CAAAATTGCAAGCCATAACCCAAAGAGGAAAGCGAAATCTAGTAGCTATT  
 ATTGATACCTGGCTTTGATATTAAACCATGATATTTTCGTTTAGATAGCCC  
 AAAAGATGATAAGCACAGCTTTAAACCTAAGGCAGAAATTTGAGGAATTAA  
 AAGCAAAACATAATATCACTTATGGGAAATGGGTTAACGATAAGATTGTT  
 TTTGCACATAACTACGCCaCAATAACAGAAACGGTGGCTGATATTGCAGC  
 AGCTATGAAAGATGGTTATGGGTGAGAAGCAAGAAATTTTCGATGGTA  
 CACACGTTGCTGGTAATTTTGTAGGTAATAGTAAACGTCAGCAATCAAT  
 GGTCTTCTTTAGAAGGTGCAGCGCAAAATGCTCAAGTCTTATTAATCGG  
 TATTCAGATAAAATTTGATTGGGCAAAATTTGGTGAAGCATATGCTAAAG  
 CAATCACAGACGCTGTTAATCTAGGAGCAAAACGATTAATATGAGCCTT  
 GGAAGAACAGCAGATTCTTTAATTGCTCTCAATGATAAAGTTAAATTAGC  
 ACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGGCTGCCGGA  
 ATGAAGGTGCAATTTGGTATGGATTATAGCAACCAATATCACTAATCCT  
 GACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGTACTTTGAGTGT  
 TGCTAGCTATGAATCACTTAAACCTATCAGTGAGGTGCGTTGAACAACTA  
 TTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTCTAAACCTTTGAC  
 AAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGGTGCAAAAAAGA  
 CTTTGAAGGTAAAGACTTTAAGGTAAGATTGCATTAATTGAGCGTGGT  
 GTGGACTGATTTTATGACTAAAACTCACTCATGCTACAAATGCAGGTGTT  
 GTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTTGGAATTTCTAAT  
 TCCCTTACCGTGAATTAACCTGTGGGGTTATAGTAAGTAGATGGCGAGC  
 GTATAAAAATACTTCAAGTCAGTTAACTTAAACAGAGTTTGTAGGTA  
 GTTGATAGCCAAAGGTGGCAATCGTATGCTGGAACCAATCAAGTTGGGGCGT  
 GACAGCTGAAGGAGCAATCAAGCCTGATGTAAACGCTTCTGGCTTTGAAA  
 TTTATTTCTCAACCTATAATAATCAATACCAACCAATGTCTGGTACAGT  
 ATGGCTTCAACCATGTTGCAGGATTAATGACAAATGCTTCAAGTCATTT

**Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)**

GGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTGCTAGAAT  
 TGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTGAAGAG  
 GATAAGGCGTTTTATTCCACCACGTCAGCAAGGTGCAGGTGTAGTTGATGC  
 TGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAAACGATGGCAAAG  
 CTAAAAATTAATCTCAACAGAGTGGGAGATAAAATTGATATCACAGTTACA  
 ATTCTAAACTTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCTAATGT  
 AGCAACAGAACAGTAAATAAAGSTAAATTTGCCCTTAAACCcAAGCCT  
 TGCTAGATACTAATTGGCAGAAAGTAATTTCTCGTGATAAAGAAACAA  
 GTTCGATTACTATTGATTCTAGTCAATTTAGTCAGAAATTTAAAGAACA  
 GATGGCAAATGGTTATTCTTAGAAGGTTTGTACGTTTAAAGAAGCCA  
 AGGATAGTAATCAGGAGTTAATGAGTATTCCTTTGTAGGATTTAATGGT  
 GATTTTGCAGACTcACAAGCACTGAAACACCGATTTATAAGACGCTTTC  
 TAAAGGTAGTTTCTACTATAAACCAAATGATACAACTCATAAGACCAAT  
 TGGAGTACAATGAATCAGCTCCTTTTGAAAGCAACCACTATCTGCTCTG  
 TTAACCAATCAGCGCTCTGGGGCTATGTTGATTATGTCAAAAAATGGTGG  
 GGAGTTAgAATTAgCACCGGAGAGTCCAAAAAGAATTATTTTAGGAACCT  
 TTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTGGAAGAGATGCA  
 CGGAATAATCCATATTTGCCATTTCTCAAATAAAGATGGAAATAGGGA  
 TGAAATCACTCCCAGGCAACTTTCTTAAGAAATGTTAAGGATATTTCTG  
 CTCAAGTTCTAGATCAAAATGGAATGTTAATTTGGCAAAGTAAGGTTTAA  
 CCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAGTGATGGTCA  
 TTATCGTATGGATGCCCTTCAGTGGAGTGGTTTAGATAAGGATGGCAAAG  
 TTGTAGCAGATGGTTTTTATACCTTATCGTTTACGTTACACACCACTAGCA  
 GAAGGAGCAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAAGTACTAA  
 GTCACCAAACTCTCCTTCAGGAGCTCAGTTTGTATGAACTAATCGAACAT  
 TAAGCTTAGCCATGCCCTAAGGAAAGTAGTTATGTTCTCATATCGTCTA  
 CAATTAGTTTATCTCATGTTGTAAAAGATGAAGAATATGGAGATGAGAC  
 TTCTTACCATTAATTTCCATATAGATCAAGAAGGTAAAGTGACACTTCTTA  
 AAACAGTTAAGATAGGAGAGAGTGGGTTGCAGTAGACCTTAAGACCTTG  
 ACCTTGTGTGGAAGATAAAGCTGGTAATTTTCGCAACGGTAAAAATTTGTC  
 TGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAACGCTATAGTAA  
 TTTCTAACAATTTCAAATATTTTGATAACTTGAAAAAGAACTATGTTT  
 ATTTCTAAAGAAGGAAAGTAGTAAACAAGAATCTAGAAGAAATAGCAAT  
 AGTTAAGCCGCAAACTACAGTTACTACTCAATCATTTGTCTAAAGAAATAA  
 CTCAATCAGGAAATGAGAAAGTCTCACTTCTACAAACAATAATAGTAGC  
 AGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTAACCA  
 TACC

SEQ ID NO. 4405

STRAIN 18RS21

GAGGAGCAAGAAATAAAAACCAAGAGCAATCACC

TGTAATTTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACCTACTAATA  
 CTGTTGAAAAAACATCTGTAAACAGCTGCTTCTGCTAGTAAATACAGCGAAA  
 GAAATGGGTGATACATCTGTAAAAAATGACAAAAACAGAAGATGAATTATT  
 AGAAGAGTTATCTAAAAACCTTGATACGTTCTAATTTGGGGGCTGATCTTG  
 AAGAAGATATCCCTCTAAACCAGAGACAACCAACAATAAAGAAAGCAAT  
 GTAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATA  
 TGAAGAGGTGAAGCCAGAAAGCAAGTCATCGCTTGTGTTCTTGATACAT  
 CTAAAAATACAAAAATTACAAGCCATAACCCAAAGAGGAAAGGAAATGTA  
 GTAGCTATTATTGATAGTGGCTTTGATATTAAACATGATATTTTTCGTTT  
 AGATAGCCCAAAAGATGATAAGCAAGCTTTAAAACTAAGACAGAATTTG  
 AGGAATTTAAAGCAAAACATAATATCACTTATGGGAAATGGGTAAACGAT  
 AAGATTGTTTTGACATAAATACGCAACAATAACAGAAACGGTGGCTGA  
 TATTGACGAGCTATGAAAGATGGTTATGGTTCAGAAGCAAGAAATATT  
 CGCATGGTACACAGCTTGTCTGTTATTTTGTAGCTAATAGTAAACGTTCCA  
 GCAATCAATGGTCTTCTTTAGAAGGTGACGCGCCAAATGCTCAAGTCTT  
 ATTAATGCGTATTCAGATAAAATTGATTCCGACAAATTTGGTGAAGCAT  
 ATGCTAAAGCAATCACAGACGCTGTTAATCTAGGAGCAAAACGATTAAT  
 ATGAGTATTGGAAAAACAGCTGATTCTTAAATTGCTCTCAATGATAAAGT  
 TAAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAAGTTGTTGTTG  
 CTGCCGGAATGAAGGCGCATTTGGTATGGATTATAGCAAAACATTATCA  
 ACTAATCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATAC  
 TTTGAGTGTGCTAGCTATGAATCACTTAAAACTATCAGTGAGGTGCTTG  
 AAACAACCTATTGAAGGTAAGTTAGTTAAGTTGCCGATTTGACTTTCTAAA  
 CCTTTTGACAAAGGTAAGGCTACGATGTGGTTTATGCCAATATGGTGC  
 AAAAAAGACTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAATTG  
 AGCGTGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAT  
 GCAGGTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAAA  
 TTTTCTAATTCCTTACCCTGAATTACCTGTGGGGATTATTAGTAAAGTAG  
 ATGGCGAGCGTATAAAAAATCACTTCAAGTCAGTTAAACATTAAACAGAGT  
 TTTGAAGTAGTTGATAGCCAGGTGGTAATCGTATGCTGGAACCAATCAAG  
 TTGGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTG  
 GCTTTGAATTTATTCTTCAACCTATAATAATCAATACCAaCAATGTCT  
 GGTACAAGTATGGCTTCAACACATGTTGCAGGATTAATGACAATGCTTCA  
 AAGTCATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAAT  
 TGCTAGAATTGTTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATAT  
 AGTGAAGAGGATAAGGCGTTTATTACCACGTCAGCAAGGTGAGGTGT  
 AGTTGATGCTGAAAAAGCTATCCAAGCTCAATATATATATTACTGGAAACG  
 ATGGCAaAGCTAAAAATTAATCTCAACGAAATGGGAGATAAATTTGATATC  
 ACAGTTACAATTCAaAACTTGTAGAAGGTGTCAAAGAATTGTATTATCA  
 AGCTAATGTAGCAACAGAAACAAGTAAATAAAGTAAATTTGCCCTTaAAC  
 CACAAGCCTTGCTAGATACTAATTGGCAGAAAGTAATTTCTTcGTGATAAA  
 GAAACACAAGTTCGATTACTATTGATGCTAGTCAATTTAGTCAGAAAT

**Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)**

AAAAGAACAGATGGCAAATGGTTATTTCTTAgAAGGTTTTGTACGTTTTA  
 AAGAAGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGA  
 TTTAATGGTGATTTTGCGAACCTTACAAGCACTTGAAACACCGATTATAA  
 GACGATTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAACTCATA  
 AAGACCAATTGGAGTACAATGAATCAGCTCCTTTTGAAGCAACAATAT  
 ACTGCCTTGTAAACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAA  
 AATGGTGGGAGTTAGAAATAGCaCCGGAGAGTCCAAAAGAAATTTATTT  
 TAGGAACCTTTTGAGAAATAAGGTTGAGGATAAAACAATTCATCTTTTGGA  
 AGAGATGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAGATGG  
 AAATAGGGACGAAATCACTCCCCAGGCAACtTTCTTAAGAAATGTTAAGG  
 ATATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGCAAAGT  
 AAGGTTTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAG  
 TGATGGTCATTATCGTATGGATGCTCTTCAGTGGAGTGGTTTAGATAAGG  
 ATGGCAAAGTTGTAGCAGATGGTTTTTATACCTTATCGCTTACGTTACACA  
 CCAGTAGCAGAAGGAGCAATAGTCAGGAGTCAGACTTTAAAGTACAAGT  
 AAGTACTAAGTCACCAATCTTCCTTCACGAGCTCAGTTTGTGAACTA  
 ATCGAACATTAAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTTACA  
 TATCGTTTACAATTAGTTTATCTCATGTTGTAAGATGAAGAAATATGG  
 GGATGAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGA  
 CACTTCTTAAACCGGTTAAGATAGGAGAGAGTGAAGTTGCGGTAGACCTT  
 AAGGCCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTGCaAACGGT  
 AAAATTGTCTGATCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAACG  
 CTATAGTAATTTCTAACAGTTTCAAATATTTTGATACTTGAAGAAAGAA  
 CCTATGTTTATTTCTAAAGAAAGAAAGTAGTAAACAAGAACTTAGAAGA  
 AATAATATTAGTTAAGCCGCAAACTACAGTTACTACTCAATCATTTGTCTA  
 AAGAAATACTAAATCAGGAAATGAGAAAGTCTCACITCTACAAACAAT  
 AATAGTAGCAGAGTAGCTAAGATCATATCACTTAAACATAACGGGGATTCT  
 TGTTAACCATACC

SEQ ID NO. 4406

STRAIN M732

CAGGAGCAAGAATTAAAAACCAAGAGCAATCACCT  
 GTAATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACTACTAATAT  
 TGTGTAAGAAACATCTGTAAACAGCTGCTTCTGCTAGTAATACAGTGAAG  
 AATGGGTGATACATCTGTAAAAAATGACAAACAGAGATGAATTATTA  
 GAAGAGTTATCTAAAAACCTTGATACGTCTAATTTGGGGCTGATCTTGA  
 AGAAGAAATATCCCTCTAAACCAAGAGACCAACAATAAAGAAAGCAATG  
 TAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTCCCTCAGCATAT  
 GAAGAGGTGAAGTCAGAAAGCAAGTCATCGCTTGCTGTTCTTGATACATC  
 TAAATAACAAAAATTACAGGCCACAACCCAAAGAGGAAAGGAAATGTAG  
 TAGCTATTTATGTAAGTGGCTTTGATATTAACCATGATATTTTTCGTTTA  
 GATAGCCCAAGAGATGATAAGCAGAGCTTTAAACTAAGGCAGAAATTTGA  
 GGAATTAAGCAAAACATAATATCACTTATGGGAATGGGTTAAGGATA  
 AGATTGTTTTTGCACATAACTACGCCAACATAACAGAAACGGTGGCTGAT  
 ATTGCAGCAGCTATGAAAGATGGTTATGGGTGCAAGCAAGAAATATTTT  
 GCATGGTACACAGCTTGTCTGGTATTTTGTAGGTAATAGTAAACGCTCCAG  
 CAATCAATAGTCTCTTTTGAAGGTGACAGCGCAAAATGCTCAAGTCTTA  
 TTAATGCGTATTCAGATAAAATGATTCGGACAAATTTGGAGAAGCATA  
 TGCTTAAAGCAATCATAGACGCTGTTAATCTAGGAGCAAAACGATTAAATA  
 TGAGCCTGGGAAAAACGGCTGATTCTTTAATTGCTCTCAATGATAAAGTT  
 AAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAAGTTGTTGTCG  
 TGCCGAAATGAAGGTGCAATTTGGTATGGATTATAGCAAAACCATTTCAA  
 CTAATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACT  
 TTGAGTGTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTGCTTGA  
 AACAACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTTGTGACTTCTAAC  
 CTTTGACAAAGGTAAAGCCTACGATGTGGTTTATGCCAATTATGGTGCA  
 AAAAAGATTTTGAAGGTAAAGACTTTAAAGGTAAGATGCAATTAATTGAG  
 CGTGTGTGGGACTTGATTTTATGACTAAAATCACTCATGCTACAAATGC  
 AGGTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAAAT  
 TTCTAATTCCTTACCGTGAATTACCTGTGGGGGTTATTAGTAAAGTAGAT  
 GCGAGCGGTATAAAAAATACTTCAAGTCAGTTAACATTTAACCAAGTTT  
 TGAAGTAGTTGATAGCCAAGGTGGCAATCGTATGCTGGAACAATCAAGTT  
 GGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGTC  
 TTTGAAATTTATCTTCAACCTATAATTAATCAATACTAAACAATGTCTGG  
 TACAAGTATGGCTTCAACCATGTTGCAAGATTAATGACAAATGCTTCAAA  
 GTCAATTTGGCTGAGAAATATAAGGGATGAATTTAGATTCTAAAAAATTG  
 CTAGAAATGCTTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAG  
 TGAAGAGGATAAGGCGTTTTATTCACCAGCTCAGCAAGGTGCAAGGTGAG  
 TTGATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAACAGAT  
 GGCAAAGTTAAATTAATCTCAACGAGAGGGAGATAAATTTGATATCAC  
 AGTTACAATTCATaAACTTGTAGAAGGTGTCAAAGAAATTTGATTATCAAG  
 CTAATGTAGCAACAGAAaCAAGTAAATAAAGGTAATTTGCCCTTAAACCA  
 CAAGCCTTGCTAGATACTAATTGGCAGAAAGTAATTTCTCGTATAAAGA  
 AACACAAGTTTCGATTTACTATTGATGCTAGTCAATTTAGTCAGAAATTA  
 AAGACAGATGGCAAATGGTTATTTCTTAGAAGGTTTTGTACGTTTTTAA  
 GAAGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGAT  
 TAATGGTGATTTTGCGAACCTTACAAGCACTTGAAACaCCGATTATATAAG  
 CGCTTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAACTCATAAA  
 GACCAATTGGAGTACAATGAATCAGCTCCTTTTGAAGCAACAATATAC  
 TGCTTTGTTAACCAATCAGCGCTTGGGGCTATGTTGATTATGTCAAAA  
 ATGTTGGGGAGTTAGAAATTAGCACCGGAGAGTCCAAAAGAAATTTATTA  
 GGAACCTTTTGAAGATAAGGTTAGGATAAAACAATTCATCTTTTGAAGAG  
 AGATGCAGCGAATAATCCATATTTTGCCATTTCTCCAATAAAGATGGA

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

ATAGGGACGAAATCACTCCCCAGGCAACTTTCTTAAGAAATGTTAAGGAT  
 ATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTGGCAAAGTAA  
 GGTTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAGCAAAGTG  
 ATGGTCATTATCGTATGGATGCTCTTCAGTGGAGTGGTTTAGATAAGGAT  
 GGCAAAGTTGTAGCAGATGGTTTTTATACTTATCGCTTACGTTACACACC  
 AGTAGCAGAAGGAGCaAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAA  
 GTACTAAGTCACCAAACTTTCCTTCACGAGCTCAGTTTGTAGAACTAAT  
 CGAACATTAAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTACATA  
 TCGTTTACAATTAGTTTATCTCATGTTGTAAAAGATGAAGAATATGGGG  
 ATGAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACA  
 CTTCTTAAACGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCTTAA  
 GGCCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTAA  
 AATTGCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAACCGCT  
 ATAGTAAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAGAAAGAACCC  
 TAGTTTATTCTTAAAGAAGGAAAGTAGTAAACAAGAATCTAGAAGAAA  
 TAACATTAGTTAAGCCTCAAACTACAGTTACTACTCAATCATGTCTTAA  
 GAAATAACTAAATCAGGAAATGAGAAAGTCCTCACTTCTCAAAACAATA  
 TAGTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTG  
 TTAACCATACC

SEQ ID NO. 4407

STRAIN COH1

GAGGAGCAAGAATTAAAAACCAAGAGCAATCACCTGT  
 AATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTaACTACTAATATTG  
 TTGAAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGTGAAAGAA  
 ATGGGcGATACATCTGTAATAAATGACAAAACAGAAGATGAATTATTAGA  
 AGAGTTATCTAAAAACCTTGATACGCTCTAATTTGGGGGCTGATCTTGAAG  
 AAGAATATCCCTCTAAACAGAGaCAACCAACAATAAAGAAGCAATGTA  
 GTAACAAATGCTTCACTGCAATAGCACAGAAGTTCCCTCAGCATATGA  
 AGAGGTGAAGTCAGAAAGCAAGTCATCGCTTGTGTTCTTGATACATCTA  
 AAATAACAAATTACAAGCCCAACCCAAAGAGGAAAGGGAATAGTAGTA  
 GCTATTATTGATACTGGCTTTGATATTAAACCATGATATTTTCGTTTGA  
 TAGCCCAAAAGATGATAAGCACAGCTTTAAACTAAGGCAGAATTGAGG  
 AaCTAAAGCAAAACATAATATCACTTATGGGAATGGGTTAACGATAAG  
 ATTGTTTTTGCACATAACTACGCCaCAATACAGAAACGGTGGCTGATAT  
 TGCAGCAGCTATGAAAGATGGTTATGGGTGAGAAGCAAGAATATTTTGC  
 ATGGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGTCACGCA  
 ATCAATAGTCTTCTTTAGAGGTGACAGCCCAATAGCTCAAGTCTTATT  
 AATGCGTATTCCAGATAAAATGATTGCGACAAATTTGGAGAAGCATATG  
 CTAAGCAATCATAGACGCTGTTAATCTAGGAGCAAAACGATTAAATATG  
 AGCCTGGGAAAAACGGCTGATTCTTTAATTGCTCTCAATGATAAAGTTAA  
 ATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAAGTTGTGTGGCTG  
 CCGGAATGAAGGTGCAATTGGTATGGATTATAGCAAAACCATTTATCACT  
 AATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGTACTTT  
 GAGTGTGTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTGCTTGA  
 CAACTATTGAAGGTAAGTTAGTTAAGTTGCGGATTGTGACTTCTAAACCT  
 TcTGACAAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGGTGCAAA  
 AAAGATTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAAATTGAGCG  
 TGGTGGTGGACTTGATTTTTATGACTAAATCACTCATGCTACAAATGCA  
 GTGTTGTGGTATCGTTATTTTAAACGATCAAGAAAACGTTGGAATTTT  
 CTAATTCCTTACCGTGAATTACCTGTGGGGTTATTAGTAAAGTAGATGG  
 CGAGCGTATAAAAAACTTCAAGTCAGTTAAACATTTAAACAGAGTTTGA  
 AAGTAGTTGATAGCCAAAGGTGGCAATCGTATGCTGGAAACATCAAGTTGG  
 GCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTT  
 TGAaATTTATTCTTCAACCTATAATAATCAATACTAAACAATGTCTGGTA  
 CRAAGTATGGCTTCAACCATGTTGCAGGATTAATGACAATGCTTCAAAGT  
 CATTTGGCTGAGAAATATAAGGGATGAATTTAGATTCTaAAAAATTGCT  
 AGaATTGCTCTaAAACATCCTCATGAGCTCAGCAACAGCATTTATATAGT  
 AAGAGGATAAGGCGTTTATTACCACGTCAGCAAGGTGCAAGGTGATGTT  
 GATGCTGAAAAAGCTATCCAAGCTCAATATATGTTACTGGAAACGATGG  
 CAAAGTTAAATTAATCTCAAAACGAGAGGGAGATAAATTTGATATCACAG  
 TTACAATTCATaAACTTGTAGAAGGTGTCAGAAGATTGATTATCAAGCT  
 AATGTAGCAaCAGAACAAGTAAATAAAGGTAAATTTGCCCTTAAACCCACA  
 AGCCTTGCTAGATACTAATTGGCAGAAAGTAATTTCTcGTGATAAGAAA  
 CACAAGTTCGATTACTATTGATGCTAGTCAATTTAGTCAGAAATTAATA  
 GAACAGATGGCAAAATGGTTATTTCTTAGAAGGTTTGTACGTTTAAAGA  
 AGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTTA  
 ATGGTATTTTGCAGACTTACAAGCACTTGAACACCGATTATAAGACG  
 CTTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAACCTATAAGA  
 CCAATTGGAGTACAATGAATCAGTCTCTTTTGAAGCAACAACCTATACTG  
 CCTTGTATAACACAATCAGCGCTTTGGGGCTATGTTGATTATGTCAAAAAT  
 GGTGGGGAGTTAGAAATAGCACCGGAGAGTCCAAAAAGAAATTTTATAGG  
 aACTTTTGAAGATAAGGTTGAGGATAAAACAATTCATCTTTTGAAGAG  
 ATGCAGGAAATATCCATATTTTGCCATTTCTCCAATAAAGATGGAAT  
 AGGAGCAAAATCACTCCCCAGGCaCTTTCTTAAGAAATGTTAAGGATAT  
 TTCTGCTCAAGTCTTAGATCAAAATGGAAATGTTATTGGCAAAGTAAGG  
 TTTTACCATCTTATCGTAAAAATTTCCATAATaATCCAAGCAAGTGAT  
 GGTCAATTATCGTATGGATGCTCTTCAGTGGAGTGGTTAgATAAGGATGG  
 CAAAGTTGTAgCAGATGGTTTATATACTTATCGCTTACGTTACACACCAG  
 TAGCAGAAGGAGCAAAATAGTCAGGAGTCAGACTTTaAGTTCAAGTAAGT  
 AcTAAGTCACCAATCTTCTTTCACGAGCTCAGTTTGATGaAACTAATCG  
 AACATTAAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTCATATC  
 GTTACAATTAGTTTATCTCATCTTGTAAAGATGAAGAATATGGGAT

**Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)**

GAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACT  
 TCCTAAACGGTTAAGTAGGAGAGAGTGAGGTTGCGGTAGACCCCTAAGG  
 CCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTAATA  
 TTGCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTAT  
 AGTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAAGAAAGAACCTA  
 TGTTTATTTCTAAAGAAGGAAAAGTAGTAAACAGAATCTAGAAGAAATA  
 ACATTAGTTAAGCCTCAAACTACAGTTACTACTCAATCATTTGTCTAAAGA  
 AATAACTAAATCAGGAAATGAGAAAGTCTCACTTCTACAAACAATAATA  
 GTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTT  
 AACCATACC

SEQ ID NO. 4408

STRAIN M781

GAGGAGCAAGAATTAAAAACCAAGAGCAATCACCTGT  
 AATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACCTACTAATATTG  
 TTGAAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGTGAAAGAA  
 ATGGGTGATACATCTGTAAAAATGACAAACAGAGATGAATTAATTAGA  
 AGAGTTATCTAAAAACCTTGATACGTTCTAATTTGGGGCTGATCTTGAAG  
 AAGAATATCCCTCTAAACAGAGACAACCAATAAAGAAAGCAATGTA  
 GTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATATGA  
 AGAGGTGAAGTCAGAAAGCAAGTCATCGCTTGTCTGTTCTTGATACATCTA  
 AAATAACAAAAATACAGGCCACAACCCAAAGAGGAAAGGGAATGTAGTA  
 GCTATTATTGATACTGGCTTTGATATTAACCATGATATTTTCGTTTAGA  
 TAGCCCAAAAGATGATAAGCACAGCTTTAAACTAAGGCAGAAATTTGAGG  
 AATTAAGCAAAAACATAATATCACTTATGGGAAATGGGTTAACGATAAG  
 ATTGTTTTTGCACATAACTACGCCAaCAATACAGAAACGGTGGCTGATAT  
 TGCAGCAGCTATGAAAGATGGTTATGGGTGAGAAGCAAGAAATATTTTGC  
 ATGGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAACCGTCCAGCA  
 ATCAATAGTCTTCTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTTATT  
 AATGGGTATTTCCAGATAAAATTGATTCCGACAAATTTGGAGAAGCATATG  
 CTAAAGCAATCATAGACGCTGTTAATCTAGGAGCAAAAACGATTAATATG  
 AGCCTGGGAAAAACGGCTGATTCTTAATTGCTCTCAATGATAAAGTTAA  
 ATTAGCACTTAAATTAGCTTTCTGAGAAGGGCGTTGCAGTTGTTGGGCTG  
 CCGGAAATGAAGGTGCATTGTTGATGGATTATAGCAAAcCATTTATCAaCT  
 AATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTT  
 GAGTGTGCTAGCTATGAATCACTtAAAACATCACTGAGGTGGTTGAAA  
 CAACATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTCTCAaACCT  
 TTTGACAAAGGTAAGGCTACGATGTGGTTTATGCCAATTATGGTGCAAA  
 AAAGATTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAATTGAGCG  
 TGGTGGTGGACTTGATTTTATGACTAAAACTCACTCATGCTACAAATCAG  
 GTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAAATTTT  
 cTAATTCCTTACCGTGAATTACCTGTGgGGGTTATTAGTAAAGTAGATGG  
 CGAGCGTATAAAAAATACTTCAAGTCAGTTAACCATTAAACAGAGTTTg  
 AAGTAGTTGATAGCCAAAGGTGGCAATCGTATGCTGGAACAATCAAGTTGG  
 GCGGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAAACAGCTTCTGGCTT  
 TGAAATTTATCTTCAACCTATAAATCAATCACTAAACAATGTCTGGTA  
 CAAGTATGGCTTCACCACATGTTGAGGATTAATGACAATGCTTCAAAGT  
 CATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTGCT  
 AGAATTGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTG  
 AAGAGGATAAGGCGTTTTATTACCACGTCAGCAAGGTGCAGGTGTAGTT  
 GATGCTGAAAAAGCTATCCAAAGCTCAATATTATGTTACTGGAACCGATGG  
 CAAAGTTAAAAATTAATCTCAAACGAGAGGGAGATAAATTTGATATCAG  
 TTACAATTCATaaACTTTGTAAGGTGTCAAAGAATTGTATTATCAAGCT  
 AATGTAGCaaCAGAAACAGTAAATaaAGGTAATTTGCCCTTaaACCaaCA  
 AGCCTTGCTAGATATAATTGGCAGaaAGTaaATTCTTcGTGATAAAGAAA  
 CACAAGTTcGATTACTAtTGATGCTAGTCAATTTAGTCAGAAATTAAAA  
 GAACAGATGGCAAAATGGTTATTCTTAGAAGGTTTGTACGTTTAAAGA  
 AGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTTA  
 ATGGTGATTTTGCAGAACTtACAAGCACTTGAACACCCGATTTATAAGACG  
 CTTTCTAAAGGTAGTTTCTACTATAaaCCAAATGATCAAACTCATAAAGA  
 CCAATTGGAGTACAATGAATCAGCTCCTTTTGAAGCAACAACCTATACTG  
 CCTTGTAAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAAT  
 GGTGGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAAATTTTTAGG  
 AACTTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTGGAAGAG  
 ATGCAGCGAATAATCCATATTTTGCATTTCTCCAATAAAGATGGAAAT  
 AGGAGCgaaATCACTCCCCAGGCaACTTCTTAAGAAATGTTAAGGATAT  
 TTCTGCTCAAGtCTTAGATCAAAATGGAATGTTATTTGGCAAAGTAAGG  
 TTTTACCATCTTATCGTAAAAATTTCCATAATaATCCAAAGCAAGTGAT  
 GGTCAATTATCGTATGGATGCTCTTCACTGGAGTGGTTTAGATAAGGATGG  
 CAAAGTTGTAGCAGATGGTTTATACTTATCGCTTACGTTACACACCAG  
 TAGCAGAGGAGCAAAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAAGT  
 ACTAAGTCACCAATCTTCCCTTACGAGCTCAGTTTGATGAAACTAATCG  
 AACATTAAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTCATATC  
 GTTTACAATTAGTTTATCTCATGTGTGTAAGATGAAGAATATGGGGAT  
 GAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACT  
 TCCTAAACCGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCCCTAAGG  
 CCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTAAAA  
 TTGTCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTAT  
 AGTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAGAAAGAACCTA  
 TGTTTATTTCTAAAGAAGGAAAGTAGTAAACAAGAATCTAGAAGAAATA  
 ACATTAGTTAAGCCTCAAACTACAGTTACTACTCAATCATTTGTCTAAAGA  
 AATAACTAAATCAGGAAATGAGAAAGTCTCACTTCTACAAACAATAATA  
 GTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTT



Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

AACCATACC

SEQ ID NO. 4409

STRAIN CJB110

GAGGAGCAAGAATTAAAAACCAAGAGCAATCACCTGTAA  
 TTGCTAAATGTTGCTCAACAGCCATCGCCATCGGTAACACTAATATTGTT  
 GAAAAACATCTGTAnCAGCTGCTTCTGCTAGTAATACAGCGAAAGAAAT  
 GGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTATTAGAAG  
 AGTTATCTAAAAACCTTGATACGTCTAATWGGGGGCTGATCTGAAGAA  
 GAATATCCCTCTAAACCAGAGACAAACCAATAAAGAAAGCAATGTAGT  
 AACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCGTATGAAG  
 AGGTGaAGCCAGAAAGCAAGTCATCGCTTGCTGTTTTTGATACATCTAAA  
 ATAACAAAATTGCAAGCCATAACCCAAAGAGGAAAGGAAATGTAGTAGC  
 TATTATTGATCTGGCTTTGATATTAAACCATGATATTTTCGTTTAGATA  
 GCCCAAAGATGATAAGCACAGCTTTAAACTTAAAGCAGAATTCGAGGAA  
 tTAAAGCAAAACATAATATCACTTATGGGAATGGGTTAACGATAAGAT  
 TGTTTTTGACATAACTACGCCAACATACAGAAACGGTGGCTGATATTG  
 CAGCAGCTATGAAAGATGGTTATGGGTGAGAAGCAAGAAATATTTGCAAT  
 GGTACACACGTTGCTGGTATTTTGTAGGTAAATAGTAAACGTCAGCAAT  
 CAATGGTCTTTCTTTAGAGGTGCGCGCAATGCTCAAGTCTTATTA  
 TGCGTATTCAGATAAAATTGATTGCGGCAAAATTTGGAGAAGCATATGCT  
 AAAGCAATCACAGACGCTCTTAATCTAGGAGCAAAACGATTAAATATGAG  
 CCTTGGAAAAACAGCAGATTCTTTAATTGCACTCAATGATAAAGTTAAAT  
 TAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAAGTGTGTGGCTGCC  
 GGAATGAAGGTGCAATTTGGTATGGATTATAGCAAAACATTATCAACTAA  
 TcCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTTGA  
 GTGTTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTGCTTGAACA  
 ACTATTGAAGGTAAGTTAGTTAAGTTGCGGATTTGTGACTTCTAAACCTTT  
 TGACAAAGGTAAAGCCTACGATGTGGTTTATGCCAATTATGGTGCAAAAA  
 AAGACTTTGAAGGTAAGGACTTTAAGGTAAGATTGCATTAATTGAGCGT  
 GGTGGTGCACTTGAATTTATGACTAAAATCACTCATGCTACAAATGCAGG  
 TGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAATTTTc  
 TAATTCCTTACCGTGAATTACCTGTGgGGGTTATTAGTAAAGTAGATGGC  
 GAGCGTATAAAAAATACITCAAGTCAGTTAACATTTAACCAgAGTTTGA  
 AGTAGTTGATAGCCAAgGTGGCAATCGTATGCTGGAACCAATCAAGTGGG  
 CGGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAAACAGCTTCTGGCTTT  
 GAAATTTTATTCTTCAACCTATAATAATCAATACCAAAACAAATGTCTGTAC  
 AAGTAGGCTTCAACCATGTGTCAGGATTAATGACAAATGCTTCAAAATC  
 ATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTGCTA  
 GAATTTGCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTGA  
 AGAGGATAAGGCGTTTATTCAACAGCTCAGCAAGGTGCGAGGTGATGTTG  
 ATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAACAGATGGC  
 AAAGCTAAAAATTAATCTCAACGAGTGGGAGATAAATTTGATATCACAGT  
 TACAATTATAAACTTGTAGAAGGTGTCAAAGAATTTGATTTATCAAGCTA  
 ATGTAGCAACAGAACCAAGTAAATAAAGTAAATTTGCCCTTaAACCAAA  
 GCCTTGCTAGATACTAATTGGCAGAAAGTAATTTCTcGTGATAAAGAAAC  
 ACAAGTTGATTTACTATcTGATGCTAGTCAATTTAGTCAGAAATTAAGAG  
 AACAGATGGCAAAATGGTTATTTCTAGaAGGTTTGTACGTTTAAAGAA  
 GCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTGTAGGATTTAA  
 TGGTGATTTTGCGAACtLACAGCACTTGAACACCGATTTATAAGACGC  
 TTTCTAAAGGTAGTtCTACTATAAACCAATGATACAACTCATAAGAC  
 CAATTTGGAGTACAATGAATCAGCTCctTTTGAAGCAACAACATACTGCT  
 CTTGTTAACCAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAAATG  
 GTGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAAATTTATTAGGA  
 ACTTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTGGAAAGAGA  
 TGCAGGAATAATCCATATTTTGCCATTCTTCCAATAAAGATGGAATA  
 GGGATGaAATCACTCCCAGGCAACtTTCTTAAGAAATGTTAAGGATATT  
 TCTGCTCAAGTTCTAGATCAAAATGGAATGTTATTGGCAAAGTAAGGT  
 TTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAGTGATG  
 GTCAATTATCGTATGGATGCCCTTTCAGTGGAGTGGTTAgATAAgGATGGC  
 AAAGTTGTAGCAGATGGTTTTTATACTTATCGCCTACGTTACACACCAGT  
 AGCAGAAgGAGCAATAGTCAGGAGTCaGACTTAAAGTTCAAGTAAGTA  
 CTAAGTCACCAATCTTCTTTACTAGCTCAGTTTGATGAAACTAATCGA  
 ACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTCATATATCG  
 TTTACAATTAGTTTATCTCATGTTGTAAAAGATGAAGAATATGGGGATG  
 AGACTTCTTACCATTATTCCATATAGATCAAGAAGGTAAAGTGACACTT  
 CCTAAAAAGGTTAAGATAGGAGAGAGTGGGTTGAGTAGACCTTAAGGC  
 CTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTaAAAT  
 TGTCTGACCTCTTGaATaAgCGAGTAGTATCAGAGAAAGAAAACGCTATA  
 GTAATTTCTAACAGTTTCAATATTTTGATAACTTGAAAAAGAACTAT  
 GTTTATTCTTAAAGAAGGAAAGTAGTAAACAAGAATCTAGAAGAATAA  
 CATTAGTTAAGCCGCAaACTACAGTTACTACTCAATCATTTGTCTAAAGAA  
 ATAACATAATCAGGAAATGAGAAAGTCCTCACTCTACAAACAATAATAG  
 TAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTA  
 ACCATACC

SEQ ID NO. 4410

STRAIN 1169NT

GAGGAGCAAGAATTAAAAACCAAGAGCAATC

ACCTGTAATTTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACACTA  
 ATATTGTTGAAAAACATCTGTAAACAGCTGCTTCTGCTAGTAATACAGCG  
 AAAGAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAAT  
 ATTAGAAGAGTTATCTAAAAACCTTGATACGCTCAATATGGGGGCTGATC

**Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)**

TTGAAGAAGAAATATCCCTCTAAACCAGAGACAACCAACAATAAGGAAAGC  
 AATGTAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGC  
 ATATGAAGAGGTGAAGCCAAAAGCAAGTCAATCGCTTGCTGTTCTTGATA  
 CATCTTAAATAACAAATATGCAAGCCATAACCCAAAGAGGAAAGGAAAT  
 GTAGTAGCTATTATTGATACTGGCTTTGATATTAAACCATGATATTTTCG  
 TTTAGATAGCCCAAAAGATGATAAGCACAGCTTTAAAAATAAGGCAGAAAT  
 TCGAGGAATTAAGCAAAACATAATATCACTTATGGGAAATGGGTTAAC  
 GATAAGATTGTTTTTGCACATAAATACGCCAACAAATACAGAAACGGTGGC  
 TGATATTGCAGCAGCTATGAAAGATGGTTATGGTTCAGAAGCAAAAGAAAT  
 TTTCCGATGGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAACGTT  
 CCAGCAATCAATGGTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAGT  
 CTTATTATGGCTATTCAGATAAAAATGATTCGGACAAATTCGGAGAAG  
 CATATGCTAAAGCAATCACAGACGCTGTTAATCTAGGAGCTAAAAACGATT  
 AATATGAGTATTGAAAAACAGCTGATTCTTTAATTTGCTCTCAATGATAA  
 AGTTAAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAAGTTGTTG  
 TGGCTGC CGGAAATGAAGGCGCAATTTGGTATGGATTATAGCAAAACCGTTA  
 TCAACTAATCTGACTACGGTACGGTAAATAGTCCAGCTATTCTGAGA  
 TACTTTGAGTGTGCTAGCTATGAATCACTTAAACATACAGTGAAGGTCG  
 TTGAACCAACTATTGAAGGTAAAGTTAGTTAAGTTCGCCATTGCGACTTCT  
 AAACCTTTTGACAAAGGTAAGGCTTACGATGTGGTTTATGCCAATTATGG  
 TGCAAAAAAGACTTTGAAGGTAAAGGCTTTAAAGGTAAGATTGCATTAA  
 TTGAGCGTGGTGGTGGACTTGATTTATGACTAAATCACTCATGCTACA  
 AATGCAGGTGTGTGGTATCGTTATTTTAAAGATCAAGAAAAACGTGG  
 AAATTTTCTAATTCCTTACCGTGAATACCTGTGGGGGTTATTAGTAAAG  
 TAGATGGCGAGCGTATAAAAAATACCTTCAAGTCAAGTTAAACATTAAACCA  
 AGATTTGAAGTAGTTGATAGCCAAAGTGGCAATCGTATGCTGGAACCAATC  
 aAGTTGGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAAACAGCTT  
 CTGGCTTCGAATTTATTTCTTCTCaaCCTATAATAATCAATACCAACAATG  
 TCTGGTACAAGTATGGCTTCAACACATGTTGCAGGATTAATGACAATGCT  
 TCAAGTCATTGGCTGAGAAATATAAGGGATGAATTTAGATTCTAAaAA  
 AATTTGCTAGAATTGTTCTAAAAACATCCCTCATGAGCTCAGCAACAGCATT  
 TATAGTGAAGAGGATAAGGCGTTTTATTCAACAGTCAAGCAAGGTCAGG  
 TGATGTTGATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAA  
 ACGATGGCAAGCTAAATTAATCTCAACAGAGTGGGAGATAAATTTGAT  
 ATCAGCTTACNATTCTATAAATCTGTAGAAGGTGTCAAGAATTTGATTA  
 TCAAGCTAATGTAGCAACAGAAACAGTAAATAAAGGTAAATTTGCCCTTA  
 AACCAAGCCTTGCTAGATACTAATTGGCAGAAAGTAATTTCTTCTGAT  
 AAAGAAACACAAGTTGATTTACTATTGATGCTAGTCAATTTAGTCAGAA  
 ATTAAAAAGAACAGATGGCAAAATGGTTATTTCTTGAAGGTTTGTACGTT  
 TTAAGAAAGCTAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTGTGA  
 GGATTTAATGGTGAATTTTGGAGCTTACAAGCACTTGAACACCGATTTA  
 TAAGACGCTTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAATC  
 ATAAAGCAATTTGGAGTATAATGAATCAGCTCCTTTTGAAAGCAACAAC  
 TATATGCTGCTTTAACACAATCAGCGCTTGGGGCTATGTTGATTTATGT  
 CaAAAATGGTGGGAGTTAGAATTAGCACCGGAGAGTcCAAAAAGAATTA  
 TTTTAGGAACCTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTG  
 GAAAGAGATGCAGCGAATAATCCATATTTTGCCTTTCTCCAATAAAGA  
 TGGAAATAGGGATGAAATCACTCCCAAGGCAACTTTCTTAAGAAATGTTA  
 AGGATATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTGGCAA  
 AGTAAGGTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCA  
 AGTGATGGTCAATTATCGTATGGATGCCCTTCAAGTGGAGTGGTTAGATA  
 AGGATGGCAAGTTGTAGCAGATGGTTTTTACTTATCGCTTACGTTAC  
 ACACAGTAGCAGAAGGAGCAAAATAGTCAGGAGTCAGACTTTAAAGTTCA  
 AGTAAGTACTAAGTCACCAATCTTCTTCAAGAGCTCAGTTTGTAGTAA  
 CTAATCGAACATTAAAGCTTAGCCATGCCCTAAGGGAAGTAGTTATGTTCT  
 ATATATCGCTACCAATTAGTTTATCTCATGTTGTAAAGATGAAGAATA  
 TGGAGATGAGACTTCTACTATTATTTCCATATAGATCAAGAAGGTAAAG  
 CGACACTTCTTAAACCGTTAAGATAGGAGAGAGTGAGTTGCAGTAGAC  
 CCTAAGGCCCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTCCGCAAC  
 CGTAAATTTGCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAA  
 ACGCTATAGTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAAAAA  
 GAACCTATGTTTATTTCTAAAAAGAAAAAGTAGTAAACAAGAACTTAGA  
 AGAaATAATATTAGTTAAGCCGCAcACTACAGTTACTACTCAaTCAATTGT  
 CTAAGAAATTAACATAATCAGGAAATGAGAAAGTCTCACTTCTACAAAC  
 AATAATAGTAGTAGTAGCTAAAAATCATATCACCTTAAACATAATGGGGA  
 TTCGTTTAAACATACC

SEQ ID NO. 4411

STRAIN **JM9130013**

GAGGAGCAAGAATTAACCAAGAGCAATCACCTGTAA  
 TTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACCTACTAATCTGTT  
 GAAAAACATCTGTAAAGCTGCTTCTGCTAGTAAATACAGCGAAAGAAAT  
 GGGTGATACATCTGTAATAAATGACAAAACAGAAAGATGAATATTAGAA  
 AGTTATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTGAAGAA  
 GAATATCCCTCTAAACAGAGACAACCAACAATAAAGAAAGCAATGTAGT  
 AACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATATGAAG  
 AGGTGAAGCCAGAAAGCAAGTCATCGCTTGTCTTCTTGATACATCTAAA  
 ATAAACAAAATTAAGGCCATAACCAAGAGGAAAGGGAAATGTAGTAGC  
 TATTATTGATACCTGCTTGTATTTAAACATGATATTTTCGTTTAGATA  
 GCCCAAGAGATGATAAGCACAGCTTAAACTAAGACAGAAATTTGAGGAA  
 TTAAGCAAAACATAATATCACTTATGGGAAATGGGTTAACGATAAGAT  
 TGTTTTTGCACATAACTACGCCAACAAATACAGAAACGGTGGCTGATATTG  
 CAGCAGCTATGAAGAGATGGTTATGGTTCAGAGCAAGAAATTTTCGCAAT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

GGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGTCAGCAAT  
 CAATGGTCTCTTTTGAAGGTGCAGCGCCAAATGCTCAAGTCTTATTA  
 TGCGTATTCAGATAAAATTGATTCGGACAAATTGGTGAAGCATATGCT  
 AAAGCAATCAGACGCTGTTAATCTAGGAGCAAAAACGATTAAATATGAG  
 TATTGAAAAACAGCTGATTCTTTAATTTGCTCTCAATGATAAAGTTAAAT  
 TAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTTGGCTGCC  
 GGAAATGAAGGCGCATTTGGTATGGATTATAGCAAAACATTATCAACTAA  
 TCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTTGA  
 GTGTTGCTAGCTATGAATCACTTAAAACTATCAGTGAGGTCGTTGAAACA  
 ACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAACCTTT  
 TGACAAAGGTAAGGCCCTACGATGTGGTTTATGCCAATTATGGTGCAAAAA  
 AAGACTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAAATGAGCGT  
 GGTGGTGGACTTGATTTTATGACTAAAATCACTCATGTACAAATGCAGG  
 TGTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTTGAAATTTTC  
 TAATTCCTTACCGTGAATTACCTGTGGGGATTATTAGTAAAGTAGATGGC  
 GAGCGTATAAAAAATACCTTCAAGTCAGTTAACATTTAACCCAGAGTTTGA  
 AGTAGTTGATAGCAAGGTCGTTAATCGTATGCTGGAACAAATCAAGTTGGG  
 GCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTTT  
 GAAATTTATTTCTCAACCTATAATAATCAATACCAAAACATGCTCGGTAC  
 AAGTATGGCTTACCACATGTTGCAGGATTATGACAATGCTTCAAAGTC  
 ATTTGGCTGAGAATATAAAGGGATGAATTTAGATTCTAAAAAATTGCTA  
 GAATTTGCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTGA  
 AGAGGATAAGGCGCTTTTATTCACCAAGTCAGCAAGGTCAGGTTAGTTG  
 ATGCTGAAAAAGCTATCCAAAGCTCAATATATATTTACTGGAACGATGGC  
 AAAGCTAAAAATTAATCTCAACGAAATGGGAGATAAATTTGATATCACAGT  
 TACAATTCATAAATCTGTAGAAGGTGTCAAGAAATGTATTATCAAGCTA  
 ATGTAGCAACAGAACAGTAAATAAAGGTAAATTTGCCCTTAAACCAAA  
 GCCTTGCTAGATACTAATTTGGCAGAAAGTAATTTCTCGTGATAAAGAAC  
 ACAAGTTTCGATTACTATTGATGCTAGTCAATTTAGTCAGAAATTAAGAG  
 AACAGATGGCAAAATGGTTATTTCTTGAAGGTTTGTACGTTTAAAGAA  
 GCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTAA  
 TGGTATTTTGGCACTTACAAGCACTTGAACACCCGATTATAAGACGC  
 TTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAACCTATAAAGAC  
 CAATTTGAGTACAATGAATCAGCTCCTTTTGAAGCAACAACTATATGCT  
 CTGTTTAAACAAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAATG  
 GTGGGGAGTTAGAAATAGCACCCGAGAGTCCAAAAAGAAATTTATTTAGGA  
 ACTTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTGGAAGAGA  
 TGCAGGGAATAATCCATATTTTGCCTTTCTCAAAATAAGATGGAATA  
 GGCACGAATCACTCCCGAGCAACTTCTTAAAGAAATGTTAAGGATATT  
 TCTGCTCAAGTTCTAGATCAAAATGGAATGTTATTTGGCAAGTAAGGT  
 TTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAGTGATG  
 GTCAATTATCGTATGGATGCTCTTCAAGTGGAGTGGTTTAGATAAGGATGGC  
 AAAGTTGTAGCAGATGGTTTATATCTATCGCTTACGTTACACACCACT  
 AGCAGAAGGAGCAAAATAGTCAGGAGTCAGACTTAAAGTACAAGTAAGTA  
 CTAAGTCACCAAAATCTTCTTACGAGCTCAGTTTGATGAACTAATCGA  
 ACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTACATATCG  
 TTTACAATTAGTTTATCTCATGTTGTAAAGATGAAGAAATATGGGGATG  
 AGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAGTGACACTT  
 CCTAAAAACGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCCCTAAGGC  
 CTGTGACACTTGTGTGAAGATAAAGCTGGTAATTTGCGCAACGGTAAAT  
 TGTCTGATCTCTGAATAAGGCAGTAGTATCAGAGAAAGAAACGCTATA  
 GTAATTTCTAACAGTTTCAAAATATTTTGATAACTTGAAGAAAGAACCTAT  
 GTTTATTTCTAAAAAGAAAAAGTAGTAAACAAGAATCTAGAAGAAATAA  
 TATTAGTTAAGCCGCAAACTACAGTTACTACTCAATCATTGTCTAAAGAA  
 ATAACATAATCAGGAAATGAGAAAGTCTCACTTCTACAAACAATAATAG  
 TAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGATTTCTGTTA  
 ACCATACC

PRETTY of: /biotmp/msa183564.2{\*} May 13, 2003 03:28 ...

	1		50
msa183564.2{147_COH1}	-----	-----	-----
msa183564.2{147_M732}	-----	-----	-----
msa183564.2{147_M781}	-----	-----	-----
msa183564.2{147_2603}	gtggataaac	atcactcaaa	aaaggctatt
msa183564.2{147_JM9130013}	-----	-----	-----
msa183564.2{147_18RS21}	-----	-----	-----
msa183564.2{147_090}	-----	-----	-----
msa183564.2{147_CJB110}	-----	-----	-----
msa183564.2{147_A909}	-----	-----	-----
msa183564.2{147_H36B}	-----	-----	-----
msa183564.2{147_1169NT}	-----	-----	-----
Consensus	*****	*****	*****

  

	51		100
msa183564.2{147_COH1}	-----	-----	GAGGAGCAAG
msa183564.2{147_M732}	-----	-----	GAGGAGCAAG
msa183564.2{147_M781}	-----	-----	GAGGAGCAAG
msa183564.2{147_2603}	aactagtatt	ttattaatgc	atagcaatca
msa183564.2{147_JM9130013}	-----	-----	agtgatgca
msa183564.2{147_18RS21}	-----	-----	GAGGAGCAAG
msa183564.2{147_090}	-----	-----	GAGGAGCAAG
msa183564.2{147_CJB110}	-----	-----	GAGGAGCAAG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_A909}	-----	-----	-----	-----	GAGGAGCAAG
msa183564.2{147_H36B}	-----	-----	-----	-----	GAGGAGCAAG
msa183564.2{147_1169NT}	-----	-----	-----	-----	GAGGAGCAAG
Consensus	*****	*****	*****	*****	*****
101					
msa183564.2{147_COH1}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_M732}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_M781}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_2603}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_JM9130013}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_18RS21}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_090}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_CJB110}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_A909}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_H36B}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_1169NT}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
Consensus	*****	*****	*****	*****	*****
151					
msa183564.2{147_COH1}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAACAT	CTGTAAcAgC
msa183564.2{147_M732}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAACAT	CTGTAAcAgC
msa183564.2{147_M781}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAACAT	CTGTAAcAgC
msa183564.2{147_2603}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAACAT	CTGTAAcAgC
msa183564.2{147_JM9130013}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAACAT	CTGTAAcAgC
msa183564.2{147_18RS21}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAACAT	CTGTAAcAgC
msa183564.2{147_090}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAACAT	CTGTAAcAgC
msa183564.2{147_CJB110}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAACAT	CTGTAAcAgC
msa183564.2{147_A909}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAACAT	CTGTAAcAgC
msa183564.2{147_H36B}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAACAT	CTGTAAcAgC
msa183564.2{147_1169NT}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAACAT	CTGTAAcAgC
Consensus	*****	*****	*****	*****	*****
201					
msa183564.2{147_COH1}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_M732}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_M781}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_2603}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_JM9130013}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_18RS21}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_090}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_CJB110}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_A909}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_H36B}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_1169NT}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
Consensus	*****	*****	*****	*****	*****
251					
msa183564.2{147_COH1}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_M732}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_M781}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_2603}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_JM9130013}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_18RS21}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_090}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_CJB110}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_A909}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_H36B}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_1169NT}	ATGACAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
Consensus	*****	*****	*****	*****	*****
301					
msa183564.2{147_COH1}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_M732}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_M781}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_2603}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_JM9130013}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_18RS21}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_090}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_CJB110}	ACGTCTAATw	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_A909}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_H36B}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_1169NT}	ACGTCTAATA	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
Consensus	*****	*****	*****	*****	*****
351					
msa183564.2{147_COH1}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG
msa183564.2{147_M732}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG
msa183564.2{147_M781}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG
msa183564.2{147_2603}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG
msa183564.2{147_JM9130013}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG
msa183564.2{147_18RS21}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG
msa183564.2{147_090}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_CJB110}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAATGCT	TCAACTGCAA	
msa183564.2{147_A909}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAATGCT	TCAACTGCAA	
msa183564.2{147_H36B}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAATGCT	TCAACTGCAA	
msa183564.2{147_1169NT}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAATGCT	TCAACTGCAA	
Consensus	*****	*****	*****	*****	*****	
msa183564.2{147_COH1}	401	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAGCAAG
msa183564.2{147_M732}	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAGCAAG	
msa183564.2{147_M781}	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAGCAAG	
msa183564.2{147_2603}	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAGCAAG	
msa183564.2{147_JM9130013}	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAGCAAG	
msa183564.2{147_18RS21}	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAGCAAG	
msa183564.2{147_090}	TAGCACAGAA	AGTTCCTCTCA	GCGtATGAAG	AGGTGAAGtC	AgAAAGCAAG	
msa183564.2{147_CJB110}	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAGCAAG	
msa183564.2{147_A909}	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAGCAAG	
msa183564.2{147_H36B}	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAGCAAG	
msa183564.2{147_1169NT}	TAGCACAGAA	AGTTCCTCTCA	GCaTATGAAG	AGGTGAAGtC	AaAAAGCAAG	
Consensus	*****	*****	**-----	*****	*-----*	
msa183564.2{147_COH1}	451	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_M732}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc	
msa183564.2{147_M781}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc	
msa183564.2{147_2603}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc	
msa183564.2{147_JM9130013}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc	
msa183564.2{147_18RS21}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc	
msa183564.2{147_090}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc	
msa183564.2{147_CJB110}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc	
msa183564.2{147_A909}	TCATCaCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc	
msa183564.2{147_H36B}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc	
msa183564.2{147_1169NT}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc	
Consensus	*****	*****	*****	*****	*****	*-----*
msa183564.2{147_COH1}	501	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG
msa183564.2{147_M732}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
msa183564.2{147_M781}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
msa183564.2{147_2603}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
msa183564.2{147_JM9130013}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
msa183564.2{147_18RS21}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
msa183564.2{147_090}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
msa183564.2{147_CJB110}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
msa183564.2{147_A909}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
msa183564.2{147_H36B}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
msa183564.2{147_1169NT}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG	
Consensus	*****	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	551	ATATTAAACCA	TGATATTTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC
msa183564.2{147_M732}	ATATTAAACCA	TGATATTTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
msa183564.2{147_M781}	ATATTAAACCA	TGATATTTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
msa183564.2{147_2603}	ATATTAAACCA	TGATATTTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
msa183564.2{147_JM9130013}	ATATTAAACCA	TGATATTTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
msa183564.2{147_18RS21}	ATATTAAACCA	TGATATTTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
msa183564.2{147_090}	ATATTAAACCA	TGATATTTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
msa183564.2{147_CJB110}	ATATTAAACCA	TGATATTTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
msa183564.2{147_A909}	ATATTAAACCA	TGATATTTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
msa183564.2{147_H36B}	ATATTAAACCA	TGATATTTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
msa183564.2{147_1169NT}	ATATTAAACCA	TGATATTTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC	
Consensus	*****	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	601	AGCTTTAAAA	cTAAggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_M732}	AGCTTTAAAA	cTAAggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT	
msa183564.2{147_M781}	AGCTTTAAAA	cTAAggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT	
msa183564.2{147_2603}	AGCTTTAAAA	cTAAgaCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT	
msa183564.2{147_JM9130013}	AGCTTTAAAA	cTAAgaCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT	
msa183564.2{147_18RS21}	AGCTTTAAAA	cTAaGaCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT	
msa183564.2{147_090}	AGCTTTAAAA	cTAAagCAGA	ATTcGAGGAA	TTAAAAGCAA	AACATAATAT	
msa183564.2{147_CJB110}	AGCTTTAAAA	cTAAagCAGA	ATTcGAGGAA	TTAAAAGCAA	AACATAATAT	
msa183564.2{147_A909}	AGCTTTAAAA	cTAAggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT	
msa183564.2{147_H36B}	AGCTTTAAAA	cTAAggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT	
msa183564.2{147_1169NT}	AGCTTTAAAA	aTAAggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT	
Consensus	*****	-***-****	***-*****	*****	*****	*****
msa183564.2{147_COH1}	651	CACCTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_M732}	CACCTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG	
msa183564.2{147_M781}	CACCTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG	
msa183564.2{147_2603}	CACCTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG	
msa183564.2{147_JM9130013}	CACCTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG	
msa183564.2{147_18RS21}	CACCTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG	

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_090}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_CJB110}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_A909}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_H36B}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_1169NT}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_M732}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_M781}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_2603}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_JM9130013}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_18RS21}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_090}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_CJB110}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_A909}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_H36B}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_1169NT}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_M732}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_M781}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_2603}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_JM9130013}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_18RS21}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_090}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_CJB110}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_A909}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_H36B}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
msa183564.2{147_1169NT}	TATGGGTCAG	AAGCAAAGAA	TATTTtGCAT	GGTACACACG	TTGCTGGTAT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_M732}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_M781}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_2603}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_JM9130013}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_18RS21}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_090}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_CJB110}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_A909}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_H36B}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
msa183564.2{147_1169NT}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATaGTCCT	CTTTTAGAAG
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_M732}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_M781}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_2603}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_JM9130013}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_18RS21}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_090}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_CJB110}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_A909}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_H36B}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_1169NT}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	GATTTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	tAGACGCTGT
msa183564.2{147_M732}	GATTTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	tAGACGCTGT
msa183564.2{147_M781}	GATTTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	tAGACGCTGT
msa183564.2{147_2603}	GATTTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_JM9130013}	GATTTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_18RS21}	GATTTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_090}	GATTTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_CJB110}	GATTTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_A909}	GATTTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_H36B}	GATTTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_1169NT}	GATTTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	ccTgGGAAAA	ACgGcTGATT
msa183564.2{147_M732}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	ccTgGGAAAA	ACgGcTGATT
msa183564.2{147_M781}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	ccTgGGAAAA	ACgGcTGATT
msa183564.2{147_2603}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	taTtGGAAAA	ACaGcTGATT
msa183564.2{147_JM9130013}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	taTtGGAAAA	ACaGcTGATT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_18RS21}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	taTtGGAAAA	ACaGcTGATT
msa183564.2{147_090}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	ccTtGGAAAA	ACaGcAGATT
msa183564.2{147_CJB110}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	ccTtGGAAAA	ACaGcAGATT
msa183564.2{147_A909}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	ccTtGGAAAA	ACaGcAGATT
msa183564.2{147_H36B}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	ccTtGGAAAA	ACaGcAGATT
msa183564.2{147_1169NT}	TAATCTAGGA	GCTAAAACGA	TAAATATGAG	taTtGGAAAA	ACaGcTGATT
Consensus	*****	**-----*	*****	--*-----*	**--*-----*
msa183564.2{147_COH1}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_M732}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_M781}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_2603}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_JM9130013}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_18RS21}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_090}	CTTTAATTGC	aCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_CJB110}	CTTTAATTGC	aCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_A909}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_H36B}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_1169NT}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
Consensus	*****	-----*	*****	*****	*****
msa183564.2{147_COH1}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGCG
msa183564.2{147_M732}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGCG
msa183564.2{147_M781}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGCG
msa183564.2{147_2603}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTGCG
msa183564.2{147_JM9130013}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTGCG
msa183564.2{147_18RS21}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTGCG
msa183564.2{147_090}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGCG
msa183564.2{147_CJB110}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGCG
msa183564.2{147_A909}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGCG
msa183564.2{147_H36B}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGCG
msa183564.2{147_1169NT}	GAGAAGGGCG	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTGCG
Consensus	*****	*****	*****	*****	*-----*
msa183564.2{147_COH1}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_M732}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_M781}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_2603}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_JM9130013}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_18RS21}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_090}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_CJB110}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_A909}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_H36B}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_1169NT}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_M732}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_M781}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_2603}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_JM9130013}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_18RS21}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_090}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_CJB110}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_A909}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_H36B}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_1169NT}	ATAGTCCAGC	TATTTCTGAA	GATACITTGA	GTGTTGCTAG	CTATGAATCA
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_M732}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_M781}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_2603}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_JM9130013}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_18RS21}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_090}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_CJB110}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_A909}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_H36B}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_1169NT}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_M732}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_M781}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_2603}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_JM9130013}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_18RS21}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_090}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_CJB110}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_A909}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_H36B}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_1169NT}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_M732}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_M781}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_2603}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_JM9130013}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_18RS21}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_090}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_CJB110}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_A909}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_H36B}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
msa183564.2{147_1169NT}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGACTTTG	AAGGTAAGGA
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_M732}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_M781}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_2603}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_JM9130013}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_18RS21}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_090}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_CJB110}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_A909}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_H36B}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_1169NT}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_M732}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_M781}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_2603}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_JM9130013}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_18RS21}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_090}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_CJB110}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_A909}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_H36B}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
msa183564.2{147_1169NT}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTATT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_M732}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_M781}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_2603}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_JM9130013}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_18RS21}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_090}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_CJB110}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_A909}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_H36B}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_1169NT}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_M732}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_M781}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_2603}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_JM9130013}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_18RS21}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_090}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_CJB110}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_A909}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_H36B}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_1169NT}	ACCTGTGGGG	GTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	CAAGTCAGTT	AACATTAAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_M732}	CAAGTCAGTT	AACATTAAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_M781}	CAAGTCAGTT	AACATTAAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT



Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_2603}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_JM9130013}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_18RS21}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_090}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_CJB110}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_A909}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_H36B}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_1169NT}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
Consensus	*****	*****	*****	*****	*****
1601	1650				
msa183564.2{147_COH1}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_M732}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_M781}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_2603}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_JM9130013}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_18RS21}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_090}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_CJB110}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_A909}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_H36B}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_1169NT}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
Consensus	*****	*****	*****	*****	*****
1651	1700				
msa183564.2{147_COH1}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_M732}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_M781}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_2603}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_JM9130013}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_18RS21}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_090}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_CJB110}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_A909}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_H36B}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_1169NT}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
Consensus	*****	*****	*****	*****	*****
1701	1750				
msa183564.2{147_COH1}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_M732}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_M781}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_2603}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_JM9130013}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_18RS21}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_090}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_CJB110}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_A909}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_H36B}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_1169NT}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
Consensus	*****	*****	*****	*****	*****
1751	1800				
msa183564.2{147_COH1}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_M732}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_M781}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_2603}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_JM9130013}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_18RS21}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_090}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_CJB110}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_A909}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_H36B}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_1169NT}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
Consensus	*****	*****	*****	*****	*****
1801	1850				
msa183564.2{147_COH1}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_M732}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_M781}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_2603}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_JM9130013}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_18RS21}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_090}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_CJB110}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_A909}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_H36B}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_1169NT}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
Consensus	*****	*****	*****	*****	*****
1851	1900				
msa183564.2{147_COH1}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTAT
msa183564.2{147_M732}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTAT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_M781}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_2603}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_JM9130013}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_18RS21}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_090}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_CJB110}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_A909}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_H36B}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_1169NT}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
Consensus	*****	*****	*****	*****	*****
1901					
msa183564.2{147_COH1}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_M732}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_M781}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_2603}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_JM9130013}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_18RS21}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_090}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_CJB110}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_A909}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_H36B}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_1169NT}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
Consensus	*****	*****	*****	*****	*****
1951					
msa183564.2{147_COH1}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_M732}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_M781}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_2603}	AGCTCAATAT	TATaTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_JM9130013}	AGCTCAATAT	TATaTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_18RS21}	AGCTCAATAT	TATaTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_090}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_CJB110}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_A909}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_H36B}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_1169NT}	AGCTCAATAT	TATgTTACTG	GAAACGATGG	CAAAGtTAAA	ATTAATCTCA
Consensus	*****	***-*****	*****	*****-*****	*****
2001					
msa183564.2{147_COH1}	AACGAgagGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_M732}	AACGAgagGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_M781}	AACGAgagGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_2603}	AACGAatGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_JM9130013}	AACGAatGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_18RS21}	AACGAatGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_090}	AACGAggGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_CJB110}	AACGAggGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_A909}	AACGAggGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_H36B}	AACGAggGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_1169NT}	AACGAggGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
Consensus	*****-****	*****	*****	*****	*****
2051					
msa183564.2{147_COH1}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_M732}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_M781}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_2603}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_JM9130013}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_18RS21}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_090}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_CJB110}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_A909}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_H36B}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_1169NT}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
Consensus	*****	*****	*****	*****	*****
2101					
msa183564.2{147_COH1}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_M732}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_M781}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_2603}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_JM9130013}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_18RS21}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_090}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_CJB110}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_A909}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_H36B}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_1169NT}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
Consensus	*****	*****	*****	*****	*****
2151					
msa183564.2{147_COH1}	GGCAGAAAGT	AATTCCTCGT	GATAAAGAAA	CACAAGTTCG	ATTACTATT
2200					

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_M732}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
msa183564.2{147_M781}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
msa183564.2{147_2603}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
msa183564.2{147_JM9130013}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
msa183564.2{147_18RS21}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
msa183564.2{147_090}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
msa183564.2{147_CJB110}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
msa183564.2{147_A909}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
msa183564.2{147_H36B}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
msa183564.2{147_1169NT}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTTCG ATTTACTATT	
Consensus	*****	*****
msa183564.2{147_COH1}	2201 GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	2250
msa183564.2{147_M732}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_M781}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_2603}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_JM9130013}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_18RS21}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_090}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_CJB110}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_A909}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_H36B}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_1169NT}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
Consensus	*****	*****
msa183564.2{147_COH1}	2251 TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	2300
msa183564.2{147_M732}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_M781}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_2603}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_JM9130013}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_18RS21}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_090}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_CJB110}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_A909}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_H36B}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_1169NT}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
Consensus	*****	*****
msa183564.2{147_COH1}	2301 AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	2350
msa183564.2{147_M732}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_M781}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_2603}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_JM9130013}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_18RS21}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_090}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_CJB110}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_A909}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_H36B}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_1169NT}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
Consensus	*****	*****
msa183564.2{147_COH1}	2351 CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	2400
msa183564.2{147_M732}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_M781}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_2603}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_JM9130013}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_18RS21}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_090}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_CJB110}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_A909}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_H36B}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_1169NT}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
Consensus	*****	*****
msa183564.2{147_COH1}	2401 CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	2450
msa183564.2{147_M732}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_M781}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_2603}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_JM9130013}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_18RS21}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_090}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_CJB110}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_A909}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_H36B}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_1169NT}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
Consensus	*****	*****

2451

2500

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_COH1}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_M732}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_M781}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_2603}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_JM9130013}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_18RS21}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_090}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_CJB110}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_A909}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_H36B}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_1169NT}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
Consensus	*****	*****	*****	*****	*****
2501					
msa183564.2{147_COH1}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_M732}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_M781}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_2603}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_JM9130013}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_18RS21}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_090}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_CJB110}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_A909}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_H36B}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_1169NT}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
Consensus	*****	*****	*****	*****	*****
2551					
msa183564.2{147_COH1}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_M732}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_M781}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_2603}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_JM9130013}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_18RS21}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_090}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_CJB110}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_A909}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_H36B}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_1169NT}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
Consensus	*****	*****	*****	*****	*****
2601					
msa183564.2{147_COH1}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_M732}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_M781}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_2603}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_JM9130013}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_18RS21}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_090}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_CJB110}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_A909}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_H36B}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_1169NT}	AGGATAAAAC	AATTCATCTT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
Consensus	*****	*****	*****	*****	*****
2651					
msa183564.2{147_COH1}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_M732}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_M781}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_2603}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_JM9130013}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_18RS21}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_090}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_CJB110}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_A909}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_H36B}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_1169NT}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
Consensus	*****	*****	*****	*****	*****
2701					
msa183564.2{147_COH1}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_M732}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_M781}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_2603}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_JM9130013}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_18RS21}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_090}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_CJB110}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_A909}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_H36B}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_1169NT}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
Consensus	*****	*****	*****	*****	*****
2750					

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

		2751			2800
msa183564.2{147_COH1}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_M732}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_M781}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_2603}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_JM9130013}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_18RS21}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_090}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_CJB110}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_A909}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_H36B}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
msa183564.2{147_1169NT}	AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA
Consensus	*****	*****	*****	*****	*****
		2801			2850
msa183564.2{147_COH1}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_M732}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_M781}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_2603}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_JM9130013}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_18RS21}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_090}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_CJB110}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_A909}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_H36B}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
msa183564.2{147_1169NT}	AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC
Consensus	*****	*****	***-*****	*****	*****
		2851			2900
msa183564.2{147_COH1}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_M732}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_M781}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_2603}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_JM9130013}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_18RS21}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_090}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_CJB110}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_A909}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_H36B}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
msa183564.2{147_1169NT}	tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT
Consensus	--*****	*****	*****	*****	*****
		2901			2950
msa183564.2{147_COH1}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_M732}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_M781}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_2603}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_JM9130013}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_18RS21}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_090}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_CJB110}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_A909}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_H36B}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
msa183564.2{147_1169NT}	TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT
Consensus	*****	***-*****	*****	*****	*****
		2951			3000
msa183564.2{147_COH1}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_M732}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_M781}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_2603}	CAGGAGTCAG	ACTTTAAAGT	aCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_JM9130013}	CAGGAGTCAG	ACTTTAAAGT	aCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_18RS21}	CAGGAGTCAG	ACTTTAAAGT	aCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_090}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_CJB110}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_A909}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_H36B}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
msa183564.2{147_1169NT}	CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTTCC
Consensus	*****	*****	-*****	*****	*****
		3001			3050
msa183564.2{147_COH1}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_M732}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_M781}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_2603}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_JM9130013}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_18RS21}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_090}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_CJB110}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_A909}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_H36B}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
msa183564.2{147_1169NT}	TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAAGC	TTAGCCATGC
Consensus	**--*****	*****	*****	*****	*****

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

	3051		3100
msa183564.2{147_COH1}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTtTTATCT		
msa183564.2{147_M732}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTtTTATCT		
msa183564.2{147_M781}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTtTTATCT		
msa183564.2{147_2603}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTtTTATCT		
msa183564.2{147_JM9130013}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTtTTATCT		
msa183564.2{147_18RS21}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTtTTATCT		
msa183564.2{147_090}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTtTTATCT		
msa183564.2{147_CJB110}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTtTACAATT AGTtTTATCT		
msa183564.2{147_A909}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTcTACAATT AGTtTTATCT		
msa183564.2{147_H36B}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTcTACAATT AGTtTTATCT		
msa183564.2{147_1169NT}	CTAAGGaAAG TAGTTATGTT CCTAcATATC GTcTACAATT AGTtTTATCT		
Consensus	*****-****	*****-****	*****-****
	3101		3150
msa183564.2{147_COH1}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_M732}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_M781}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_2603}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_JM9130013}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_18RS21}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_090}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_CJB110}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_A909}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_H36B}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
msa183564.2{147_1169NT}	CATGTTGTAA AAGATGAAGA ATATGGgGAT GAGACTTCTT AccATTATTT		
Consensus	*****-****	*****-****	*****-****
	3151		3200
msa183564.2{147_COH1}	CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAAGATAG		
msa183564.2{147_M732}	CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAAGATAG		
msa183564.2{147_M781}	CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAAGATAG		
msa183564.2{147_2603}	CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAAGATAG		
msa183564.2{147_JM9130013}	CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAAGATAG		
msa183564.2{147_18RS21}	CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAAGATAG		
msa183564.2{147_090}	CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAAGATAG		
msa183564.2{147_CJB110}	CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACg GTTAAAGATAG		
msa183564.2{147_A909}	CCATATAGAT CgAGAAGGTA AAGtGACACT TCCTAAAACa GTTAAAGATAG		
msa183564.2{147_H36B}	CCATATAGAT CaAGAAGGTA AAGtGACACT TCCTAAAACa GTTAAAGATAG		
msa183564.2{147_1169NT}	CCATATAGAT CaAGAAGGTA AAGcGACACT TCCTAAAACg GTTAAAGATAG		
Consensus	*****-****	*****-****	*****-****
	3201		3250
msa183564.2{147_COH1}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGg CCTTGACACT TGTGTGGAA		
msa183564.2{147_M732}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGg CCTTGACACT TGTGTGGAA		
msa183564.2{147_M781}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGg CCTTGACACT TGTGTGGAA		
msa183564.2{147_2603}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGg CCTTGACACT TGTGTGGAA		
msa183564.2{147_JM9130013}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGg CCTTGACACT TGTGTGGAA		
msa183564.2{147_18RS21}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGg CCTTGACACT TGTGTGGAA		
msa183564.2{147_090}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGg CCTTGACACT TGTGTGGAA		
msa183564.2{147_CJB110}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGg CCTTGACACT TGTGTGGAA		
msa183564.2{147_A909}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGa CCTTGACACT TGTGTGGAA		
msa183564.2{147_H36B}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGa CCTTGACACT TGTGTGGAA		
msa183564.2{147_1169NT}	GAGAGAGTGA GGTTCGcGTA GACCCTAAGg CCTTGACACT TGTGTGGAA		
Consensus	*****-****	*****-****	*****-****
	3251		3300
msa183564.2{147_COH1}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_M732}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_M781}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_2603}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_JM9130013}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_18RS21}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_090}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_CJB110}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_A909}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_H36B}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
msa183564.2{147_1169NT}	GATAAAGCTG GTAATTTtGC AACGGTAAAA TTGTCTGAcC TCTTGAATAA		
Consensus	*****-****	*****-****	*****-****
	3301		3350
msa183564.2{147_COH1}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA		
msa183564.2{147_M732}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA		
msa183564.2{147_M781}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA		
msa183564.2{147_2603}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA		
msa183564.2{147_JM9130013}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA		
msa183564.2{147_18RS21}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA		
msa183564.2{147_090}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA		
msa183564.2{147_CJB110}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA		
msa183564.2{147_A909}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA		
msa183564.2{147_H36B}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA		
msa183564.2{147_1169NT}	GGCAGTAGTA TCAGAGAAAG AAAACGCTAT AGTAATTTCT AACAgTTTCA		

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

Consensus	*****	*****	*****	*****	*****
	3351				3400
msa183564.2{147_COH1}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_M732}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_M781}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_2603}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_JM9130013}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_18RS21}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_090}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_CJB110}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_A909}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_H36B}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_1169NT}	AATATTTTGA	TAACCTGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
Consensus	*****	*****	*****	*****	*****
	3401				3450
msa183564.2{147_COH1}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_M732}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_M781}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_2603}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_JM9130013}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_18RS21}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_090}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_CJB110}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_A909}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_H36B}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_1169NT}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
Consensus	*****	*****	*****	*****	*****
	3451				3500
msa183564.2{147_COH1}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_M732}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_M781}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_2603}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_JM9130013}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_18RS21}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_090}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_CJB110}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_A909}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_H36B}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_1169NT}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
Consensus	*****	*****	*****	*****	*****
	3501				3550
msa183564.2{147_COH1}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_M732}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_M781}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_2603}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_JM9130013}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_18RS21}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_090}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_CJB110}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_A909}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_H36B}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
msa183564.2{147_1169NT}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaAGATC
Consensus	*****	*****	*****	*****	*****
	3551				3600
msa183564.2{147_COH1}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_M732}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_M781}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_2603}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_JM9130013}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_18RS21}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_090}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_CJB110}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_A909}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_H36B}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_1169NT}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
Consensus	*****	*****	*****	*****	*****
	3601				3650
msa183564.2{147_COH1}	-----	-----	-----	-----	-----
msa183564.2{147_M732}	-----	-----	-----	-----	-----
msa183564.2{147_M781}	-----	-----	-----	-----	-----
msa183564.2{147_2603}	atcagataga	gcaacgaatg	gtctatttgg	tggtactttg	gcattgttat
msa183564.2{147_JM9130013}	-----	-----	-----	-----	-----
msa183564.2{147_18RS21}	-----	-----	-----	-----	-----
msa183564.2{147_090}	-----	-----	-----	-----	-----
msa183564.2{147_CJB110}	-----	-----	-----	-----	-----
msa183564.2{147_A909}	-----	-----	-----	-----	-----
msa183564.2{147_H36B}	-----	-----	-----	-----	-----

**Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)**

msa183564.2{147_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	3651				3700
msa183564.2{147_COH1}	-----	-----	-----	-----	-----
msa183564.2{147_M732}	-----	-----	-----	-----	-----
msa183564.2{147_M781}	-----	-----	-----	-----	-----
msa183564.2{147_2603}	ctagtttact	tctttatttg	aaacccaaaa	agactaaaaa	taatagtaaa
msa183564.2{147_JM9130013}	-----	-----	-----	-----	-----
msa183564.2{147_18RS21}	-----	-----	-----	-----	-----
msa183564.2{147_090}	-----	-----	-----	-----	-----
msa183564.2{147_CJB110}	-----	-----	-----	-----	-----
msa183564.2{147_A909}	-----	-----	-----	-----	-----
msa183564.2{147_H36B}	-----	-----	-----	-----	-----
msa183564.2{147_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****

**SEQ ID NO. 4412****STRAIN 2603**

VDKHHSSKAILKLTITLTTSSILLMHSNQVNAEEQELKNQEQSPVIANVAQQPSPSVTTNTIV  
 EKTSTVTAASANTAKEMGDTSVKNDKTEDELEELSKNLDTSNLGADLEEEYPSKPKETTIN  
 NKESNVVTNASTAIAQKVPSAYEEVKEPKSSSLAVLDTSKITKLQAITQRGKGNVVAIID  
 TGFDINHDI FRLDSPKDDKHSFKTKTEFEELKAKHNITYGKWNVDKI VFAHNYANNNTETV  
 ADIAAAMKDGYSSEAKNISHGTHVAGIFVGNKRPAINGLLLEGAAPNAQVLLMRIPDKI  
 DSDKFGEAYAKAITDAVNLGAKTINMSIGKTADSLIALNDKVKLALKLASEKGVAVVVAA  
 GNEGAFGMDYSKPLSTNPDYGTVNSPAISEDTLSVASYESLKTISEVVETTIEGKLVKLP  
 IVTSKPFKDGKAYDVVYANYGAKKDFEGKDFGKIALIERGGGLDFMTKI THATNAGVVG  
 IVIDQEKGRGNFLIPYRELPGVIISKVDGERIKNTSSQLTFNQSFVVDSSQGNRMLEQ  
 SSWGVTABGAIKPDVTASGFYIYSTYNNQYQTMSTGSMASPHVAGLMTMLQSHLAEKYK  
 GMLNLSKLLLELSKNILMSSATALYSEEDKAFYSPRQQGAGVVDAAEKAIQAQYYITGNDG  
 KAKINLKRMDGDFDITVTIHKLVGKELYQANVATEQVNGKGFALKPQALLDNTWQKV  
 ILRDKETQVRFTIDASQFSQKLKEQMANGYFLEGFVRFEAKDSNQELMSIPFVGFGNDF  
 ANLQALETPITYKTLKGSFYKPNDDTHKDQLEYNESAPFESNNYTALLTQSASWGYVDY  
 VKNGGELELAPESPKRIILGTFFENKVEDKTIHLLERDAANNPYFAISPNDGNGRDEITPQ  
 ATFLRNVDKISAQVLDQNGNVIWQSKVLPSYRKNFHNPKQSDGHYRMDALQWSGLDKDG  
 KVVADGFYTYRLRYTPVAEGANSQESDFKVQVSTKSPNLPRAQFDETNRTLSLAMPKES  
 SYVPTYRLQLVLSHVVKDEEYGDTSYHYFHIHQEGKVTLPKTVKIGESEVAVDPKALTL  
 VVEDKAGNFATVKLSDDLKAVVSEKENAIVISNSFKYFDNLKKEPMFISKKEKVVNKNL  
 BEIILVKPQTITVTQSLSKETKSGNEKVLSTNNNSSRVAKII SPKHNGDSVNHTLPST  
 SDRATNGLVGTLALLSSLLLYLKPKTKNNKS

**SEQ ID NO. 4413****STRAIN A909**

EEQELKNQEQSPVIANVAQQPSPSVTTNTVEKTSVTSASANTAKEMGDTSVKNDKTEDE  
 LLEELSKNLDTSNLGADLEEEYPSKPKETTNNKESNVVTNASTAIAQKVPSAYEEVKEPKES  
 SSLAVLDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE  
 LKAKHNITYGKWNVDKI VFAHNYANNNTETVADIAAAMKDGYSSEAKNISHGTHVAGIFVG  
 NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDFGEAYAKAITDAVNLGAKTINMSLGK  
 TADSLIALNDKVKLALKLASEKGVAVVVAAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
 DTLVASYESLKTISEVVETTIEGKLVKLP IVTSKPFKDGKAYDVVYANYGAKKRL.R.G  
 L.R.DCIN.AWWT.FYD.NHSCYKCRCCWYRYF.RSRKTWKFSNSLP.ITCGGY..SRW  
 RAYKKYFKSVNT.PEF.SS..PRWQSYAGTIKLRDS.RSNQA.CNSFWL.NLFFNL..S  
 IPNNVWYKGYFTTCCIRINDNASKSFG.EI.RDEFRF.KIARIV.KHPHELSNSII..RG.  
 GVLFTTSARCRC.S.C.KSYPSSILCYWKRWS.N.SQTSGR.I.YHSYNS.TCRRCORIV  
 LSS.CSNRTSK.R.ICP.TTSLARY.LAESNSS..RNTSSIIY.F.SI.SEIKRTDGKWL  
 FLRRFCTF.RSQQ..SGVNEYSFCRI.W.FCELTST.NTDL.DAF.R.FLL.TK.YNS.R  
 PIGVQ.ISSF.KQQLYCLVNTISVLGLC.LCQKWGWVRI STGESKKNYFRNF.E.G.G.N  
 NSSFGKRCSE.SIFCHFSK.RWK.G.NHSPGNFLKCC.GYFCSSSRSKWKCYLAK.GFTI  
 LS.KFP..SKAK.WLSYGCPSVEWFR.GWQSCSRWFLYLSFTLHTSSRRSK.SGVRL.S  
 SSKY.VTKSSFTSSV..N.SNIKLSHA.GK.LCSYISSTISFISCKR.RIWR.DFLPLF  
 PYRSRR.SDTS.NS.DRRE.GCSR.P.DLDTCCGR.SW.FRNGKIV.PLE.GSSIRERKRY  
 SNF.QFQIF..LEKRTYVYF.RRKSSQESRRNSIS.AANYSSYSIIV.RNNSIRK.ESP  
 HFYKQ...QSS.DHIT.T.RGFC.PY

**SEQ ID NO. 4414****STRAIN H36B**

EEQELKNQEQSPVIANVAQQPSPSVTTNTVEKTSVTSASANTAKEMGDTSVKNDKTEDE  
 LLEELSKNLDTSNLGADLEEEYPSKPKETTNNKESNVVTNASTAIAQKVPSAYEEVKEPKES  
 SSLAVLDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE  
 LKAKHNITYGKWNVDKI VFAHNYANNNTETVADIAAAMKDGYSSEAKNISHGTHVAGIFVG  
 NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDFGEAYAKAITDAVNLGAKTINMSLGK  
 TADSLIALNDKVKLALKLASEKGVAVVVAAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
 DTLVASYESLKTISEVVETTIEGKLVKLP IVTSKPFKDGKAYDVVYANYGAKKDFEGK  
 FKGKIALIERGGGLDFMTKI THATNAGVVGIVIFNDQEKGRGNFLIPYRELPGVIISKVDG  
 ERIKNTSSQLTFNQSFVVDSSQGNRMLEQSSWGVTABGAIKPDVTASGFYIYSTYNNQ  
 YQTMSTGSMASPHVAGLMTMLQSHLAEKYKGMNLSKLLLELSKNILMSSATALYSEEDK  
 AFYSPRQQGAGVVDAAEKAIQAQYYITGNDGKAKINLKRVDGKFDITVTIHKLVGKELY  
 YQANVATEQVNGKGFALKPQALLDNTWQKVIILRDKETQVRFTIDSSQFSQKLKEQMANGY  
 FLEGFVRFEAKDSNQELMSIPFVGFGNDFANLQALETPITYKTLKGSFYKPNDDTHKD  
 QLEYNESAPFESNNYTALLTQSASWGYVDYVKNGGELELAPESPKRIILGTFFENKVEDKTI  
 HLLERDAANNPYFAISPNDGNGRDEITPQATFLRNVDKISAQVLDQNGNVIWQSKVLPS  
 YRKNFHNPKQSDGHYRMDALQWSGLDKDGKVVADGFYTYRLRYTPVAEGANSQESDFKV  
 QVSTKSPNLPRAQFDETNRTLSLAMPKESYVPTYRLQLVLSHVVKDEEYGDTSYHYF



**Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)**

HIDQEGKVTLPKTVKIGESEVAVDPKTLTLVVEDKAGNFATVKLSDLLNKAVVSEKENAI  
 VTSNNFKYFDNLKKEPMFI SKKGVVNNKLEBIALVKPQTIVTTQSLSKETQSGNEKVL  
 TSTNNSSSRVAKI ISPKHNGDSVNHT

**SEQ ID NO. 4415****STRAIN 18RS21**

EEQELKNQEQSPVIANVAQOPSPSVTNTVEKTSVTAASASNTAKEMGDTSVKNDKTEDE  
 LLEELSKNLDTSNGLADLEEEYPSKPETTNKESNVVTNASTAIAQKVPSAYEEVKPESK  
 SSLAVLDTSKITKLQATTQRGKGNVVAI IDTGFDINHDI FRLDSPKDDKHSFKTKTEFEE  
 LKAKHNIYTGKWNVDKI VFAHNYANNNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG  
 NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDFGEAYAKA I DAVNLGAKTINMSIGK  
 TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
 DTLSVASYESLKTISEVVETIIEGKLVKLP I VTSKPFDDGKAYDVVYANYGAKKDFEGKD  
 FKGKIALIERGGGLDMTKI THATNAGVVGIV I FNDQEKRGNFILPYRELPVGI ISKVDG  
 BRIKNTSSQLTFNQSFVVDSDQGNRMLEQSSWGVTAEGA IKPDVTAAGFEIYSSYNNQ  
 YQTMSTGSMASPHVAGLMTMLQSHLAEKYKGMNLDSSKLLLELSKNILMSSATALYSEEDK  
 AFYSPRQOQAGVVDAAEKAIQAQYITGNDGKAKINLKRMDGKDFITVTIHLKVEGVKELY  
 YQANVATEQVNVKGFALKPQALLDTNWQKVLIRDKETQVRFT IDASQFSQKLKEQMANGY  
 FLEGGVRFKEAKDSNQLMSI PFVGFNGDFANLQALETP I YKTI SKGSFYYPNDTTHKD  
 QLEYNESAPFESNNY TALLTQSASWGYVDVYKNGGELELAPESPKRI ILGT FENKVEDKT  
 IHLLEDAANNPYFAISPNDGGRDEITPQATFLRNVDI SAQVLDQNGNVIWQSKVLPS  
 YRKNPHNNPKQSDGHRMDALQWGLDKDKGVVADGFYTYRLRYTPVAEGANSQESDFKV  
 QVSTKSPNLPRAQFDETNRTL SLAMPKESYVPTYRLQLVLSHVVDKEEYGDTSYHYF  
 HIDQEGKVTLPKTVKIGESEVAVDPKALTTLVVEDKAGNFATVKLSDLLNKAVVSEKENAI  
 VTSNNFKYFDNLKKEPMFI SKKGVVNNKLEBIALVKPQTIVTTQSLSKETITSGNEKVL  
 TSTNNSSSRVAKI ISPKHNGDSVNHT

**SEQ ID NO. 4416****STRAIN M732**

EEQELKNQEQSPVIANVAQOPSPSVTNI VEKTSVTAASASNTVKEMGDTSVKNDKTEDE  
 LLEELSKNLDTSNGLADLEEEYPSKPETTNKESNVVTNASTAIAQKVPSAYEEVKSEK  
 SSLAVLDTSKITKLQATTQRGKGNVVAI IDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE  
 LKAKHNIYTGKWNVDKI VFAHNYANNNTETVADIAAAMKDGYGSEAKNILHGTHVAGIFVG  
 NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDFGEAYAKA I DAVNLGAKTINMSLGK  
 TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
 DTLSVASYESLKTISEVVETIIEGKLVKLP I VTSKPFDDGKAYDVVYANYGAKKILKVRT  
 LKVRILH. LSVVVDLIL. LKSLMLQMQLLVSLFLT I KKNVEIF. FLT VNYLWGLLVK. MA  
 SV. KILQVS. HLTRVLK. LIAKVAIVCWNQVGA. QLKEQSSLM. QLLALKFILQPI I IN  
 TKQCLVQVWLHMLQD. .QCCKVIWLRNIG. I. ILKNC. NCLKTSS. AQQHYIVKRI  
 RFIHHVSKVQV. LMLKKLSKLNIMLETMAKLLISNEREINLISQLQFINL. KVSKNCI  
 IKLM. QONK. IKVNLPLNHKPC. ILIGRK. FFVKKHKFDLLMLVNLVRN. KNRQWMI  
 S. KVLVVLKPRIVIRS. .VFL. DLMVILRTYKHLKHFIRRFKVVSTINQMIQLIKT  
 NWSTNQMLLLKATTILPC. HNQLGAMLIMSKMVG. N. HRRVQKELF. ELLRIRLRIKQ  
 FIFWKEMQRI I HILPFLQIKMEIGTKSLPRQLS. EMLRIFLLKF. IKMEMLFGKVRFYHL  
 IVKISII IQSKVMVI I VMLFSGVV. IRMAKL. QMVFI LIAVTHQ. QKEQIVRSQTLKF  
 K. VLSHQIFLHLSLMLKLIH. A. PCLRKVVMFLHIVYN. FYLML. KMKNMGMRLLTII S  
 I. IKKVK. HFLKRLR. ERVRLR. TLRP. HLLWKIKLVILQR. NCLTS. IRQ. YQKKTIL.  
 .FLT VSNILIT. RKNLCLFLKKEK. .TRI. KK. H. LSLKLQLLLNHCLLK. LNQEMRKSS  
 LLQTIIVAE. LRSYHLNITGILTI

**SEQ ID NO. 4417****STRAIN COH1**

EEQELKNQEQSPVIANVAQOPSPSVTNI VEKTSVTAASASNTVKEMGDTSVKNDKTEDE  
 LLEELSKNLDTSNGLADLEEEYPSKPETTNKESNVVTNASTAIAQKVPSAYEEVKSEK  
 SSLAVLDTSKITKLQATTQRGKGNVVAI IDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE  
 LKAKHNIYTGKWNVDKI VFAHNYANNNTETVADIAAAMKDGYGSEAKNILHGTHVAGIFVG  
 NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDFGEAYAKA I DAVNLGAKTINMSLGK  
 TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
 DTLSVASYESLKTISEVVETIIEGKLVKLP I VTSKPFDDGKAYDVVYANYGAKKILKVRT  
 LKVRILH. LSVVVDLIL. LKSLMLQMQLLVSLFLT I KKNVEIF. FLT VNYLWGLLVK. MA  
 SV. KILQVS. HLTRVLK. LIAKVAIVCWNQVGA. QLKEQSSLM. QLLALKFILQPI I IN  
 TKQCLVQVWLHMLQD. .QCCKVIWLRNIG. I. ILKNC. NCLKTSS. AQQHYIVKRI  
 RFIHHVSKVQV. LMLKKLSKLNIMLETMAKLLISNEREINLISQLQFINL. KVSKNCI  
 IKLM. QONK. IKVNLPLNHKPC. ILIGRK. FFVKKHKFDLLMLVNLVRN. KNRQWMI  
 S. KVLVVLKPRIVIRS. .VFL. DLMVILRTYKHLKHFIRRFKVVSTINQMIQLIKT  
 NWSTNQMLLLKATTILPC. HNQLGAMLIMSKMVG. N. HRRVQKELF. ELLRIRLRIKQ  
 FIFWKEMQRI I HILPFLQIKMEIGTKSLPRQLS. EMLRIFLLKF. IKMEMLFGKVRFYHL  
 IVKISII IQSKVMVI I VMLFSGVV. IRMAKL. QMVFI LIAVTHQ. QKEQIVRSQTLKF  
 K. VLSHQIFLHLSLMLKLIH. A. PCLRKVVMFLHIVYN. FYLML. KMKNMGMRLLTII S  
 I. IKKVK. HFLKRLR. ERVRLR. TLRP. HLLWKIKLVILQR. NCLTS. IRQ. YQKKTIL.  
 .FLT VSNILIT. RKNLCLFLKKEK. .TRI. KK. H. LSLKLQLLLNHCLLK. LNQEMRKSS  
 LLQTIIVAE. LRSYHLNITGILTI

**SEQ ID NO. 4418****STRAIN M781**

EEQELKNQEQSPVIANVAQOPSPSVTNI VEKTSVTAASASNTVKEMGDTSVKNDKTEDE  
 LLEELSKNLDTSNGLADLEEEYPSKPETTNKESNVVTNASTAIAQKVPSAYEEVKSEK  
 SSLAVLDTSKITKLQATTQRGKGNVVAI IDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE  
 LKAKHNIYTGKWNVDKI VFAHNYANNNTETVADIAAAMKDGYGSEAKNILHGTHVAGIFVG  
 NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDFGEAYAKA I DAVNLGAKTINMSLGK  
 TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
 DTLSVASYESLKTISEVVETIIEGKLVKLP I VTSKPFDDGKAYDVVYANYGAKKILKVRT  
 LKVRILH. LSVVVDLIL. LKSLMLQMQLLVSLFLT I KKNVEIF. FLT VNYLWGLLVK. MA

**Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)**

SV.KILQVS.HLTRVLK.LIAKVAIVCWNQVGA.QLKEQSSLM.QLLALKFILQPIIIN  
TKQCLVQVWLHMLQD..QCCKVILWRNIKG.I.ILKNC.NCLKTSS.AQQOYHIVKRIR  
RFIHHVSKVQV.LMLKKLSKLNIMLLETMAKLKLSNEREINLISQLQFINL.KVSKNCI  
IKLM.QQNK.IKVNPLPLNHKPC.ILIGRK.FFVVKKHKFDLLMLVNLVRN.KNRWQMI  
S.KVLYVLKKPRIVIRS..VPLL.DLMVILRTYKHLKHFIRFLKVVSTINQMIQLIKT  
NWSTMNQLLLKATTILPC.HNQLGAMLIMSKMVGS.N.HRRVQKELF.ELLRIRLRIKQ  
IFPWKEMQRIIHLFPFLQIKMEIGTKSLPRQLS.EMLRIFLLKF.IKMEMFLGKVRFYHL  
IVKISII IQSKVMVIVVMFLFSGVV.IRMAKL.QMVFLIAYVTHQ.QKEQIVRSQTLKF  
K.VLSHQIFLHLSMLKLIH.A.PCLRKVVMLHIVYN.FYLM.L.KMKMGMRLLTIIS  
I.IKKVK.HFLKRLR.ERVRLR.TLRP.HLLWKIKLVILQR.NCLTS.IRQ.YQRKKTIL.  
.FLTVSNILIT.RKNLCLFLKKEK..TRI.KK.H.LSLKLQLLNHCLKK.LNQEMRKSS  
LLQTIIVAE.LRSYHLNITGILLTI

SEQ ID NO. 4419

STRAIN JM9130013

EEQELKNQEQSPVIANVAQQPSPSVTTNTVEKTSVTAASANTAKEMGDTSVKNDKTEDE  
LLEELSKNLDTSNLGADLEEEYPSKPEPTNNKESNVVNTASTAIAQKVPSAYEEVKPESK  
SSLAVFDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI.FRLDSPKDDKHSFKTKTEFEE  
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG  
NSKRPAINGLLLEGAAPNAQVLLMRI.PDKIDSDFGEAYAKAITDAVNLGAKTINMSIGK  
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
DTLSVASYESLKITSEVVETIEGKLVKLP.IVTSKPFDKGKAYDVVYANYGAKKDFEGKD  
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKRGNFILPYRELPGVISKVDG  
ERIKNTSSQLTFNQSFVVDSSQGNRMLEQSSWGVTAEAGIKPDVTASGFEIYSSTYNNQ  
YQTMSTGSMASPHVAGLMTMLQSHLAEKYKGMNLD SKKLELSKNILMSSATALYSEEDK  
AFYSRQGGAGVVDAAEKAIQAQYYITGNDGKAKINLKRMDKFDITVTIHKLVEGVKELY  
YQANVATEQVNGKGFALKPQALLDTNWQKVLIRDKETQVRFTIDASQFSQKLKEQMANGY  
FLEGFVRFEKAKDSNQELMSIPFVGFGNDFANLQALETPITYKLSKGSFYKPNDTTHKD  
QLEYNESAPFESNNYTALLTQASWGYVDYVKNNGGELELAPESPKRIILGTFFENKVEDKT  
IHLLERDAANNPYFAISPENKDGNRDEITPQATFLRNVDISAQVLDQNGNVIWQSKVLPS  
YRKNFHNPKQSDGHYRMDALQWSGLDKDGKVVADGFTYRLRYTPVAEGANSQESDFKV  
QVSTKSPNLPSRAQFDETNRTLSLAMPKESYVPTYRLQLVLSHVVKDEEYGDSETS YHYF  
HIDQEGKVTLPTKTVKIGESEVAVDPKALTIVVEDKAGNFATVKLSDDLKNAVVSEKENAI  
VISNSFKYFNLKKEPMFISKEGKVVKNLEEBITLVKPQTTVTTQSLSKETKSGNEKVL  
TSTNNSSRVAKIISPKNHGDVSNHT

SEQ ID NO. 4420

STRAIN 090

EEQELKNQEQSPVIANVAQQPSPSVTTNIVEKTSVTAASANTVKEMGDTSVKNDKTEDE  
LLEELSKNLDTSNLGADLEEEYPSKPEPTNNKESNVVNTASTAIAQKVPSAYEEVKPESK  
SSLAVFDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI.FRLDSPKDDKHSFKTKAEFEE  
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG  
NSKRPAINGLLLEGAAPNAQVLLMRI.PDKIDSDFGEAYAKAITDAVNLGAKTINMSLGK  
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
DTLSVASYESLKITSEVVETIEGKLVKLP.IVTSKPFDKGKAYDVVYANYGAKKDFEGKD  
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKRGNFILPYRELPGVISKVDG  
ERIKNTSSQLTFNQSFVVDSSQGNRMLEQSSWGVTAEAGIKPDVTASGFEIYSSTYNNQ  
YQTMSTGSMASPHVAGLMTMLQSHLAEKYKGMNLD SKKLELSKNILMSSATALYSEEDK  
AFYSRQGGAGVVDAAEKAIQAQYYVTGNDGKAKINLKRVDKFDITVTIHKLVEGVKELY  
YQANVATEQVNGKGFALKPQALLDTNWQKVLIRDKETQVRFTIDASQFSQKLKEQMANGY  
FLEGFVRFEKAKDSNQELMSIPFVGFGNDFANLQALETPITYKLSKGSFYKPNDTTHKD  
QLEYNESAPFESNNYTALLTQASWGYVDYVKNNGGELELAPESPKRIILGTFFENKVEDKT  
IHLLERDAANNPYFAISPENKDGNRDEITPQATFLRNVDISAQVLDQNGNVIWQSKVLPS  
YRKNFHNPKQSDGHYRMDAFQWSGLDKDGKVVADGFTYRLRYTPVAEGANSQESDFKV  
QVSTKSPNLPLLAQFDETNRTLSLAMPKESYVPTYRLQLVLSHVVKDEEYGDSETS YHYF  
HIDQEGKVTLPTKTVKIGESEVAVDPKALTIVVEDKAGNFATVKLSDDLKNAVVSEKENAI  
VISNSFKYFNLKKEPMFISKEGKVVKNLEEBITLVKPQTTVTTQSLSKETKSGNEKVL  
TSTNNSSRVAKIISPKNHGDVSNHT

SEQ ID NO. 4421

STRAIN CJB110

EEQELKNQEQSPVIANVAQQPSPSVTTNIVEKTSVTAASANTAKEMGDTSVKNDKTEDE  
LLEELSKNLDTSNLGADLEEEYPSKPEPTNNKESNVVNTASTAIAQKVPSAYEEVKPESK  
SSLAVFDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI.FRLDSPKDDKHSFKTKAEFEE  
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG  
NSKRPAINGLLLEGAAPNAQVLLMRI.PDKIDSDFGEAYAKAITDAVNLGAKTINMSLGK  
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
DTLSVASYESLKITSEVVETIEGKLVKLP.IVTSKPFDKGKAYDVVYANYGAKKDFEGKD  
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKRGNFILPYRELPGVISKVDG  
ERIKNTSSQLTFNQSFVVDSSQGNRMLEQSSWGVTAEAGIKPDVTASGFEIYSSTYNNQ  
YQTMSTGSMASPHVAGLMTMLQNHLEEKYKGMNLD SKKLELSKNILMSSATALYSEEDK  
AFYSRQGGAGVVDAAEKAIQAQYYVTGNDGKAKINLKRVDKFDITVTIHKLVEGVKELY  
YQANVATEQVNGKGFALKPQALLDTNWQKVLIRDKETQVRFTIDASQFSQKLKEQMANGY  
FLEGFVRFEKAKDSNQELMSIPFVGFGNDFANLQALETPITYKLSKGSFYKPNDTTHKD  
QLEYNESAPFESNNYTALLTQASWGYVDYVKNNGGELELAPESPKRIILGTFFENKVEDKT  
IHLLERDAANNPYFAISPENKDGNRDEITPQATFLRNVDISAQVLDQNGNVIWQSKVLPS  
YRKNFHNPKQSDGHYRMDAFQWSGLDKDGKVVADGFTYRLRYTPVAEGANSQESDFKV  
QVSTKSPNLPLLAQFDETNRTLSLAMPKESYVPTYRLQLVLSHVVKDEEYGDSETS YHYF  
HIDQEGKVTLPTKTVKIGESEVAVDPKALTIVVEDKAGNFATVKLSDDLKNAVVSEKENAI  
VISNSFKYFNLKKEPMFISKEGKVVKNLEEBITLVKPQTTVTTQSLSKETKSGNEKVL  
TSTNNSSRVAKIISPKNHGDVSNHT

SEQ ID NO. 4422

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

**STRAIN 1169NT**

EEQELKNQEQSPVIANVAQQSPSVTTNI VEKTSVTAASANTAKEMGDTSVKNDKTEDE  
 LLEELSKNLDTSNMGADLEEYPSKPETTNNKESNVVTINASTAIAQKVPSAYEEVKPKSK  
 SSLAVLDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI FRLDSPKDDKHSPFNKAEEFEE  
 LKAKHNITYGKWNVDKIVFAHNYANTTETVADIAAAMKDGYSKAKNISHGTHVAGIFVG  
 NSKRPAINGLLLEGAAPNAQVLLMRI PDKIDSDKFGEAYAKAITDAVNLGAKTINMSIGK  
 TADSLIALNDKVLKALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE  
 DTLASVASYESLKTISEVVETITIEGKLVKLPVITVSKPFDKGAIDVYVANYGAKDFEGKD  
 FKQKIALIERGGGLDMFTKITHTATNAGVVGIVIFNDQEKRGNFILPYRELPVGVISKVDG  
 ERIKNTSSQLTFNQRFEVVDSSQGGNRMLEQSSWGVTAAGAIKPDVTASGFEIYSSTYNNQ  
 YQTMSTGSMASPHVAGLMTMLQSHLAEKYKGMNLDKSKLLELSKNILMSSATALYSEEDK  
 AFYSPRQGGAGVVDAAEKAIQAQYVVTGNDGKAKINLKRVDGKFDITVTIHKLVGVKELY  
 YQANVATEQVNGKGFALKPQALLDTNWQKVIILRDKETQVRFTIDASQFSQKLKEQMANGY  
 FLEGFVRFKKAKSDNQBLMSIPFVGFNGDFASLQALEPTIYKTLKSGSFYYPNDTTHKD  
 QLEYNESAPPFESNNYATALLQSSASWGYVDVYKNGGELELAPESPKRIILGTFENKVEDKT  
 IHLERDAANNPYFAISPNDGGRDEITPQATFLRNVKDISAQVLDQNGNVIWQSKVLPS  
 YRKNFHNPNKQSDGHYRMDALQWGLDKDKGVVADGFTYRLRYTPVABGANSQESDPKV  
 QVSTKSPNLPSSRAQFDETNRTLSLAMPKGSYVPIYRLQLVLSHVVKDEYGEDTSYFF  
 HLDQEGKATLPKTVKIGESEVAVDPKALTIVVEDKAGNFATVKLSDDLNKAVVSEKENAI  
 VISNSPKYFDNLKKEPMFISKKEKVVNKNLEBIIIVKPHTTVTITQSLKEITKSGNEKVL  
 TSTNNSSRVAKIISPKNHGSVNHT

PRETTY of: /biotmp/msa209368.2{\*} February 10, 2003 02:09 ..

	1	50
msa209368.2{147_COH1}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_M732}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_M781}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_18RS21}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_2603}	vdkhhskkai lkltlittsi lhmshngvna	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_JM9130013}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_090}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_CJB110}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_1169NT}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_H36B}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_A909}	-----	EEQELKNQEQ SPVIANVAQQ
Consensus	*****	*****

	51	100
msa209368.2{147_COH1}	PSPSVTtNiV EKTsvTaASA SNTvKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_M732}	PSPSVTtNiV EKTsvTaASA SNTvKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_M781}	PSPSVTtNiV EKTsvTaASA SNTvKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_18RS21}	PSPSVTtntV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_2603}	PSPSVTtntV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_JM9130013}	PSPSVTtntV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_090}	PSPSVTtNiV EKTsvTaASA SNTvKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_CJB110}	PSPSVTtNiV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_1169NT}	PSPSVTtNiV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_H36B}	PSPSVTtntV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_A909}	PSPSVTtntV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
Consensus	*****	*****

	101	150
msa209368.2{147_COH1}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKseSK
msa209368.2{147_M732}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKseSK
msa209368.2{147_M781}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKseSK
msa209368.2{147_18RS21}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_2603}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_JM9130013}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_090}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_CJB110}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_1169NT}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_H36B}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKpeSK
msa209368.2{147_A909}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAIAQKVPS	AYEEVKpeSK
Consensus	***-*****	*****

	151	200
msa209368.2{147_COH1}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_M732}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_M781}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_18RS21}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_2603}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_JM9130013}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_090}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_CJB110}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_1169NT}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_H36B}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_A909}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
Consensus	*****	*****

	201	250
msa209368.2{147_COH1}	SPKtKaEFEE LKAKHNITYG KWNVDKIVFA HNYANTTETV ADIAAAMKDG	

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa209368.2{147_M732}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_M781}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_18RS21}	SFKtKtEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_2603}	SFKtKtEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_JM9130013}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_090}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_CJB110}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_1169NT}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_H36B}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_A909}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
Consensus	*****-*****	*****-*****	*****-*****	*****-*****	*****-*****
msa209368.2{147_COH1}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_M732}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_M781}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_18RS21}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_2603}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_JM9130013}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_090}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_CJB110}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_1169NT}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_H36B}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_A909}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
Consensus	*****-*****	*****-*****	*****-*****	*****-*****	*****-*****
msa209368.2{147_COH1}	DSDKFGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_M732}	DSDKFGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_M781}	DSDKFGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_18RS21}	DSDKFGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_2603}	DSDKFGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_JM9130013}	DSDKFGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_090}	DSDKFGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_CJB110}	DSDKFGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_1169NT}	DSDKFGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_H36B}	DSDKFGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_A909}	DSDKFGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
Consensus	*****-*****	*****-*****	*****-*****	*****-*****	*****-*****
msa209368.2{147_COH1}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_M732}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_M781}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_18RS21}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_2603}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_JM9130013}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_090}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_CJB110}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_1169NT}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_H36B}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_A909}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
Consensus	*****-*****	*****-*****	*****-*****	*****-*****	*****-*****
msa209368.2{147_COH1}	LKTISeVVET	TIEGKLvKLP	IVTSKPFdKG	KAYDVVYANY	GAKKilkvrt
msa209368.2{147_M732}	LKTISeVVET	TIEGKLvKLP	IVTSKPFdKG	KAYDVVYANY	GAKKilkvrt
msa209368.2{147_M781}	LKTISeVVET	TIEGKLvKLP	IVTSKPFdKG	KAYDVVYANY	GAKKilkvrt
msa209368.2{147_18RS21}	LKTISeVVET	TIEGKLvKLP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_2603}	LKTISeVVET	TIEGKLvKLP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_JM9130013}	LKTISeVVET	TIEGKLvKLP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_090}	LKTISeVVET	TIEGKLvKLP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_CJB110}	LKTISeVVET	TIEGKLvKLP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_1169NT}	LKTISeVVET	TIEGKLvKLP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_H36B}	LKTISeVVET	TIEGKLvKLP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_A909}	LKTISeVVET	TIEGKLvKLP	IVTSKPFdKG	KAYDVVYANY	GAKKrl.r.g
Consensus	*****-*****	*****-*****	*****-*****	*****-*****	*****-*****
msa209368.2{147_COH1}	lkvrhlh.lsv	vvdlil.lks	lmlqmqvllv	slfltkiknv	eiF.fltnvny
msa209368.2{147_M732}	lkvrhlh.lsv	vvdlil.lks	lmlqmqvllv	slfltkiknv	eiF.fltnvny
msa209368.2{147_M781}	lkvrhlh.lsv	vvdlil.lks	lmlqmqvllv	slfltkiknv	eiF.fltnvny
msa209368.2{147_18RS21}	fkgkialier	ggglldfntki	thatnagvvg	ivifndqekr	gnFlippyrel
msa209368.2{147_2603}	fkgkialier	ggglldfntki	thatnagvvg	ivifndqekr	gnFlippyrel
msa209368.2{147_JM9130013}	fkgkialier	ggglldfntki	thatnagvvg	ivifndqekr	gnFlippyrel
msa209368.2{147_090}	fkgkialier	ggglldfntki	thatnagvvg	ivifndqekr	gnFlippyrel
msa209368.2{147_CJB110}	fkgkialier	ggglldfntki	thatnagvvg	ivifndqekr	gnFlippyrel
msa209368.2{147_1169NT}	fkgkialier	ggglldfntki	thatnagvvg	ivifndqekr	gnFlippyrel
msa209368.2{147_H36B}	fkgkialier	ggglldfntki	thatnagvvg	ivifndqekr	gnFlippyrel
msa209368.2{147_A909}	l.r.dcin.a	wwwt.fyd.n	hscykrcrcw	yyrf.rsrkt	wkFsnslp.i
Consensus	*****-*****	*****-*****	*****-*****	*****-*****	*****-*****

501

550

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa209368.2{147_COH1}	lwGllvk.ma	sv.Kilqvs.	hltrvlk.li	akvaivcwnn	qvga.qlkeq
msa209368.2{147_M732}	lwGllvk.ma	sv.Kilqvs.	hltrvlk.li	akvaivcwnn	qvga.qlkeq
msa209368.2{147_M781}	lwGllvk.ma	sv.Kilqvs.	hltrvlk.li	akvaivcwnn	qvga.qlkeq
msa209368.2{147_18RS21}	pvGiiskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_2603}	pvGiiskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_JM9130013}	pvGiiskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_090}	pvGviskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_CJB110}	pvGviskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_1169NT}	pvGviskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_H36B}	pvGviskvdg	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_A909}	tcGgy..srw	rayKkyfksv	ni..pef..ss.	.prwqsyagt	iklgrds.rs
Consensus	-----	-----	-----	-----	-----
msa209368.2{147_COH1}	sslm.qllal	kfilqpiiin	tkqclvqvwl	hhmlqd..qc	fkviwlrnk
msa209368.2{147_M732}	sslm.qllal	kfilqpiiin	tkqclvqvwl	hhmlqd..qc	fkviwlrnk
msa209368.2{147_M781}	sslm.qllal	kfilqpiiin	tkqclvqvwl	hhmlqd..qc	fkviwlrnk
msa209368.2{147_18RS21}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_2603}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_JM9130013}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_090}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_CJB110}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_1169NT}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_H36B}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmtm	lqshlaekyk
msa209368.2{147_A909}	nqa.cnsfwl	.nlffnl..s	ipnnvwykyg	fttccrindn	asksfg.ei.
Consensus	-----	-----	-----	-----	-----
msa209368.2{147_COH1}	g.i.ilknc.	nclktss.aq	qghyivkrir	rflhhvskvq	v.lmlkKlSk
msa209368.2{147_M732}	g.i.ilknc.	nclktss.aq	qghyivkrir	rflhhvskvq	v.lmlkKlSk
msa209368.2{147_M781}	g.i.ilknc.	nclktss.aq	qghyivkrir	rflhhvskvq	v.lmlkKlSk
msa209368.2{147_18RS21}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_2603}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_JM9130013}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_090}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_CJB110}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_1169NT}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_H36B}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_A909}	rdefrf.kia	riv.khphel	nsii...rg.	gvlfettsarc	rscs.c.Ksyp
Consensus	-----	-----	-----	-----	-----
msa209368.2{147_COH1}	lnimlletma	klklisnere	inlisqlqfi	nl.kvsknci	iklm.qgnk.
msa209368.2{147_M732}	lnimlletma	klklisnere	inlisqlqfi	nl.kvsknci	iklm.qgnk.
msa209368.2{147_M781}	lnimlletma	klklisnere	inlisqlqfi	nl.kvsknci	iklm.qgnk.
msa209368.2{147_18RS21}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_2603}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_JM9130013}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_090}	aqyyvtgndg	kakinlkrvg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_CJB110}	aqyyvtgndg	kakinlkrvg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_1169NT}	aqyyvtgndg	kakinlkrvg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_H36B}	aqyyvtgndg	kakinlkrvg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_A909}	ssilcywkrw	qs.n.sqtsg	r.i.yhsyns	.tcrrcqriv	lss.csnrts
Consensus	-----	-----	-----	-----	-----
msa209368.2{147_COH1}	ikvnlpnlhk	pc.iligrk.	ffvikkhkfd	lllmlvnlvr	n.Knrwqmvi
msa209368.2{147_M732}	ikvnlpnlhk	pc.iligrk.	ffvikkhkfd	lllmlvnlvr	n.Knrwqmvi
msa209368.2{147_M781}	ikvnlpnlhk	pc.iligrk.	ffvikkhkfd	lllmlvnlvr	n.Knrwqmvi
msa209368.2{147_18RS21}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_2603}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_JM9130013}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_090}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_CJB110}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_1169NT}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_H36B}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_A909}	k.r.icp.tt	slary.laes	nss..rntss	iyf.f.si.s	eiKrtgdgkw
Consensus	-----	-----	-----	-----	-----
msa209368.2{147_COH1}	s.kvlyvlkk	privirs..v	fl1.dlmvil	rtykhkhkrf	irrfkvvst
msa209368.2{147_M732}	s.kvlyvlkk	privirs..v	fl1.dlmvil	rtykhkhkrf	irrfkvvst
msa209368.2{147_M781}	s.kvlyvlkk	privirs..v	fl1.dlmvil	rtykhkhkrf	irrfkvvst
msa209368.2{147_18RS21}	flegfvrkke	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgsfy
msa209368.2{147_2603}	flegfvrkke	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgsfy
msa209368.2{147_JM9130013}	flegfvrkke	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgsfy
msa209368.2{147_090}	flegfvrkke	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgsfy
msa209368.2{147_CJB110}	flegfvrkke	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgsfy
msa209368.2{147_1169NT}	flegfvrkke	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgsfy
msa209368.2{147_H36B}	flegfvrkke	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgsfy
msa209368.2{147_A909}	flrrfctf.r	sqq..sgvne	ysfcrl.w.f	celtat.ntd	l.daf.r.fl
Consensus	-----	-----	-----	-----	-----

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

	801			850	
msa209368.2{147_COH1}	inqmiglikt	nwstmnglll	kattilpc.h	nqrlgamlim	skmvgs.n.h
msa209368.2{147_M732}	inqmiglikt	nwstmnglll	kattilpc.h	nqrlgamlim	skmvgs.n.h
msa209368.2{147_M781}	inqmiglikt	nwstmnglll	kattilpc.h	nqrlgamlim	skmvgs.n.h
msa209368.2{147_18RS21}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_2603}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_JM9130013}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_090}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_CJB110}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_1169NT}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_H36B}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_A909}	l.tk.yns.r	pigvq.issf	.kqglyclvn	tisvlglc.l	cqkwwgvriss
Consensus	-----	-----	-----	-----	-----
	851			900	
msa209368.2{147_COH1}	rrvqKelf.e	llrirlrikq	fifwkemqri	ihilpflqik	meigtkslpr
msa209368.2{147_M732}	rrvqKelf.e	llrirlrikq	fifwkemqri	ihilpflqik	meigtkslpr
msa209368.2{147_M781}	rrvqKelf.e	llrirlrikq	fifwkemqri	ihilpflqik	meigtkslpr
msa209368.2{147_18RS21}	pespKriilg	tfnkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_2603}	pespKriilg	tfnkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_JM9130013}	pespKriilg	tfnkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_090}	pespKriilg	tfnkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_CJB110}	pespKriilg	tfnkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_1169NT}	pespKriilg	tfnkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_H36B}	pespKriilg	tfnkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_A909}	tgesKlNyfr	nf.e.g.g.n	nssfgkrcse	.sifchfsk.	rwk.g.nhsp
Consensus	-----	-----	-----	-----	-----
	901			950	
msa209368.2{147_COH1}	qls.emlrif	llkf.ikmem	lfgkvrfyhl	ivkisiisq	kvmviiivwml
msa209368.2{147_M732}	qls.emlrif	llkf.ikmem	lfgkvrfyhl	ivkisiisq	kvmviiivwml
msa209368.2{147_M781}	qls.emlrif	llkf.ikmem	lfgkvrfyhl	ivkisiisq	kvmviiivwml
msa209368.2{147_18RS21}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_2603}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_JM9130013}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_090}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_CJB110}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_1169NT}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_H36B}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_A909}	gnflkkc.gy	fcssrsrskwk	cylak.gfti	ls.kfp..sk	ak.wslsygc
Consensus	-----	-----	-----	-----	-----
	951			1000	
msa209368.2{147_COH1}	fsgvv.irma	kl.qmvFili	ayvthq.qke	qivrsqtlkf	k.vlshqifl
msa209368.2{147_M732}	fsgvv.irma	kl.qmvFili	ayvthq.qke	qivrsqtlkf	k.vlshqifl
msa209368.2{147_M781}	fsgvv.irma	kl.qmvFili	ayvthq.qke	qivrsqtlkf	k.vlshqifl
msa209368.2{147_18RS21}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_2603}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_JM9130013}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_090}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_CJB110}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_1169NT}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_H36B}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_A909}	psvewfr.gw	qscsrwFlly	sftlhtsarr	sk.sgvrl.s	ssky.vtkss
Consensus	-----	-----	-----	-----	-----
	1001			1050	
msa209368.2{147_COH1}	helslmkllie	h.a.pclrkv	vmflhivyn.	fyml.Knkn	mgmrl1tiis
msa209368.2{147_M732}	helslmkllie	h.a.pclrkv	vmflhivyn.	fyml.Knkn	mgmrl1tiis
msa209368.2{147_M781}	helslmkllie	h.a.pclrkv	vmflhivyn.	fyml.Knkn	mgmrl1tiis
msa209368.2{147_18RS21}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetsyhyf
msa209368.2{147_2603}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetsyhyf
msa209368.2{147_JM9130013}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetsyhyf
msa209368.2{147_090}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetsyhyf
msa209368.2{147_CJB110}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetsyhyf
msa209368.2{147_1169NT}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetsyhyf
msa209368.2{147_H36B}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetsyhyf
msa209368.2{147_A909}	ftssv..n.s	niklsha.gk	.lcsyissti	sfisccKr.r	iwr.dflplf
Consensus	-----	-----	-----	-----	-----
	1051			1100	
msa209368.2{147_COH1}	i.ikkvk.hf	lkrlr.ervr	lr.tlrlp.hl	lwkiklvilq	r.nc1ts.ir
msa209368.2{147_M732}	i.ikkvk.hf	lkrlr.ervr	lr.tlrlp.hl	lwkiklvilq	r.nc1ts.ir
msa209368.2{147_M781}	i.ikkvk.hf	lkrlr.ervr	lr.tlrlp.hl	lwkiklvilq	r.nc1ts.ir
msa209368.2{147_18RS21}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_2603}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_JM9130013}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_090}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_CJB110}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_1169NT}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_H36B}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_A909}	pyrsrr.sdt	s.ns.drre.	gcsrp.dldt	ccgr.sw.fr	ngkiv.ple.
Consensus	-----	-----	-----	-----	-----

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

	1101		1150
msa209368.2{147_COH1}	q.yqrkktl. .fltvsnili t.rKnlclfl kkeK..tri. kk.h.lslkl		
msa209368.2{147_M732}	q.yqrkktl. .fltvsnili t.rKnlclfl kkeK..tri. kk.h.lslkl		
msa209368.2{147_M781}	q.yqrkktl. .fltvsnili t.rKnlclfl kkeK..tri. kk.h.lslkl		
msa209368.2{147_18RS21}	avvsekenai visnsfkyfd nlkKepmfis kkeKvvknkl eeilvvpqt		
msa209368.2{147_2603}	avvsekenai visnsfkyfd nlkKepmfis kkeKvvknkl eeilvvpqt		
msa209368.2{147_JM9130013}	avvsekenai visnsfkyfd nlkKepmfis kkeKvvknkl eeilvvpqt		
msa209368.2{147_090}	avvsekenai visnsfkyfd nlkKesmfis kegKvvknkl eeitlvkpqt		
msa209368.2{147_CJB110}	avvsekenai visnsfkyfd nlkKesmfis kegKvvknkl eeitlvkpqt		
msa209368.2{147_1169NT}	avvsekenai visnsfkyfd nlkKepmfis kkeKvvknkl eeilvvpqt		
msa209368.2{147_H36B}	avvsekenai visnsfkyfd nlkKepmfis kegKvvknkl eeilvvpqt		
msa209368.2{147_A909}	gssirerkry snf.qfqif. .leKrtvyvf .rrKsskqes rrnsis.aan		
Consensus	-----	---*-----	-----
	1151		1200
msa209368.2{147_COH1}	qlllnhclkk .lngemrkss llqtiivae. lrsyhlnitg illti-----		
msa209368.2{147_M732}	qlllnhclkk .lngemrkss llqtiivae. lrsyhlnitg illti-----		
msa209368.2{147_M781}	qlllnhclkk .lngemrkss llqtiivae. lrsyhlnitg illti-----		
msa209368.2{147_18RS21}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhT-----		
msa209368.2{147_2603}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhTlpst		
msa209368.2{147_JM9130013}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhT-----		
msa209368.2{147_090}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhT-----		
msa209368.2{147_CJB110}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhT-----		
msa209368.2{147_1169NT}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhT-----		
msa209368.2{147_H36B}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhT-----		
msa209368.2{147_A909}	ysyysiiv.r nnsirk.esp hfykq...qs s.dhit.t.r gfc.py-----		
Consensus	-----	-----	-----*****
	1201		1233
msa209368.2{147_COH1}	-----	-----	---
msa209368.2{147_M732}	-----	-----	---
msa209368.2{147_M781}	-----	-----	---
msa209368.2{147_18RS21}	-----	-----	---
msa209368.2{147_2603}	sdratnglfv gtlallsl1 lylpkpktkn nsk		
msa209368.2{147_JM9130013}	-----	-----	---
msa209368.2{147_090}	-----	-----	---
msa209368.2{147_CJB110}	-----	-----	---
msa209368.2{147_1169NT}	-----	-----	---
msa209368.2{147_H36B}	-----	-----	---
msa209368.2{147_A909}	-----	-----	---
Consensus	*****	*****	***

**Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)****SEQ ID NO. 4501****STRAIN 2603**

ATGAAAAAGATTAGAAAAAGTTTAGGACTTCTACTATGTTGCTTTTATAGGATTGGTACAA  
 TTAGCGTTTTTTTCGGTAGCCAGTGTAATGCTGATACCCCTAATCAACTAACAATCACA  
 CAGATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATGGACTGTG  
 ACTGACAACTTAAAAGTTGATTATTGAGCCAAATGACAGATAGCGAATTGAACCAGAAG  
 TATAAGAGTATCTTGACTTCTCTACTGATACTAATGGTCAGACAAAGATAGCACTCCCA  
 AATGGTTTCGTACTTTGGTCGTCTTATAAGCTGATCAAAGCGTTTCAACAATAGTACCT  
 TTTTATATTGAATTACAGATGATAAGTTTATCAAAATCAATTACAGATAAATCCTAAGCGA  
 AAAGTTGAAACAGGCCGATTAAAACCTTATTAAATATACAAAAGAAGGAAAGATAAAGAAA  
 AGGCTATCCGGAGTAAATTGTTATTATACGATAACCAGAATCAGCCAGTTTCGCTTTAAA  
 AATGGACGATTACGACCGATCAAGATGGGATTACTTCATTAGTAAGTATGATAAGGGA  
 GAAATTGAGGTTGAAGGTTTATACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTA  
 ACTGGTTACCGTATATCTATGAAGGATGCTGATGTTGCTGTAGTTGCTAATAAAACACAG  
 GAAGTAGAGGTAGAAAACGAAAAGAACTCCTCCACCAACAAATCCTAAACCATCACAA  
 CCGCTTTTTCAGCAATCTTTCTTCTAAAACAGGAATGATTATTGGTGGAGGACTGACA  
 ATTCTTGGTTGTATTATTTTGGGAATTTTGTATTCTTTTAAAGAAAACTAAAAATAGC  
 AAATCTGAAGAAACGATACAGTA

**SEQ ID NO. 4502****STRAIN 090**

GATACCCCTAATCAACTAACAATCACAC  
 AGATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTA  
 TGGACTGTGACTGACAACTTAAAAGTTGATTATTGAGCCAAATGACAGA  
 TAGCGAATTGAACCAGAAGTATAAGAGTATCTTGACTTCTCTACTGATA  
 CTAATGGTCAGACAAAGATAGCACTCCCAAATGGTTTCGTACTTTGGTCGT  
 GCTTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGA  
 ATTACAGATGATAAGTTTATCAAAATCAATTACAGATAAATCCTAAGCGAA  
 AAGTTGAAACAGGCCGATTAAAACCTTATTAAATATACAAAAGAAGGAAAG  
 ATAAAGAAAAGGCTATCAGGAGTAAATTGTTATTATACGATAACAGAA  
 TCAGCCAGTTTCGCTTTAAAAATGGACGATTTCAGACCGATCAAGATGGGA  
 TTACTTCATTAGTAAGTATGATGATAAGGGAGAAATTGAGGTTGAAGGTTTA  
 TTACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTTACCG  
 TATATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGG  
 AAGTAgAGGTAAGAAAACGAAAAGAACTCCTCCACCAACAAATCCTAAA  
 CCAATCAACCG

**SEQ ID NO. 4503****STRAIN H36B**

GATACCCCTAATCAACTAACAATCACACAGA  
 TAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATGG  
 ACTGTGACTGACAACTTAAAAGTTGATTATTGAGCCAAATGACAGATAG  
 CGAATTGAACCAGAAGTATAAGAGTATCTTGACTTCTCTACTGATACTA  
 ATGGTCAGACAAAGATAGCACTCCCAAATGGTTTCGTACTTTGGTCGTGCT  
 TATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGAATT  
 ACCAGATGATAAGTTTATCAAAATCAATTACAGATAAATCCTAAGCGAAAAG  
 TTGAAAACAGGCCGATTAAAACCTTATTAAATATACAAAAGAAGGAAAGATA  
 AAGAAAAGGCTwTCCGGAGTAAATTGTTATTATACGATAACAGAAATCA  
 CGCAGTTTCGCTTTAAAAATGGACGATTTCAGACCGATCAAGATGGGATTA  
 CTTTATTAGTAAGTATGATAAGGGAGAAATTGAGGTTGAAGGTTTATTA  
 CCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTTACCGTAT  
 ATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGAAG  
 TAGAGGTAGAAAACGAAAAGAACTCCTCCACCAACAAATCCTAAACCA  
 TCACAACCGC

**SEQ ID NO. 4504****STRAIN 18RS21**

GATACCCCTAATCAACTAACAATCACACAG  
 ATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATG  
 GACTGTGACTGACAACTTAAAAGTTGATTATTGAGCCAAATGACAGATA  
 GCGAATTGAACCAGAAGTATAAGAGTATCTTGACTTCTCTACTGATACT  
 ATGGTCAGACAAAGATAGCACTCCCAAATGGTTTCGTACTTTGGTCGTGCT  
 TTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGAAT  
 TACCAGATGATAAGTTTATCAAAATCAATTACAGATAAATCCTAAGCGAAAA  
 GTTGAAAACAGGCCGATTAAAACCTTATTAAATATACAAAAGAAGGAAAGAT  
 AAAGAAAGGCTATCCGGAGTAAATTGTTATTATACGATAACAGAAATC  
 AGCCAGTTTCGCTTTAAAAATGGACGATTTCAGACCGATCAAGATGGGATT  
 ACTTCATTAGTAAGTATGATAAGGGAGAAATTGAGGTTGAAGGTTTATTA  
 ACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTTACCGTAT  
 TATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGAAG  
 GTAGAGGTAGAAAACGAAAAGAACTCCTCCACCAACAAATCCTAAACCA  
 ATCAACACC

**SEQ ID NO. 4505****STRAIN CJB110**

GATACCCCTAATCAACTAACAATCACACA  
 GATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTAT  
 GGACTGTGACTGACAACTTAAAAGTTGATTATTGAGCCAAATGACAGAT  
 AGCGAATTGAACCAGAAGTATAAGAGTATCTTGACTTCTCTACTGATACT  
 TAAATGGTCAGACAAAGATAGCACTCCCAAATGGTTTCGTACTTTGGTCGTG  
 CTTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGAA  
 TTACCAGATGATAAGTTTATCAAAATCAATTACAGATAAATCCTAAGCGAAA  
 AGTTGAAAACAGGCCGATTAAAACCTTATTAAATATACAAAAGAAGGAAAGGA



Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

TAAAGAAAAGGCTaTCAGGAGTAATATTTGTATTATACGATAACCAAGAT  
 CAGCCAGTTTCGCTTTAAAAATGGACGATTTCAGCCGATCAAGATGGGAT  
 TACTTCATTAGTAAGTATGATGATAAGGGAGAAATTGAGGTTGAAGGTTTAT  
 TACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTTaCCGT  
 ATATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGA  
 AGTAGAGGTAGAAAACGAAAAAGAACTCCTCCACCAACAAATCCTAAAC  
 CATCACACC

SEQ ID NO. 4506

STRAIN 1169NT

GATACCCCTAATCAACTAACATCACACAG  
 ATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATG  
 GACTGTGACTGACAACTTAAAGTTGATTTATTGAGCCAAATGACAGATA  
 GCGAATTGAACCAAGATATAAGAGTATCTTGACTTCTCCTACTGATACT  
 AATGGtCagaCAAAGATAGCACTCCCAATGGTTTCGTACTTTGGTCGTGC  
 TTATAAAGCTGATCAAGCGTTTCAACAATAGTACCTTTTATATGAAT  
 TACCAGATGATAAGTTATCAAATCAATTACAGATAAATCCTAAGCGAAAA  
 GTTGAACACAGGCCGATTAAAACTTATTAATATACAAAGAGGAAAGAT  
 AAAGAAAAGGCTATCAGGAGTAATATTTGTATTATACGATAACCAAGATC  
 AGCCAGTTTCGCTTTAAAAATGGACGATTTCAGCCGATCAAGATGGGAT  
 ACTTCATTAGTAAGTATGATGATAAGGAGAAATTGAGGTTGAAGGTTTAT  
 ACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTTACCGTA  
 TATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGA  
 GTAGAGGTAGAAAACGAAAAAGAACTCCTCCACCAACAAATCCTAAACC  
 ATCACACC

PRETTY of: /biotmp/msa184750.2{\*} May 13, 2003 06:23 ..

	1				50
msa184750.2{150_090}	-----	-----	-----	-----	-----
msa184750.2{150_1169NT}	-----	-----	-----	-----	-----
msa184750.2{150_CJB110}	-----	-----	-----	-----	-----
msa184750.2{150_18RS21}	-----	-----	-----	-----	-----
msa184750.2{150_2603}	atgaaaaaga	ttagaaaaag	tttaggactt	ctactatgtt	gctttttagg
msa184750.2{150_H36B}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa184750.2{150_090}	-----	-----	-----	-----	---GATACCC
msa184750.2{150_1169NT}	-----	-----	-----	-----	---GATACCC
msa184750.2{150_CJB110}	-----	-----	-----	-----	---GATACCC
msa184750.2{150_18RS21}	-----	-----	-----	-----	---GATACCC
msa184750.2{150_2603}	attggtacaa	ttagcgtttt	tttcggtagc	cagtgtaaat	gctGATACCC
msa184750.2{150_H36B}	-----	-----	-----	-----	---GATACCC
Consensus	*****	*****	*****	*****	*****
	101				150
msa184750.2{150_090}	CTAATCAACT	AACAATCACA	CAGATAGGAC	TTCAGCCAAA	TACTACAGAG
msa184750.2{150_1169NT}	CTAATCAACT	AACAATCACA	CAGATAGGAC	TTCAGCCAAA	TACTACAGAG
msa184750.2{150_CJB110}	CTAATCAACT	AACAATCACA	CAGATAGGAC	TTCAGCCAAA	TACTACAGAG
msa184750.2{150_18RS21}	CTAATCAACT	AACAATCACA	CAGATAGGAC	TTCAGCCAAA	TACTACAGAG
msa184750.2{150_2603}	CTAATCAACT	AACAATCACA	CAGATAGGAC	TTCAGCCAAA	TACTACAGAG
msa184750.2{150_H36B}	CTAATCAACT	AACAATCACA	CAGATAGGAC	TTCAGCCAAA	TACTACAGAG
Consensus	*****	*****	*****	*****	*****
	151				200
msa184750.2{150_090}	GAGGGGATTT	CTTATCGTTT	ATGGACTGTG	ACTGACAACT	TAAAAGTTGA
msa184750.2{150_1169NT}	GAGGGGATTT	CTTATCGTTT	ATGGACTGTG	ACTGACAACT	TAAAAGTTGA
msa184750.2{150_CJB110}	GAGGGGATTT	CTTATCGTTT	ATGGACTGTG	ACTGACAACT	TAAAAGTTGA
msa184750.2{150_18RS21}	GAGGGGATTT	CTTATCGTTT	ATGGACTGTG	ACTGACAACT	TAAAAGTTGA
msa184750.2{150_2603}	GAGGGGATTT	CTTATCGTTT	ATGGACTGTG	ACTGACAACT	TAAAAGTTGA
msa184750.2{150_H36B}	GAGGGGATTT	CTTATCGTTT	ATGGACTGTG	ACTGACAACT	TAAAAGTTGA
Consensus	*****	*****	*****	*****	*****
	201				250
msa184750.2{150_090}	TTTATTGAGC	CAAATGACAG	ATAGCGAATT	GAACCAGAAG	TATAAGAGTA
msa184750.2{150_1169NT}	TTTATTGAGC	CAAATGACAG	ATAGCGAATT	GAACCAGAAG	TATAAGAGTA
msa184750.2{150_CJB110}	TTTATTGAGC	CAAATGACAG	ATAGCGAATT	GAACCAGAAG	TATAAGAGTA
msa184750.2{150_18RS21}	TTTATTGAGC	CAAATGACAG	ATAGCGAATT	GAACCAGAAG	TATAAGAGTA
msa184750.2{150_2603}	TTTATTGAGC	CAAATGACAG	ATAGCGAATT	GAACCAGAAG	TATAAGAGTA
msa184750.2{150_H36B}	TTTATTGAGC	CAAATGACAG	ATAGCGAATT	GAACCAGAAG	TATAAGAGTA
Consensus	*****	*****	*****	*****	*****
	251				300
msa184750.2{150_090}	TCTTGACTTC	TCCTACTGAT	ACTAATGGTC	AGACAAAGAT	AGCACTCCCA
msa184750.2{150_1169NT}	TCTTGACTTC	TCCTACTGAT	ACTAATGGTC	AGACAAAGAT	AGCACTCCCA
msa184750.2{150_CJB110}	TCTTGACTTC	TCCTACTGAT	ACTAATGGTC	AGACAAAGAT	AGCACTCCCA
msa184750.2{150_18RS21}	TCTTGACTTC	TCCTACTGAT	ACTAATGGTC	AGACAAAGAT	AGCACTCCCA
msa184750.2{150_2603}	TCTTGACTTC	TCCTACTGAT	ACTAATGGTC	AGACAAAGAT	AGCACTCCCA
msa184750.2{150_H36B}	TCTTGACTTC	TCCTACTGAT	ACTAATGGTC	AGACAAAGAT	AGCACTCCCA
Consensus	*****	*****	*****	*****	*****
	301				350

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

msa184750.2{150_090}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_1169NT}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_CJB110}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_18RS21}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_2603}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_H36B}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	351				400
msa184750.2{150_1169NT}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_CJB110}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_18RS21}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_2603}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_H36B}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	401				450
msa184750.2{150_1169NT}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACCTTATT
msa184750.2{150_CJB110}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACCTTATT
msa184750.2{150_18RS21}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACCTTATT
msa184750.2{150_2603}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACCTTATT
msa184750.2{150_H36B}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACCTTATT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	451				500
msa184750.2{150_1169NT}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTCaG	GAGTAATATT
msa184750.2{150_CJB110}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTCaG	GAGTAATATT
msa184750.2{150_18RS21}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTCcG	GAGTAATATT
msa184750.2{150_2603}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTCcG	GAGTAATATT
msa184750.2{150_H36B}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTwTCcG	GAGTAATATT
Consensus	*****	*****	*****	*****_--_*	*****
msa184750.2{150_090}	501				550
msa184750.2{150_1169NT}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_CJB110}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_18RS21}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_2603}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_H36B}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	551				600
msa184750.2{150_1169NT}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_CJB110}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_18RS21}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_2603}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_H36B}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	601				650
msa184750.2{150_1169NT}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_CJB110}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_18RS21}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_2603}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_H36B}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	651				700
msa184750.2{150_1169NT}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_CJB110}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_18RS21}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_2603}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_H36B}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	701				750
msa184750.2{150_1169NT}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAAACT
msa184750.2{150_CJB110}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAAACT
msa184750.2{150_18RS21}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAAACT
msa184750.2{150_2603}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAAACT
msa184750.2{150_H36B}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAAACT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	751				800
msa184750.2{150_1169NT}	CCTCCACCAA	CAAATCCTAA	ACCATCACAA	CCg-----	-----
	CCTCCACCAA	CAAATCCTAA	ACCATCACAA	CC-----	-----

**Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)**

```

msa184750.2{150_CJB110} CCTCCACCAA CAAATCCTAA ACCATCACAA CC-----
msa184750.2{150_18RS21} CCTCCACCAA CAAATCCTAA ACCATCACAA CC-----
msa184750.2{150_2603} CCTCCACCAA CAAATCCTAA ACCATCACAA CCgCtttttc cacaatcatt
msa184750.2{150_H36B} CCTCCACCAA CAAATCCTAA ACCATCACAA CCgC-----
Consensus *****

```

801 850

```

msa184750.2{150_090} -----
msa184750.2{150_1169NT} -----
msa184750.2{150_CJB110} -----
msa184750.2{150_18RS21} -----
msa184750.2{150_2603} tcttcctaaa acaggaatga ttattggtgg aggactgaca attccttggtt
msa184750.2{150_H36B} -----
Consensus *****

```

851 900

```

msa184750.2{150_090} -----
msa184750.2{150_1169NT} -----
msa184750.2{150_CJB110} -----
msa184750.2{150_18RS21} -----
msa184750.2{150_2603} gtattatttt gggaattttt ttatctttt taagaaaaac taaaaatagc
msa184750.2{150_H36B} -----
Consensus *****

```

901 924

```

msa184750.2{150_090} -----
msa184750.2{150_1169NT} -----
msa184750.2{150_CJB110} -----
msa184750.2{150_18RS21} -----
msa184750.2{150_2603} aaatctgaaa gaaacgatac agta
msa184750.2{150_H36B} -----
Consensus *****

```

**SEQ ID NO. 4507****STRAIN 2603**

MKKIRKSLGGLLCCFLGLVQLAFFSVASVNADTPNQLTITQIGLQPNTEEGISYRLWTV  
 TDNLKVDLLSQMTDSELNQKYKSILTSPTDTNGQTKIALPNGSYFGRAYKADQSVSTIVP  
 FYIELPDDKLSNQLQINPKRKVETGRLKLIK YTKEGKIKKRLSGVIFVLVDNQNPQVRFK  
 NGRFTTDDGITSVLVTDKGEIEVEGLLPKYIFREAKALTYRISMKDVAVVAVVANKTQ  
 EVEVEKEKETPPPTNPKPSQPLFPQSFLPKTGMIGGGLTILGCIILGILFIFLRKTKNS  
 KSERNDTV

**SEQ ID NO. 4508****STRAIN 090**

DTPNQLTITQIGLQPNTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT  
 NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK  
 YTKEGKIKKRLSGVIFVLVDNQNPQVRFKNGRFTTDDGITSVLVTDKGEIEVEGLLPKG  
 YIFREAKALTYRISMKDVAVVAVVANKTQEVENEKETPPPTNPKPSQ

**SEQ ID NO. 4509****STRAIN H36B**

DTPNQLTITQIGLQPNTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT  
 NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK  
 YTKEGKIKKRLSGVIFVLVDNQNPQVRFKNGRFTTDDGITSVLVTDKGEIEVEGLLPKG  
 YIFREAKALTYRISMKDVAVVAVVANKTQEVENEKETPPPTNPKPSQ

**SEQ ID NO. 4510****STRAIN 18RS21**

DTPNQLTITQIGLQPNTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT  
 NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK  
 YTKEGKIKKRLSGVIFVLVDNQNPQVRFKNGRFTTDDGITSVLVTDKGEIEVEGLLPKG  
 YIFREAKALTYRISMKDVAVVAVVANKTQEVENEKETPPPTNPKPSQ

**SEQ ID NO. 4511****STRAIN 1169NT**

DTPNQLTITQIGLQPNTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT  
 NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK  
 YTKEGKIKKRLSGVIFVLVDNQNPQVRFKNGRFTTDDGITSVLVTDKGEIEVEGLLPKG  
 YIFREAKALTYRISMKDVAVVAVVANKTQEVENEKETPPPTNPKPSQ

PRETTY of: /biotmp/msa184868.2{\*} May 13, 2003 06:25 ..

```

msa184868.2{150_090} 1 ----- 50
msa184868.2{150_2603} mkkirkslgl llccflglvq laffsvasvn -DTPNQLTIT QIGLQPNTE
msa184868.2{150_H36B} ----- -DTPNQLTIT QIGLQPNTE
msa184868.2{150_1169NT} ----- -DTPNQLTIT QIGLQPNTE
msa184868.2{150_18RS21} ----- -DTPNQLTIT QIGLQPNTE
Consensus *****

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51 100

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msa184868.2{150_090} EGISYRLWTV TDNLKVDLLS QMTDSELNQK YKSILTSPTD TNGQTKIALP

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**Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)**

```

msa184868.2{150_2603} EGISYRLWTV TDNLKVDLLS QMTDSELNQK YKSILTSPTD TNGQTKIALP
msa184868.2{150_H36B} EGISYRLWTV TDNLKVDLLS QMTDSELNQK YKSILTSPTD TNGQTKIALP
msa184868.2{150_1169NT} EGISYRLWTV TDNLKVDLLS QMTDSELNQK YKSILTSPTD TNGQTKIALP
msa184868.2{150_18RS21} EGISYRLWTV TDNLKVDLLS QMTDSELNQK YKSILTSPTD TNGQTKIALP
Consensus *****

101
msa184868.2{150_090} NGSYFGRAYK ADQSVSTIVP FYIELPDDKL SNQLQINPKR KVGTRGLKLI
msa184868.2{150_2603} NGSYFGRAYK ADQSVSTIVP FYIELPDDKL SNQLQINPKR KVGTRGLKLI
msa184868.2{150_H36B} NGSYFGRAYK ADQSVSTIVP FYIELPDDKL SNQLQINPKR KVGTRGLKLI
msa184868.2{150_1169NT} NGSYFGRAYK ADQSVSTIVP FYIELPDDKL SNQLQINPKR KVGTRGLKLI
msa184868.2{150_18RS21} NGSYFGRAYK ADQSVSTIVP FYIELPDDKL SNQLQINPKR KVGTRGLKLI
Consensus *****

151
msa184868.2{150_090} KYTKEGKIKK RLSGVIFVLY DNQNPVRFK NGRFTTDQDG ITSLVTDDKG
msa184868.2{150_2603} KYTKEGKIKK RLSGVIFVLY DNQNPVRFK NGRFTTDQDG ITSLVTDDKG
msa184868.2{150_H36B} KYTKEGKIKK RLSGVIFVLY DNQNPVRFK NGRFTTDQDG ITSLVTDDKG
msa184868.2{150_1169NT} KYTKEGKIKK RLSGVIFVLY DNQNPVRFK NGRFTTDQDG ITSLVTDDKG
msa184868.2{150_18RS21} KYTKEGKIKK RLSGVIFVLY DNQNPVRFK NGRFTTDQDG ITSLVTDDKG
Consensus *****

201
msa184868.2{150_090} EIEVEGLLPG KYIFREAKAL TGYRISMKDA VVAVVANKTQ EVEVENEKET
msa184868.2{150_2603} EIEVEGLLPG KYIFREAKAL TGYRISMKDA VVAVVANKTQ EVEVENEKET
msa184868.2{150_H36B} EIEVEGLLPG KYIFREAKAL TGYRISMKDA VVAVVANKTQ EVEVENEKET
msa184868.2{150_1169NT} EIEVEGLLPG KYIFREAKAL TGYRISMKDA VVAVVANKTQ EVEVENEKET
msa184868.2{150_18RS21} EIEVEGLLPG KYIFREAKAL TGYRISMKDA VVAVVANKTQ EVEVENEKET
Consensus *****

251
msa184868.2{150_090} PPPTNPKPSQ p----- tgmiigggt ilgciilgil fiflrktkns
msa184868.2{150_2603} PPPTNPKPSQ plfpqsfllpk tgmiigggt ilgciilgil fiflrktkns
msa184868.2{150_H36B} PPPTNPKPSQ p----- tgmiigggt ilgciilgil fiflrktkns
msa184868.2{150_1169NT} PPPTNPKPSQ p----- tgmiigggt ilgciilgil fiflrktkns
msa184868.2{150_18RS21} PPPTNPKPSQ p----- tgmiigggt ilgciilgil fiflrktkns
Consensus *****

301
msa184868.2{150_090} -----
msa184868.2{150_2603} kserndtv
msa184868.2{150_H36B} -----
msa184868.2{150_1169NT} -----
msa184868.2{150_18RS21} -----
Consensus *****

```

**Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)**

SEQ ID NO. 4601

**STRAIN A909**

TGACAAATATTTTACCCAACTGGTTTAGAGCAAGCAGGTGTAACATATTTACCTTT  
 CTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGACGGAATGCTTTTCGTCCAGA  
 TAACATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATCATTTTAAACGATATCATGA  
 ATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGTGTAGCTGGGGCAGATGGAAA  
 AACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAATATTACAGACACTTCTTTCTCT  
 AATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATTACTTTGTGTTTGAAGCTGA  
 TGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACTCAATTATTACCAATATTGA  
 TTTTGACCATCCTGATTATTTACAGGCCATAGAGGACGTATTCAATGCCTTTAATGACTA  
 TGCTAAGCAAGTTCAAAAAGGTTTATTCATTTTGGAGAAGATCCAAAACCTTCATGAAAT  
 CACTTCTGAGGCACCAATATATTATTGGTTTGAAGATTCAAATGATTTTATAGCAAA  
 AGACATCACTCGAAGCTGTTAATGGTTCTGACTTTAAGGTTTCTATAACCAAGAAAGAAAT  
 TGGTCAGTTTTCATGTACCGATACGGTAAACATAATATCTTAAATGCAACTGCTGTTAT  
 TGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCTGAGCATTGAAGACATT  
 TTCAGGGGTAAAGCGTCGTTTACTGAGAAGATTATTGACGATCTGTCATTATTGATGA  
 CTTTGGCTCACCATCCTACTGAGATTATTGCGACATTAGATGCTGCTCGACAAAAATACCC  
 GTCAAAAGAAATTTAGCTAATTTTCCAACCGCATACGTTCACTCGTACGATAGCTCTTTT  
 AGACGAATTTGCCCATGCTTGGAGTCAAGCGGATAGCGTTTATCTCGCTCAAAATATATGG  
 TTCTGCTAGAGAAGTAGATAATGGTGAAGGTAGAAGATTAGCTGCTAAGATTGT  
 CAAACACTCAGATTAGTGACAGTCGAAAATGTCTCGCCTTTACTCAATCATGATATATGC  
 TGTCTATGTCCTTATGGGTGCTGGAGACATTCAATTGTATGAGCGCTCTTTTGAAGAATT  
 ATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4602

**STRAIN 1169NT**

AAAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACCCAACTGGTTTAGAGCAAGC  
 AGGTGTAACATATATTTACCTTTCTCACCAGAATAATATCAGTGAGGATTTAGAGATTATTGC  
 AGGAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTA  
 TCATTTTAAACGATATCATGAATTTCTCGGAGATTATTATGCGTCAGTTCACTAGTCTAGG  
 TGTAGCTGGGGCAGATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAA  
 TATTACAGACACTTCTTTCTTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAA  
 TTACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATA  
 CTCATTTATACCAANTATGATTTTGACCATCCTGATTATTTTACAGGCTAGAGGACGT  
 ATTCAATGCCCTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGA  
 AGATCCAAACCTTCATGAATTCACCTTCTGAGGCACCAATATATTATTATGGTTTGAAGA  
 TTCAAATGATTTTATAGCAAAAGACATCACTCGAAGCTTAAATGGTTCTGACTTTAAGGT  
 TTTCTATAACCAAGAAAGAAATTTGGTCAGTTTTCATGTACCGATACGGTAAACATAATAT  
 CTTAAATGCAACTGCTGTTTATGCTAACCCTTTACATAATGGGAATTGATATGGCATTAGT  
 AGCTGAGCATTTGAAGACATTTTACGGGGTAAAGCGTCGTTTACTGAGAAGATTATTGA  
 CGATACCTGTCATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGA  
 TGCTGCTCGACAAAAATACCCGTCAAAAGAAATTTAGCTAATTTTCCAACCGCATACGTT  
 CACTCGTACGATAGCTCTTTTACAGCAATTTGCCATGCCCTTGGTCAAGCGGATAGCGT  
 TTATCTCGCTCAAAATATGATGGTTCTGCTAGAGAAGTAGATAATGGTGAAGGTAGA  
 AGATTAGCTGCTAAGATTGTCAAACTCAGATTAGTGACAGTCGAAAATGTCTCGCC  
 TTACTCAATCATGATAATGCTGTCTATGTCCTTATGGGTGCTGGAGACATTCAATTGTA  
 TGAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4603

**STRAIN 090**

AAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACCCAACTGGTTTAGAGCAAGCA  
 GGTGTAACATATATTTACCTTTCTCACCAGAATAATATCAGTGAGGATTTAGAGATTATTGCA  
 GGAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTAT  
 CATTTTAAACGATATCATGAATTTCTCGGAGATTATTATGCGTCAGTTCACTAGTCTAGGT  
 GTAGCTGGGGCAGATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAA  
 ATTACAGACACTTCTTTCTTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAAT  
 TACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATA  
 TCAATTTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCTAGAGGACGTA  
 TTCATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAA  
 GATTCAAAACCTTCATGAAATCACCTCTAAGGCACCAATATATTATTATGGTTTGAAGAT  
 TCAATGATTTTATAGCAAAAGACATCACTCGAAGCTTAAATGGTTCTGACTTTAAGGT  
 TTCTATAACCAAGAAAGAAATTTGGTCAGTTTTCATGTACCGATACGGTAAACATAATAT  
 TTAATGCAACTGCTGTTTATGCTAACCCTTTACATAATGGGAATTGATATGGCATTAGTA  
 GCTGAGCATTTGAAGACATTTTACGGGGTAAACGTCGTTTACTGAGAAGATTATTGAC  
 GATACTGTCATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGAT  
 GCTGCTCGACAAAAATACCCGTCAAAAGAAATTTAGCTAATTTTCCAACCGCATACGTT  
 ACTCGTACGATAGCTCTTTTACAGCATTTTGCCATGCTTTGAGTCAAGCGGATAGCGTT  
 TATCTTGTCTCAAAATATGCTTCTGCTAGAGAAGTAGATAATGGTGAAGGTAGA  
 GATTAGCTGCTAAGATTGTCAAACTCAGATTAGTGACAGTCGAAAATGTCTCGCC  
 TTACTCAATCATGATAATGCTGTCTATGTCCTTATGGGTGCTGGAGACATTCAATTGTAT  
 GAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4604

**STRAIN H36B**

AAAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACTCAACGTCGTTTAGAGCAAGCAGGT  
 ATAACATATATTTACCTTTCTCACCAGAATAATATCAGTGAGGATTTAGAGATTATTGCAAGGA  
 AATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATCAT  
 TTTAAACGATATCATGAATTTCTCGGAGATTATTATGCGTCAGTTCACTAGTCTAGGTGTA  
 GCTGGGGCAGATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAATATT  
 ACAGACACTTCTTTCTTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATTAC  
 TTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACTCA  
 ATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCTAGAGGACGTATTC  
 AATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAAGAT

**Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)**

CCAAAACCTTCATGAAATCACTTCTGAGGCACCAATATATTATTATGGTTTGAAGATTCA  
AATGATTTTATAGCAAAAGATATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTTTC  
TATAACCAAGAAGAAATTGGTCAGTTTACGTAACCATACGATACGGTAAACATAATATCTTA  
AATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCT  
GAGCAITTTGAAGACATTTTCAGGGGTAACCGTCTGTTTACTGAGAAAATTATTGACGAT  
ACTGTCAITTTATGATGACTTTGCTCACCATCCTACTGAGATTATTGCGCATTAGATGCT  
GCTCGACAAAATACCCCTCAAAAGAAATGTAGCTATTTTCCAACCGCATACGTTCACT  
CGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGTTTAT  
CTCGCTCAAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAAGAT  
TTAGTCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCTTTA  
CTCAATCATGATAATGCTGTCTATGCTTTTATGGGTGCTGGAGACATTCAATTGTATGAG  
CGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4605

STRAIN 18RS21

AAAGCAGGCTCTAGTGACGTTGACAAATATTTTACCACCGTGGTTTAGAGCAAGCA  
GGTGTAACCTATATACCTTTCTCACCGAATAATATCAGTGAGGATTAGAGATTATTGCA  
GGAAATGCTTTTCGTCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTAT  
CATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT  
GTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAAT  
ATTACAGACACTCTTTTCTAATTTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAAT  
TACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATA  
TCAATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCTTAGAGGACGTA  
TTCAATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTATGGAGAA  
GATCCAAAACCTTCATGAATCACTTCTGAGGCACCAATATATTTATGGTTTGAAGAT  
TCAAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTT  
TTCTATAACCAAGAAGAAATTGGTCAGTTTCTGTAACGACATACGGTAAACATAATATC  
TTAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTA  
GCTGAGCAITTTGAAGACGTTTTCAGGGGTAAAGCGTCTGTTTACTGAGAAGATTATTGAC  
GATACGTGCTATTATTTAGTACCTTTGCTCACCATCCTACTGAGATTATTGCGCATTAGAT  
GCTGCTCGACAAAATACCCGTCAAAAGAAATTTAGTACTATTTTCCAACCGCATACGTTT  
ACTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGTT  
TATCTCGCTCAAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGA  
AGTTTATAGTCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCT  
TTACTCAATCATGATAATGCTGTCTATGCTTTTATGGGTGCTGGAGACATTCAATTGTAT  
GAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4606

STRAIN M732

AAAAGCAGGCTCTAGTGACGTTGACAAATATTTTACCACCGTGGTTTAGAGCAAGCAG  
GTGTAACCTATATACCTTTCTCACCGAATAATATCAGTGAGGATTAGAGATTATTGCA  
GAAATGCTTTTCGTCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATC  
ATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT  
TAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAATA  
TTACAGACACTCTTTTCTAATTTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAAT  
ACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACT  
CAATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCTTAGAGGACGTA  
TCAATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTATGGAGAA  
ATCCAAAACCTTCATGAATCACTTCTGAGGCACCAATATATTTATGGTTTGAAGAT  
CAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTT  
TTCTATAACCAAGAAGAAATTGGTCAGTTTCTGTAACGACATACGGTAAACATAATATCT  
TAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAG  
CTGAGCAITTTGAAGACATTTTCAGGGGTAAAGCGTCTGTTTACTGAGAAGATTATTGAC  
ATACTGTCTATTATTTAGTACTTTGCTCACCATCCTACTGAGATTATTGCGCATTAGAT  
CTGCTCGACAAAATACCCGTCAAAAGAAATTTAGTACTATTTTCCAACCGCATACGTTTCA  
CTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGTT  
ATCTCGCTCAAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGA  
AGTTTATAGTCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCCT  
TACTCAATCATGATAATGCTGTCTATGCTTTTATGGGTGCTGGAGACATTCAATTGTAT  
AGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4607

STRAIN M781

AAAGCAGGCTCTAGTGACGTTGACAAATATTTTACCACCGTGGTTTAGAGCAAGCAG  
GTGTAACCTATATACCTTTCTCACCGAATAATATCAGTGAGGATTAGAGATTATTGCA  
GAAATGCTTTTCGTCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATC  
ATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT  
GTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAA  
TATTACAGACACTCTTTTCTAATTTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAA  
TTACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATA  
TCAATTATTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCTTAGAGGACGT  
ATTCAATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTATGGAGA  
AGATCCAAAACCTTCATGAATCACTTCTGAGGCACCAATATATTTATGGTTTGAAGA  
TTCAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGT  
TTTCTATAACCAAGAAGAAATTTGGTCAGTTTCTGTAACGACATACGGTAAACATAATAT  
CTTAAATGCAACTGCTGTTTATTTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGT  
AGCTGAGCAITTTGAAGACATTTTCAGGGGTAAAGCGTCTGTTTACTGAGAAGATTATTGA  
CGATACTGTCAATATTAGTACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGA  
TGCTGCTCGACAAAATACCCGTCAAAAGAAATTTAGTACTATTTTCCAACCGCATACGTT  
CACTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCCTTGAGTCAAGCGGATAGCGT  
TTATCTCGCTCAAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGA  
AGATTAGTCTGCTAAGATTGTCAAACACTCAGATTTAGTGACAGTCGAAAATGTCTCGCC  
TTTACTCAATCATGATAATGCTGTCTATGCTTTTATGGGTGCTGGAGACATTCAATTGTAT

**Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)**

TGAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4608

STRAIN CJB110

AAAAAGCAGGCTCTAGTGACGTGACAAATATATTTTACCCAACGTGGTTAGAGCAAGCA  
 GGTGTAACATAATACCTTTCTCACCAGAAATATATCAGTGAGGATTTAGAGATTTAGGCA  
 GGAAATGCTTTTCTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTTGAAAAGGGCTAT  
 CATTTTAAACGATATCATGAATTTCTCGGAGATTTATGCGTCAGTTCACTAGTCTAGGT  
 GTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAAT  
 ATTACAGACACTTCTTTCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAAT  
 TACTTTGTGTTGAAGCTGATGAATACGACGTCATTTTATGCCGTACCATCCAGAATAC  
 TCAATTATTACCAATATGATTGTTGACCATCTGATTATTTTACAGGCCCTAGAGGACGTA  
 TTCAATGCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTATGGAGAA  
 GATTCAAAACCTTCATGAATCACTTCTAAGGCACCAATATATATTATGTTTGAAGAT  
 TCAAATGATTTTATAGCAAAAGACATCACTCGAAGCTTAAATGGTTCTGACTTTAAGGTT  
 TTCTATAACCAAGAGAAATTTGGTCAGTTTCATGTACAGCATACGGTAAACATAATATC  
 TTAATATCAACTGCTGTTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTA  
 GCTGAGGATTTGAAGACATTTTCAAGGGTAAAACGTCGTTTACTGAGAAGATTATTGAC  
 GATACTGTCAATTATGATGACTTTGCTCACCATCTACTGAGATTATTCGACATTAGAT  
 GCTGCTCGACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCAACCCGCATACGTTT  
 ACTCGTACGATAGCTCTTTTAGACGATTTTGCCCATGCTTTGAGTCAAGCGGATAGCGTT  
 TATCTTGCTCAAAATATGTTGCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAA  
 GATTTAGCTGCTAAGATTGTTCAAACTCAGATTAGTGACAGTCGAAAATGTCTCGCCT  
 TTACTCAATCATGATAATGCTGCTATGCTTTTATGGGTGCTGGAGACATTCAATTGTAT  
 GAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4609

STRAIN JM9130013 (reverse complement)

GTTCAAAAAGCAGGCTCTAGTGACGTGACAAATATTTTACTCAACGTGGTTTGA  
 GCAAGCAGGTATACCTATATTAACCTTTCTCACCAGAAATATATCAGTGAGGATTTAGAGAT  
 TATGTCAGGAAATGCTTTTCCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTTGAAA  
 GGGCTATCATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAG  
 TCTAGGTGATAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTT  
 AAAAAATATTACAGACACTTCTTTCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAA  
 TGCTAATTACTTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCC  
 AGAATACCTCAATATATTACCAATATTGATTTTGACCATCTGATTATTTTACAGGCCCTAGA  
 GGACGTATTCAATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATT  
 TGGAGAAGATCCAAAACCTCATGAATCACTTCTGAGGCACCAATATATATTATGTTT  
 TGAAGATTCAATGATTTTATAGCAAAAGATATCACTCGAAGCTTAAATGGTTCTGACTT  
 TAAGGTTTCTTATAACCAAGAGAAATTTGGTCAGTTTCAAGTACAGCATACGGTAAACA  
 TAATATCTTAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGC  
 ATTAGTAGCTCAGCATTTGAAGACATTTTCAAGGGTAAAACGTCGTTTACTGAGAAAAT  
 TATTGACGATACCTGCTATTATTGATGACTTTGCTCACCATCTACTGAGATTATTGCGAC  
 ATTAGATGCTGCTCGACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCCAAACCGCA  
 TACGTTCACTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCTTTGAGTCAAGCGGA  
 TAGCGTTTATCTCGCTCAAAATATGTTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAA  
 GGTAGAAGATTATGCTGCTTAAGATTGTCAAACTCAGATTATTAGTGACAGTCGAAAATGT  
 CTCGCCCTTACTCAATCATGATAATGCTGCTATGCTCTTTATGGGTGCTGGAGACATTCA  
 ATTGTATGAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4610

STRAIN COH1 reverse complement

CAGGCTCTAGTGACGTGACAAATATTTTACCCAACGTGGTTAGAGCAAGCAGGTGTAA  
 CTATATTACCTTTCTCACCAGAAATATATCAGTGAGGATTTAGAGATTTATGTCAGGAAATG  
 CTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTTGAAAAGGGCTCATTTTAA  
 AACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGTGTAGCTG  
 GGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAATATTACAG  
 ACACCTCTTTCTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATTACTTTG  
 TGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACTCAATTA  
 TTACCAATATTGATTTTGACCATCTGATTATTTTACAGGCCCTAGAGGACGTATTCAATG  
 CCTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTATGGAGAAGATCCAA  
 AACCTCATGAATCACTTCTGAGGCACCAATATATATTATGTTTGAAGATTCAATG  
 ATTTTATAGCAAAAGACATCACTCGAAGCTTAAATGGTTCTGACTTTAAGGTTTCTATA  
 ACCAAGAAGAAATTTGGTCAGTTTCAATGATACAGCATACGGTAAACATAATATCTTAAATG  
 CAACTGCTGTTTATGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCTGAGC  
 ATTTGAAGACATTTTCAAGGGTAAAACGTCGTTTACTGAGAAGATTATTGACGATACCTG  
 TCATTATTGATGACTTTGCTCACCATCTACTGAGATTATTGCGACATTAGATGCTGCTC  
 GACAAAAATACCCGTCAAAAGAAATTTAGCTATTTTCCAAACCGCATACGTTCACTCGTA  
 CGATAGCTCTTTTAGACGAATTTGCCCATGCTTTGAGTCAAGCGGATAGCGTTTATCTCG  
 CTCAAATATATTGTTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAAGATTGAG  
 CTGCTAAGATTGTCAAACTCAGATTATTAGTGACAGTCGAAAATGTCTCGCCTTACTCA  
 ATCATGATAATGCTGCTATGCTCTTTATGGGTGCTGGAGACATTCAATTGTATGAGCGCT  
 CTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4611

STRAIN 2603

atgtcaaaaacttatcattttattgggtattaaaggatccggaatgagtgccctagcactg  
 atgcttcacatacaaatgggacataacgtccaaggaagtgacgttgacaaatattattttacc  
 caacgtgggttagaggaagcaggtgtaactatattacctttctcaccgaataatcagc  
 gaggatttagagattattgcaggaatgcttttctgctccagataacaatgaagagttggct  
 tatgttattgaaaagggtatcaatttaaacgataatgaattttctcgagattttatg  
 cgtcagttcaactagtcaggtgtagctggggcacatggaaaaacctcaacgacaggttta  
 ttagctcatgttttaaaaaatattacagacacttctttcctaattggagatgggtacagga

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

cgtgggtctgctaattgctaattactttgtgtttgaagctgatgaatacgaacgtcatttt  
 atgccgtaccatccagaataactcaattattaccaatattgattttgaccatcctgattat  
 tttacaggcttagaggacgtattcaatgcctttaatgactatgctaagcaagttcaaaaa  
 ggtttattcatttatggagaagatccaaaacttcatgaaatcacttctgaggcaccaata  
 tattattatgggttttgaagattcaaatgattttatagcaaaagacatcactcgactgtt  
 aatgggtctgactttaagggtttctataaccaagaagaatttggtcagtttcatgtacca  
 gcatacggtaaaacataatattctaaatgcaactgctgtttatgctaaccctttacataatg  
 ggaatttgatattggcatttagtagctgagcatttgaagacgttttcaggggtaagcgtcgt  
 ttactgagaagattattgacgatactgtcattattgatgactttgctcaccatcctact  
 gagattattgcgacatttagatgctgctcgacaaaaataccggtcaaaagaattttagct  
 attttccaacccgatacgttcaactgtagcagtagctcttttagacgaatttgcccatgcc  
 ttgagtcaagcgataagcgtttatctcgctcaaatataggttctgctagagaagtagat  
 aatgggtgaggtgaaggtagaagatttagctgctaagattgtcaaacactcagatttagtg  
 acagtcgaaaaatgtctcgcttactcaatcatgataatgctgtctatgtctttaggggt  
 gctggagacattcaattgtatgagcgtcttttgaagaattatttagtaacctaaactaaa  
 aatacacia

SEQ ID NO. 4612

STRAIN COH1 reverse complement

CAGGCTCTAGTGACGTTGACAAATATATTTTACCCCAACGTGGTGTAGAGCAAGCAGGTGTAA  
 CTATATTACTCTTTCTCACCGAATAATATCAGTGAGGATTTAGAGATTATGCAGGAAATG  
 CTTTTCGTCAGATAACAAATGAAGAGTTGGCTTATGTTATTGAAAAGGCTATCATTTTA  
 AACGATATCATGAATTTCTCGGAGATTTATGCGTCAGTTCACTAGTCTAGGTGTAGCTG  
 GGGACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAATATACAG  
 ACACCTCTTTCTTAATTGGAGATGGTACAGGACGTGGTCTGCTAATGCTAATTACTTTG  
 TGTTTGAAGCTGATGAATACGACGTCATTTTATGCCGTACCATCCAGAATACTCAATTA  
 TTACAATATTGATTTTGACCATCTGATTATTTTACAGGCTTAGAGGACGTATTCAATG  
 CCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAAGATCCAA  
 AACTTCATGAAATCACTTCTGAGGCACCAATATATTTATTTGTTTGAAGATTCAAATG  
 ATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTTTCTATA  
 ACCAAGAAGAAATGGTCAGTTTATGTAACGACATACGGTAACATAATATCTTAAATG  
 CACTGCTGTTTATGCTAACCCTTTACATAATGGGAATTGATATGGCATTAGTAGCTGAGC  
 ATTTGAAGACATTTTCAGGGGTAAGCGTCTGTTTACTGAGAAGATTATTGACGACTACTG  
 TCATTTATGATGACTTTGCTCACCATCTACTGAGATTATTGCGACATTAGATGCTGCTC  
 GACAAAAATACCCGTCAAAAGAAATTTGTAGCTATTTTCCAACCGCATACGTTCACTCGTA  
 CGATAGCTCTTTTAGACGAATTTGCCCATGCTTGAAGTCAAGCGGATAGCGTTTATCTCG  
 CTCAAATATATGTTTCTAGAGAAGTAGATAATGGTGAGGTGAAGTGAAGAAGATTTCAG  
 CTGCTAAGATTGTCAAACACTCAGATTATTAGTGACAGTCAAAAAATGCTCTCGCTTTACTCA  
 ATCATGATAATGCTGTCTATGCTCTTTATGGGTGCTGGAGACATTCAATTGTATGAGCGCT  
 CTTTGAAGAATTTATAGCTAACCTAACCTAATAAAAAATACACAA

PRETTY of: /biotmp/msa56524.2{\*} November 26, 2002 08:06 ..  
 PRETTY of: /biotmp/msa253045.2{\*} January 31, 2003 03:51 ..

	1				50
msa253045.2{157_090}	-----	-----	-----	-----	-----
msa253045.2{157_CJB110}	-----	-----	-----	-----	-----
msa253045.2{157_H36B}	-----	-----	-----	-----	-----
msa253045.2{157_JM9130013}	-----	-----	-----	-----	-----
msa253045.2{157_1169NT}	-----	-----	-----	-----	-----
msa253045.2{157_A909}	-----	-----	-----	-----	-----
msa253045.2{157_COH1}	-----	-----	-----	-----	-----
msa253045.2{157_M732}	-----	-----	-----	-----	-----
msa253045.2{157_M781}	-----	-----	-----	-----	-----
msa253045.2{157_18RS21}	-----	-----	-----	-----	-----
msa253045.2{157_2603}	atgtcaaaaa	cttatcattt	tattgggatt	aaaggatccg	gaatgagtcg
Consensus	*****	*****	*****	*****	*****
	51				100
msa253045.2{157_090}	-----	-----	-----	-aaagcaggc	tctagtgcg
msa253045.2{157_CJB110}	-----	-----	-----	-Aaaaagcaggc	tctagtgcg
msa253045.2{157_H36B}	-----	-----	-----	-Aaaaagcaggc	tctagtgcg
msa253045.2{157_JM9130013}	-----	-----	-----	-GttcaAaaaagcaggc	tctagtgcg
msa253045.2{157_1169NT}	-----	-----	-----	-Aaaaagcaggc	tctagtgcg
msa253045.2{157_A909}	-----	-----	-----	-----	-----
msa253045.2{157_COH1}	-----	-----	-----	-----caggc	tctagtgcg
msa253045.2{157_M732}	-----	-----	-----	-Aaaaagcaggc	tctagtgcg
msa253045.2{157_M781}	-----	-----	-----	-aaagcaggc	tctagtgcg
msa253045.2{157_18RS21}	-----	-----	-----	-aaagcaggc	tctagtgcg
msa253045.2{157_2603}	cctagcactg	atgcttcac	aaatGggacA	taacgtccaa	ggaagtgcg
Consensus	*****	*****	*****	*****	*****
	101				150
msa253045.2{157_090}	tTGACAAATA	TTATTTTACc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
msa253045.2{157_CJB110}	tTGACAAATA	TTATTTTACc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
msa253045.2{157_H36B}	tTGACAAATA	TTATTTTACt	CAACGTGGTT	TAGAGCAAGC	AGGTaTAACT
msa253045.2{157_JM9130013}	tTGACAAATA	TTATTTTACt	CAACGTGGTT	TAGAGCAAGC	AGGTaTAACT
msa253045.2{157_1169NT}	tTGACAAATA	TTATTTTACc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
msa253045.2{157_A909}	-TGACAAATA	TTATTTTACc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
msa253045.2{157_COH1}	tTGACAAATA	TTATTTTACc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
msa253045.2{157_M732}	tTGACAAATA	TTATTTTACc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
msa253045.2{157_M781}	tTGACAAATA	TTATTTTACc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
msa253045.2{157_18RS21}	tTGACAAATA	TTATTTTACc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT



Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_2603}	tTGACAAATA	TTATTTTAcc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
Consensus	*****	*****	*****	*****	*****
	151				200
msa253045.2{157_090}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_CJB110}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_H36B}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_JM9130013}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_1169NT}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_A909}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_COH1}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_M732}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_M781}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_18RS21}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_2603}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
Consensus	*****	*****	*****	*****	*****
	201				250
msa253045.2{157_090}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_CJB110}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_H36B}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_JM9130013}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_1169NT}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_A909}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_COH1}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_M732}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_M781}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_18RS21}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_2603}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
Consensus	*****	*****	*****	*****	*****
	251				300
msa253045.2{157_090}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_CJB110}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_H36B}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_JM9130013}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_1169NT}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_A909}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_COH1}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_M732}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_M781}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_18RS21}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_2603}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
Consensus	*****	*****	*****	*****	*****
	301				350
msa253045.2{157_090}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_CJB110}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_H36B}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_JM9130013}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_1169NT}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_A909}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_COH1}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_M732}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_M781}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_18RS21}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_2603}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
Consensus	*****	*****	*****	*****	*****
	351				400
msa253045.2{157_090}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_CJB110}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_H36B}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_JM9130013}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_1169NT}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_A909}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_COH1}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_M732}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_M781}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_18RS21}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_2603}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
Consensus	*****	*****	*****	*****	*****
	401				450
msa253045.2{157_090}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_CJB110}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_H36B}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_JM9130013}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_1169NT}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_A909}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_COH1}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_M732}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_M781}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_18RS21}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_2603}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
Consensus	*****	*****	*****	*****	*****
	451				500
msa253045.2{157_090}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_CJB110}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_H36B}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_JM9130013}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_1169NT}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_A909}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_COH1}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_M732}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_M781}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_18RS21}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_2603}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
Consensus	*****	*****	*****	*****	*****
	501				550
msa253045.2{157_090}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_CJB110}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_H36B}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_JM9130013}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_1169NT}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_A909}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_COH1}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_M732}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_M781}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_18RS21}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_2603}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
Consensus	*****	*****	*****	*****	*****
	551				600
msa253045.2{157_090}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_CJB110}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_H36B}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_JM9130013}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_1169NT}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_A909}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_COH1}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_M732}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_M781}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_18RS21}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_2603}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
Consensus	*****	*****	*****	*****	*****
	601				650
msa253045.2{157_090}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACTTCTaA
msa253045.2{157_CJB110}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACTTCTaA
msa253045.2{157_H36B}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACTTCTgA
msa253045.2{157_JM9130013}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACTTCTgA
msa253045.2{157_1169NT}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACTTCTgA
msa253045.2{157_A909}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACTTCTgA
msa253045.2{157_COH1}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACTTCTgA
msa253045.2{157_M732}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACTTCTgA
msa253045.2{157_M781}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACTTCTgA
msa253045.2{157_18RS21}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACTTCTgA
msa253045.2{157_2603}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACTTCTgA
Consensus	*****	*****	*****	*****	*****
	651				700
msa253045.2{157_090}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_CJB110}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_H36B}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_JM9130013}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_1169NT}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_A909}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_COH1}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_M732}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_M781}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_18RS21}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_2603}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
Consensus	*****	*****	*****	*****	*****
	701				750
msa253045.2{157_090}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_CJB110}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_H36B}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_JM9130013}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_1169NT}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_A909}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_COH1}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_M732}	AAGAcATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_M781}	AAGACATCAC	TCGAAC <b>TGTT</b>	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC	
msa253045.2{157_18RS21}	AAGACATCAC	TCGAAC <b>TGTT</b>	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC	
msa253045.2{157_2603}	AAGACATCAC	TCGAAC <b>TGTT</b>	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC	
Consensus	*****	*****	*****	*****	*****	
751						800
msa253045.2{157_090}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_CJB110}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_H36B}	CAAGAAGAAA	TTGGTCAGTT	TCAGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_JM9130013}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_1169NT}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_A909}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_COH1}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_M732}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_M781}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_18RS21}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_2603}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
Consensus	*****	*****	*****	*****	*****	
801						850
msa253045.2{157_090}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_CJB110}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_H36B}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_JM9130013}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_1169NT}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_A909}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_COH1}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_M732}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_M781}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_18RS21}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_2603}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
Consensus	*****	*****	*****	*****	*****	
851						900
msa253045.2{157_090}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGT <b>CGT</b>	
msa253045.2{157_CJB110}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGT <b>CGT</b>	
msa253045.2{157_H36B}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGT <b>CGT</b>	
msa253045.2{157_JM9130013}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGT <b>CGT</b>	
msa253045.2{157_1169NT}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGT <b>CGT</b>	
msa253045.2{157_A909}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGT <b>CGT</b>	
msa253045.2{157_COH1}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGT <b>CGT</b>	
msa253045.2{157_M732}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGT <b>CGT</b>	
msa253045.2{157_M781}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGT <b>CGT</b>	
msa253045.2{157_18RS21}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACgT	TTTCAGGGGT	AAAaCGT <b>CGT</b>	
msa253045.2{157_2603}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACgT	TTTCAGGGGT	AAAaCGT <b>CGT</b>	
Consensus	*****	*****	*****	*****	*****	
901						950
msa253045.2{157_090}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_CJB110}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_H36B}	TTTACTGAGA	AaATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_JM9130013}	TTTACTGAGA	AaATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_1169NT}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_A909}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_COH1}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_M732}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_M781}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_18RS21}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_2603}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
Consensus	*****	*-*****	*****	*****	*****	
951						1000
msa253045.2{157_090}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_CJB110}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_H36B}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_JM9130013}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_1169NT}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_A909}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_COH1}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_M732}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_M781}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_18RS21}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_2603}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
Consensus	*****	*****	*****	*****	*****	
1001						1050
msa253045.2{157_090}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	
msa253045.2{157_CJB110}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	
msa253045.2{157_H36B}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	
msa253045.2{157_JM9130013}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	
msa253045.2{157_1169NT}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	
msa253045.2{157_A909}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	
msa253045.2{157_COH1}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_M732}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG		
msa253045.2{157_M781}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG		
msa253045.2{157_18RS21}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG		
msa253045.2{157_2603}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG		
Consensus	*****	*****	*****	*****	*****		
msa253045.2{157_090}	1051	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT	1100
msa253045.2{157_CJB110}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_H36B}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_JM9130013}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_1169NT}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_A909}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_COH1}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_M732}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_M781}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_18RS21}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_2603}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
Consensus	*****	*****	*****	*****	*****		
msa253045.2{157_090}	1101	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG	1150
msa253045.2{157_CJB110}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_H36B}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_JM9130013}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_1169NT}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_A909}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_COH1}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_M732}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_M781}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_18RS21}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_2603}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
Consensus	*****	*****	*****	*****	*****		
msa253045.2{157_090}	1151	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG	1200
msa253045.2{157_CJB110}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_H36B}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_JM9130013}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_1169NT}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_A909}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_COH1}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_M732}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_M781}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_18RS21}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_2603}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
Consensus	*****	*****	*****	*****	*****		
msa253045.2{157_090}	1201	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT	1250
msa253045.2{157_CJB110}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_H36B}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_JM9130013}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_1169NT}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_A909}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_COH1}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_M732}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_M781}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_18RS21}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_2603}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
Consensus	*****	*****	*****	*****	*****		
msa253045.2{157_090}	1251	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT	1300
msa253045.2{157_CJB110}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_H36B}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_JM9130013}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_1169NT}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_A909}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_COH1}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_M732}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_M781}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_18RS21}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_2603}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
Consensus	*****	*****	*****	*****	*****		
msa253045.2{157_090}	1301	TATTAGCTAA	CCTAACTAAA	AATACACAA			1329
msa253045.2{157_CJB110}	TATTAGCTAA	CCTAACTAAA	AATACACAA				
msa253045.2{157_H36B}	TATTAGCTAA	CCTAACTAAA	AATACACAA				
msa253045.2{157_JM9130013}	TATTAGCTAA	CCTAACTAAA	AATACACAA				
msa253045.2{157_1169NT}	TATTAGCTAA	CCTAACTAAA	AATACACAA				
msa253045.2{157_A909}	TATTAGCTAA	CCTAACTAAA	AATACACAA				

**Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)**

msa253045.2{157_COH1}	TATTAGCTAA	CCTAACTAAA	AATACACAA
msa253045.2{157_M732}	TATTAGCTAA	CCTAACTAAA	AATACACAA
msa253045.2{157_M781}	TATTAGCTAA	CCTAACTAAA	AATACACAA
msa253045.2{157_18RS21}	TATTAGCTAA	CCTAACTAAA	AATACACAA
msa253045.2{157_2603}	TATTAGCTAA	CCTAACTAAA	AATACACAA
Consensus	*****	*****	*****

SEQ ID NO. 4613  
STRAIN A909 frame: 2  
DKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGYHFKRYHE  
FLGDGFMROFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANANYFVFEAD  
EYERHFMPIYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGEDPKLHEI  
TSEAPIYYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNILNATAVI  
ANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLDAARQKYP  
SKEIVAI FQPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVKVEDLAAKIV  
KHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTNTQ

SEQ ID NO. 4614  
STRAIN 1169NT frame: 2  
KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY  
HFKRYHEFLGDGFMROFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN  
YFVFEADEYERHFMPIYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE  
DPKLHEITSEAPIYYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL  
NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLD  
AARQKYPSEKEIVAI FQPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVKVE  
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTNTQ

SEQ ID NO. 4615  
STRAIN 090 FRAME:1  
KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY  
HFKRYHEFLGDGFMROFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN  
YFVFEADEYERHFMPIYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE  
DSKLHEITSEAPIYYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL  
NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLD  
AARQKYPSEKEIVAI FQPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVKVE  
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTNTQ

SEQ ID NO. 4616  
STRAIN H36B frame: 2  
KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY  
HFKRYHEFLGDGFMROFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN  
YFVFEADEYERHFMPIYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE  
DPKLHEITSEAPIYYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL  
NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLD  
AARQKYPSEKEIVAI FQPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVKVE  
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTNTQ

SEQ ID NO. 4617  
STRAIN 18RS21 frame: 1  
KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY  
HFKRYHEFLGDGFMROFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN  
YFVFEADEYERHFMPIYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE  
DPKLHEITSEAPIYYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL  
NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLD  
AARQKYPSEKEIVAI FQPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVKVE  
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTNTQ

SEQ ID NO. 4618  
STRAIN M732 frame: 2  
KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY  
HFKRYHEFLGDGFMROFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN  
YFVFEADEYERHFMPIYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE  
DPKLHEITSEAPIYYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL  
NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IATLD  
AARQKYPSEKEIVAI FQPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVKVE  
DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTNTQ

SEQ ID NO. 4619  
STRAIN JM9130013 frame: 2  
FKKAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEK  
GYHFKRYHEFLGDGFMROFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN  
YFVFEADEYERHFMPIYHPEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIY  
GEDPKLHEITSEAPIYYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKH  
NILNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEI IAT  
LDAARQKYPSEKEIVAI FQPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVK  
VEDLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTNTQ

SEQ ID NO. 4620  
STRAIN M781 frame: 1  
KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY  
HFKRYHEFLGDGFMROFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

YFVFEADEYERHFMPYHPEYSIIITNIDFDHPDYFTGLEDFVNAFNDYAKQVQKGLFIYGE  
 DPKLHEITSEAPIYYYGFEDSNDFFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAKGKHN  
 LNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDTVIIDFAHHPTTEIIATLD  
 AARQKYPSEKIVAI FQPHFTFTRTIALLDFAHALSQADSVYLAQIYGSAREVDNGEVKVE  
 DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4621

STRAIN CJB110 frame: 3

KAGSSDVVKYYFTQRLGQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY  
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVKNITDTSFLIGDGTGRGSANAN  
 YFVFEADEYERHFMPYHPEYSIIITNIDFDHPDYFTGLEDFVNAFNDYAKQVQKGLFIYGE  
 DSKLHEITSEAPIYYYGFEDSNDFFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAKGKHN  
 LNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDTVIIDFAHHPTTEIIATLD  
 AARQKYPSEKIVAI FQPHFTFTRTIALLDFAHALSQADSVYLAQIYGSAREVDNGEVKVE  
 DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4622

STRAIN 2603 frame: 1

MSKTYHFIGIKGSGMSALALMLHQMGNHVQGSVDVKYYFTQRLGQAGVTILPFPSPNNIS  
 EDLEIIAGNAFRPDNNEELAYVIEKGYQFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGL  
 LAHVKNITDTSFLIGDGTGRGSANANYFVFEADEYERHFMPYHPEYSIIITNIDFDHPDY  
 FTGLEDFVNAFNDYAKQVQKGLFIYGEDPKLHEITSEAPIYYYGFEDSNDFFIAKDITRTV  
 NGSDFKVFYNQEEIGQFHVPAKGKHNILNATAVIANLYIMGIDMALVAEHLKTFSGVKRR  
 FTEKIIDTVIIDFAHHPTTEIIATLDAARQKYPSEKIVAI FQPHFTFTRTIALLDFAHA  
 LSQADSVYLAQIYGSAREVDNGEVKVEDLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMG  
 AGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4623

STRAIN COH1 frame: 3

GSSDVVKYYFTQRLGQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGYHF  
 KRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVKNITDTSFLIGDGTGRGSANANYF  
 VFEADEYERHFMPYHPEYSIIITNIDFDHPDYFTGLEDFVNAFNDYAKQVQKGLFIYGEDP  
 KLHEITSEAPIYYYGFEDSNDFFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAKGKHNILN  
 ATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDTVIIDFAHHPTTEIIATLDAAR  
 QKYPSEKIVAI FQPHFTFTRTIALLDFAHALSQADSVYLAQIYGSAREVDNGEVKVEDL  
 AAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

PRETTY of: /biotmp/msa56635.2{\*} November 26, 2002 08:08 ..

	1		50
msa253220.2{157_090}	-----kag	ssdvDKYYFT	QRLGQAGvT
msa253220.2{157_CJB110}	-----kag	ssdvDKYYFT	QRLGQAGvT
msa253220.2{157_1169NT}	-----kag	ssdvDKYYFT	QRLGQAGvT
msa253220.2{157_18RS21}	-----kag	ssdvDKYYFT	QRLGQAGvT
msa253220.2{157_M732}	-----kag	ssdvDKYYFT	QRLGQAGvT
msa253220.2{157_M781}	-----kag	ssdvDKYYFT	QRLGQAGvT
msa253220.2{157_COH1}	-----g	ssdvDKYYFT	QRLGQAGvT
msa253220.2{157_H36B}	-----kag	ssdvDKYYFT	QRLGQAGiT
msa253220.2{157_JM9130013}	-----fkkag	ssdvDKYYFT	QRLGQAGiT
msa253220.2{157_2603}	msktyhfigi ksgsgmsalal mlhqmghnvq	gsdvDKYYFT	QRLGQAGvT
msa253220.2{157_A909}	-----DKYYFT	QRLGQAGvT	
Consensus	*****	*****	*****
	51		100
msa253220.2{157_090}	ILPFPSPNNIS	EDLEIIAGNA	FRPDNNEELA
msa253220.2{157_CJB110}	ILPFPSPNNIS	EDLEIIAGNA	FRPDNNEELA
msa253220.2{157_1169NT}	ILPFPSPNNIS	EDLEIIAGNA	FRPDNNEELA
msa253220.2{157_18RS21}	ILPFPSPNNIS	EDLEIIAGNA	FRPDNNEELA
msa253220.2{157_M732}	ILPFPSPNNIS	EDLEIIAGNA	FRPDNNEELA
msa253220.2{157_M781}	ILPFPSPNNIS	EDLEIIAGNA	FRPDNNEELA
msa253220.2{157_COH1}	ILPFPSPNNIS	EDLEIIAGNA	FRPDNNEELA
msa253220.2{157_H36B}	ILPFPSPNNIS	EDLEIIAGNA	FRPDNNEELA
msa253220.2{157_JM9130013}	ILPFPSPNNIS	EDLEIIAGNA	FRPDNNEELA
msa253220.2{157_2603}	ILPFPSPNNIS	EDLEIIAGNA	FRPDNNEELA
msa253220.2{157_A909}	ILPFPSPNNIS	EDLEIIAGNA	FRPDNNEELA
Consensus	*****	*****	*****
	101		150
msa253220.2{157_090}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD
msa253220.2{157_CJB110}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD
msa253220.2{157_1169NT}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD
msa253220.2{157_18RS21}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD
msa253220.2{157_M732}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD
msa253220.2{157_M781}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD
msa253220.2{157_COH1}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD
msa253220.2{157_H36B}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD
msa253220.2{157_JM9130013}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD
msa253220.2{157_2603}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD
msa253220.2{157_A909}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD
Consensus	*****	*****	*****
	151		200
msa253220.2{157_090}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY
			FTGLEDFVNA
			FNDYAKQVQK

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253220.2{157_CJB110}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_1169NT}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_18RS21}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_M732}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_M781}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_COH1}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_H36B}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_JM9130013}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_2603}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_A909}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
Consensus	*****	*****	*****	*****	*****
msa253220.2{157_090}	GLFIYGEDsK	LHEITskAPI	YYYGFEDSND	FIKIDITRTV	NGSDFKVFYN
msa253220.2{157_CJB110}	GLFIYGEDsK	LHEITskAPI	YYYGFEDSND	FIKIDITRTV	NGSDFKVFYN
msa253220.2{157_1169NT}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKIDITRTV	NGSDFKVFYN
msa253220.2{157_18RS21}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKIDITRTV	NGSDFKVFYN
msa253220.2{157_M732}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKIDITRTV	NGSDFKVFYN
msa253220.2{157_M781}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKIDITRTV	NGSDFKVFYN
msa253220.2{157_COH1}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKIDITRTV	NGSDFKVFYN
msa253220.2{157_H36B}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKIDITRTV	NGSDFKVFYN
msa253220.2{157_JM9130013}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKIDITRTV	NGSDFKVFYN
msa253220.2{157_2603}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKIDITRTV	NGSDFKVFYN
msa253220.2{157_A909}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKIDITRTV	NGSDFKVFYN
Consensus	*****	*****	*****	*****	*****
msa253220.2{157_090}	QEEIGQFHPV	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_CJB110}	QEEIGQFHPV	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_1169NT}	QEEIGQFHPV	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_18RS21}	QEEIGQFHPV	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_M732}	QEEIGQFHPV	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_M781}	QEEIGQFHPV	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_COH1}	QEEIGQFHPV	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_H36B}	QEEIGQFHPV	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_JM9130013}	QEEIGQFHPV	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_2603}	QEEIGQFHPV	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_A909}	QEEIGQFHPV	AYGKHNLNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
Consensus	*****	*****	*****	*****	*****
msa253220.2{157_090}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_CJB110}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_1169NT}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_18RS21}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_M732}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_M781}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_COH1}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_H36B}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_JM9130013}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_2603}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_A909}	FTEKIIDDTV	IIDDFAHHPT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
Consensus	*****	*****	*****	*****	*****
msa253220.2{157_090}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_CJB110}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_1169NT}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_18RS21}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_M732}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_M781}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_COH1}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_H36B}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_JM9130013}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_2603}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_A909}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
Consensus	*****	*****	*****	*****	*****
msa253220.2{157_090}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_CJB110}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_1169NT}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_18RS21}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_M732}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_M781}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_COH1}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_H36B}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_JM9130013}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_2603}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_A909}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
Consensus	*****	*****	*****	*****	*****

**Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)****SEQ ID NO. 4701****STRAIN A909**

TATTTTTTAAACAACAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA  
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA  
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACITTTAAAGAT  
 TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC  
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG  
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACCTGCTAAAAAAGAA  
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCAITGATTATAAAGA  
 AAACACAGAAGATAAAGAAAAA

**SEQ ID NO. 4702****STRAIN H36B**

TATTTTTTAAACAACAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA  
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA  
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACITTTAAAGAT  
 TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC  
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG  
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACCTGCTAAAAAAGAA  
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCAITGATTATAAAGA  
 AAACACAGAAGATAAAGAAAAA

**SEQ ID NO. 4703****STRAIN 18RS21**

TATTTTTTAAACAACAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA  
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA  
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACITTTAAAGAT  
 TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC  
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG  
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACCTGCTAAAAAAGAA  
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCAITGATTATAAAGA  
 AAACACAGAAGATAAAGAAAAA

**SEQ ID NO. 4704****STRAIN M732**

TATTTTTTAAACAACAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA  
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA  
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACITTTAAAGAT  
 TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC  
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG  
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACCTGCTAAAAAAGAA  
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCAITGATTATAAAGA  
 AAACACAGAAGATAAAGAAAAA

**SEQ ID NO. 4705****STRAIN COH1**

TATTTTTTAAACAACAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA  
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA  
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACITTTAAAGAT  
 TATAAAGGTAAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC  
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG  
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACCTGCTAAAAAAGAA  
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCAITGATTATAAAGA  
 AAACACAGAAGATAAAGAAAAA

**SEQ ID NO. 4706****STRAIN M781**

TATTTTTTAAACAACAAAAAGGAAAAGAGC  
 TAAGGAAAAATGCAGAAAAATTTCTATGGAGAATATAAAGAAAATCCAGAA  
 GAATATCATCAAATAGCTAAAGATAAAGCAAGTGAATATTCAAATTTAGC  
 TGTGATACITTTAAAGATTATAAAGGTAAATTTGAATCAGGTGAATTGA  
 CAACAGAGGATATCGTCTCAGCCGTTAAGGAAAAAAGCGGAGAAGTAGTT  
 GACTTTGCTAATGATTTTGTCAATCAAGCTAAATCAAATTTCTCAGACGA  
 GGATACCTGCTAAAAAAGAGATAAGGCTCCTGAAACAAAAGTAGAAGATA  
 TTGTCAITGATTATAAAGAAAACACAGAAGATAAAGAAAAA

**SEQ ID NO. 4707****STRAIN 2603**

tatTTTTTAAACAACAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA  
 attctatggagaatataaagaaaatccagaagaatcatcaaataagcta  
 aagataaagcaagtgaaattcaaaatttagctgttgatacttttaagat  
 tataaaggtaaatTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC  
 agccgttaaggaaaaaagcggaagtagttgactttgctaatgattttg  
 tcaatcaagctaaatcaaaattctcagacgaggatactgctaaaaaagaa  
 gataaggctcctgaacaaaagtagaagatattgtcattgattataaaga  
 aaacacagaagataaagaaaaa

**SEQ ID NO. 4708****STRAIN 090**

TATTTTTTAAACAACAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA  
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA  
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACITTTAAAGAT



Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

TATAAAGGTTAAATTGAATCAGGTGAATTGACACAGAGGATATCGTCTC  
 AGCCCGTTAAGGAAAAAGCGGAGAGTAGTTGACTTTGCTAATGATTTTG  
 TCAATCAAGCTAAATCAAAATTTCTCAGACGAGGATCTGCTAAAAAGAA  
 GATAAGGCTCTGAAACAAAAAGTAGAAGATATTGTCATTGATTATAAAGA  
 AAACACAGAAGATAAGAAAA

SEQ ID NO. 4709

STRAIN CJB110

TATTTTAAACAACAAAAAGGAAAAAGGCTAAGGAAAA  
 ATGCAGAAAAATTTCTATGGAGAATATAAAGAAAAATCCAGAAGATATCAT  
 CAAATAGCTAAAGATAAAGCAAGTGAATATTTCAAATTTAGCTGTTGATAC  
 TTTTAAAGATTATAAAGGTAATTTGAATCAGGTGAATTGACACAGAGG  
 ATATCGTCTCAGCCGTAAAGGAAAAAGCGGAGAAGTAGTTGACTTTGCT  
 AATGATTTTGTCAATCAAGCTAAATCAAAATTTCTCAGACGAGGATACTGC  
 TAAAAAGAAGATAAGGCTCTGAAACAAAAAGTAGAAGATATTGTCATTG  
 ATTATAAAGAAAAACAGAAGATAAAGAAAA

SEQ ID NO. 4710

STRAIN 1169NT

TATTTTAAACAACAAAAAGGAAAAAGGCTAAGGAAAA  
 AATGCAGAAAAATTTCTATGGAGAATATAAAGAAAAATCCAGAAGATATCAT  
 TCAATAGCTAAAGATAAAGCAAGTGAATATTTCAAATTTAGCTGTTGATA  
 CTTTTAAAGATTATAAAGGTAATTTGAATCAGGTGAATTGACACAGAG  
 GATATCGTCTCAGCCGTAAAGGAAAAAGCGGAGAAGTAGTTGACTTTGCT  
 TAATGATTTTGTCAATCAAGCTAAATCAAAATTTCTCAGATGAGGATACTGC  
 CTAAAAAGAAAAATAAGGCTCTGAAACAAAAAGTAGAAGATATTGTCATT  
 GATTATAAAGAAAAACAGAAGATAAAGAAAA

SEQ ID NO. 4711

STRAIN JM9130013

TATTTTAAACAACAAAAAGGAAAAAGGCTAAGGAAAA  
 ATGCAGAAAAATTTCTATGGAGAATATAAAGAAAAATCCAGAAGATATCAT  
 CAAATAGCTAAAGATAAAGCAAGTGAATATTTCAAATTTAGCTGTTGATAC  
 TTTTAAAGATTATAAAGGTAATTTGAATCAGGTGAATTGACACAGAGG  
 ATATCGTCTCAGCCGTAAAGGAAAAAGCGGAGAAGTAGTTGACTTTGCT  
 AATGATTTTGTCAATCAAGCTAAATCAAAATTTCTCAGACGAGGATACTGC  
 TAAAAAGAAGATAAGGCTCTGAAACAAAAAGTAGAAGATATTGTCATTG  
 ATTATAAAGAAAAACAGAAGATAAAGAAAA

PRETTY of: /biotmp/msa68511.2{\*} January 22, 2003 05:47 ..

	1	50
msa68511.2{164_090}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_18RS21}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_2603}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_A909}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_CJB110}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_COH1}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_H36B}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_JM9130013}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_M732}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_M781}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
msa68511.2{164_1169NT}	TATTTTAA CAACAAAAA AGGAAAAGAG CTAAGGAAAA ATGCAGAAAA	
Consensus	*****	*****
	51	100
msa68511.2{164_090}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_18RS21}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_2603}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_A909}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_CJB110}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_COH1}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_H36B}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_JM9130013}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_M732}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_M781}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
msa68511.2{164_1169NT}	ATTCTATGGA GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA	
Consensus	*****	*****
	101	150
msa68511.2{164_090}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_18RS21}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_2603}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_A909}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_CJB110}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_COH1}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_H36B}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_JM9130013}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_M732}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_M781}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
msa68511.2{164_1169NT}	AAGATAAAGC AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT	
Consensus	*****	*****

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

	151		200
msa68511.2{164_090}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_18RS21}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_2603}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_A909}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_CJB110}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_COH1}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_H36B}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_JM9130013}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_M732}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_M781}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_1169NT}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
Consensus	*****	*****	*****
	201		250
msa68511.2{164_090}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_18RS21}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_2603}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_A909}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_CJB110}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_COH1}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_H36B}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_JM9130013}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_M732}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_M781}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_1169NT}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
Consensus	*****	*****	*****
	251		300
msa68511.2{164_090}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_18RS21}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_2603}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_A909}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_CJB110}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_COH1}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_H36B}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_JM9130013}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_M732}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_M781}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_1169NT}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
Consensus	*****	*****	*****
	301		350
msa68511.2{164_090}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_18RS21}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_2603}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_A909}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_CJB110}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_COH1}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_H36B}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_JM9130013}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_M732}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_M781}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_1169NT}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
Consensus	*****	*****	*****
	351		372
msa68511.2{164_090}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_18RS21}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_2603}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_A909}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_CJB110}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_COH1}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_H36B}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_JM9130013}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_M732}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_M781}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_1169NT}	AAACACAGAA	GATAAAGAAA	AA
Consensus	*****	*****	**

SEQ ID NO. 4712

STRAIN 2603

YFLITTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSLNLAVDTFKDYKGFESGEL  
 TTEDIVSAVKEKSGEVDFDFVNFQAKSKFSDDEDATKEDKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4713

STRAIN A909 frame: 1

YFLITTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSLNLAVDTFKDYKGFESGEL  
 TTEDIVSAVKEKSGEVDFDFVNFQAKSKFSDDEDATKEDKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4714

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

STRAIN H36B frame: 1  
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL  
 TTEDIVSAVKEKSGEVVDFAFNDVFNQAKSKFSDDETAKKEDKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4715  
 STRAIN 18RS21 frame: 1  
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL  
 TTEDIVSAVKEKSGEVVDFAFNDVFNQAKSKFSDDETAKKEDKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4716  
 STRAIN M732 frame: 1  
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL  
 TTEDIVSAVKEKSGEVVDFAFNDVFNQAKSKFSDDETAKKEDKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4717  
 STRAIN COH1 frame: 1  
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL  
 TTEDIVSAVKEKSGEVVDFAFNDVFNQAKSKFSDDETAKKEDKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4718  
 STRAIN M781 frame: 1  
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL  
 TTEDIVSAVKEKSGEVVDFAFNDVFNQAKSKFSDDETAKKEDKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4719  
 STRAIN 090 frame: 1  
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL  
 TTEDIVSAVKEKSGEVVDFAFNDVFNQAKSKFSDDETAKKEDKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4720  
 STRAIN CJB110 frame: 1  
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL  
 TTEDIVSAVKEKSGEVVDFAFNDVFNQAKSKFSDDETAKKEDKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4721  
 STRAIN 1169NT frame: 1  
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL  
 TTEDIVSAVKEKSGEVVDFAFNDVFNQAKSKFSDDETAKKENKAPETKVEDIVIDYKENTE  
 DKEK

SEQ ID NO. 4722  
 STRAIN JM9130013 frame: 1  
 YFLTTKKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL  
 TTEDIVSAVKEKSGEVVDFAFNDVFNQAKSKFSDDETAKKEDKAPETKVEDIVIDYKENTE  
 DKEK

PRETTY of: /biotmp/msa68746.2(\*) January 22, 2003 05:54 ..

	1		50
msa68746.2{164_090}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_1169NT}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_18RS21}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_2603}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_A909}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_CJB110}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_COH1}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_H36B}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_JM9130013}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_M732}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_M781}	YFLTTKKGKE	LRKNAEKFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
Consensus	*****	*****	*****
	51		100
msa68746.2{164_090}	YKGFESGEL	TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_1169NT}	YKGFESGEL	TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_18RS21}	YKGFESGEL	TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_2603}	YKGFESGEL	TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_A909}	YKGFESGEL	TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_CJB110}	YKGFESGEL	TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_COH1}	YKGFESGEL	TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_H36B}	YKGFESGEL	TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_JM9130013}	YKGFESGEL	TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_M732}	YKGFESGEL	TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_M781}	YKGFESGEL	TTEDIVSAVK EKSSEVVDFA NDFVNQAKSK FSDEDTAKKE	

**Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)**

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Consensus *****
msa68746.2{164_090} 101 dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_1159NT} nKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_18RS21} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_2603} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_A909} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_CJB110} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_COH1} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_H36B} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_JM9130013} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_M732} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_M781} dKAPETKVED IVIDYKENTE DKEK
Consensus *****

```

Table 48: Comparative Sequences relating to SAG1474

SEQ ID NO: 4801

STRAIN 2603

aatagtactgagacaagtgccttcagtagttcctactacaaatactatcgt  
 tcaaactaatgacagtaaatcctaccgcaaaatttggatcagaatcaggac  
 aatctgtataatagggtcaagtaaaaccagataattctcgccgcttacaaca  
 gttgacacgcctcatcatatttcagctccagatgctttaaaacaactca  
 atcaagtcctgtcgttgagagtacttctactaagttactgaagagactt  
 acaaacaaaaagatgggtcaagatttagccaacatgggtgagaagtggtcaa  
 gttactagttaggaactcgttaatatggcatacagataatttctgctaaaga  
 aaacccatctttaatgcagtcattactactagacgccaagaagctattg  
 aagaggctagaaaacttaagataccaatcagccgtttttaggtgttccc  
 ttggtagtcaaggggttagggcacagtattaaagggtggtaaaccaataa  
 tggcttgatctatgcagatggaaaaattagcacatttgacagtatgctatg  
 tcaaaaaataaaagatttaggatttattattttaggacaaacgaacttt  
 ccagagtatgggtggcgtaataataacagatttctaaattatcgggtctaac  
 gcataatccttgggatcttgcctcataatgctgggtgctcttctgggtgaa  
 gtgcagcagccattgctagcggaatgacgccaattgctagcggtagtgat  
 gctgggtgggttctatccgtattccatctcttggacgggttggtaggtt  
 aaaaccaacaagaggattgggtgagtaaatgaaaagccagattcgtatagta  
 cagcagtttcatcttccattactaagtcattagagacgcagaaaactta  
 ttaacttatctaaagaaaagcgatcaaacgctagtatcagttaatgattt  
 aaaatctttaccaattgcttatactttgaaatcaccaatgggaacagaag  
 ttagtcaagatgctaaaaacgctatttaggacaacgctcacattcttaaga  
 aaacaaggattcaagtaaacagagatagacttaccatttgatggttagagc  
 ataatgctgattattcaacctgggtattggcatgggaggagcttttt  
 caacaattgaaaaagacttaaaaaaacatgggttttactaaagaagacgtt  
 gatcctattacttgggcagttcatgttatttatcaaaatcagataaaggc  
 tgaacttaagaaatctattatggaagcccaaaaacataggatgattatc  
 gtaaggcaatggagaagcttcacaagcaatttccatcttcttatcgcca  
 acgacgcgaagtttagccctctaaatacagatccatagttaacagagga  
 agataaaaagagcgatttataatattggaacttgagccaagaagaagaa  
 ttgctctctttaaactgcagctgggagcctatgttgcttagaacaccttt  
 acacaaattgctaatatgacaggaactccagctatcagtatcccgactta  
 ctatctgagtcgtgttaccatagggacgagtgtaatggcaggtgcaa  
 actatgatgggtatttaattaaatttgcaacttctttgaaaaacatcat  
 gggtttaatgttaaatggcaagaataatagataaagaagtgaaccatc  
 tactggcctaataacagcctaactacccctctttaaagctcattcatcat  
 tagtaaaattagaagaaaattcacagttactcaagtatctatctctaaa  
 aatggatgaaatcgtctgttataaaataaacatccgtaattggcatatca  
 aaaagca

SEQ ID NO: 4802

STRAIN 090

AATAGTACTGAGACAAGTGCCTTCAGTAGTTCCTACTACAA  
 ATACTATCGTTCAAACTAATGACAGTAATCCTACCGCAAAATTTGTATCA  
 GAATCAGGACAATCTGTAATAGGTCAAGTAAAACAGATAATTTCTCGGC  
 GCTTACAACAGTTGACACGCCTCATCATATTTAGCTCCAGATGCTTTAA  
 AAACAACCTCAATCAAGTCTGTGCTGAGAGTACTTCTACTAAGTTAACT  
 GAAGAGACTTACAACAAAAAGATGGTAAAGATTTAGCCAACATGGTGAG  
 AAGTGGTCAAGTTACTAGTGAGGAACCTCGTTAATATGGCATAACGATATTA  
 TTGCTAAAGAAAAACCCATCTTTAAATGCACTTACTACTAGACGCCAA  
 GAAGCTTATTGAAGAGGCTAGAAAACTTAAAGATACCAATCAGCCGTTT  
 AGGTGTTCCCTTTGTTAGTCAAGGGGTTAGGGCACAGTATTAAAGGTGGTG  
 AAACCAATAATGGCTTGATCTATGCAGATGGAAAAATTAGCACATTTGAC  
 AGTAGCTATGTCAAAAAATATAAAGATTTAGGATTTATTATTTTAGGACA  
 AACGAACCTTCCAGAGTATGGGTGGCGTAATAAACAAGATTCTAAATTT  
 ACGGTCTAACGCATAATCCTTGGGATCTTGCTCATAATGCTGGTGGCTCT  
 TCTGGTGGAAAGTGCAGCAGCCATTGCTAGCGGAATGACGCCAATTGCTAG  
 CGGTAGTGATGCTGGTGGTTCTATCCGTATTCCATCTCTTGGACGGGCT  
 TGGTAGGTTTAAACCAACAAGAGGATTGGTGAGTAATGAAAGCCAGAT  
 TCGTATAGTACAGCAGTTCAATTTCCATTAACTAAGTCATCTAGAGACGC  
 AGAAACATTATTAACCTTATCTAAAGAAAAGCGATCAACCGCTAGTATCAG  
 TTAATGATTTAAATCTTTACCAATTGCTTATACTTTGAAATCACCAATG  
 GGAACAGAAGTTAGTCAAGATGCTAAAAACGCTATTATGGACAACGTCAC  
 ATTCTTAAGAAAAACAAGGATTCAAAGTAACAGAGATAGACTTACCAATTG  
 ATGGTAGAGCATTAAATGCGTGATTATTCAACCTTGGCTATTGGCATGGGA  
 GGAGCTTTTCAACAATTGAAAAAGACTTAAAAAACATGGTTTACTAA  
 AGAAGACGTTGATCCTATTACTTGGGCAGTTCAATGTTATTATCAAAAT  
 CAGATAAGGCTGAACCTTAAGAAATCTATTATGGAAGCCCAAAACATATG  
 GATGATTATCGTAAGGCAATGGAGAAGCTTCACAAGCAATTTCTATTTT  
 CTTATCGCCCAACGACCGCAAGTTTAGCCCTCTAAATACAGATCCATATG  
 TAACAGAGGAAGATAAAGAGCGATTATAATATGGAACCTTGAGCCAA  
 GAAGAAGAATTGCTCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAG  
 AACACCTTTTACACAAATGCTAATATGACAGGACTCCAGCTATCAGTA  
 TCCCCGCTTACTTATCTGAGTCTGGTTTACCCATAGGGACGATGTTAATG  
 GCAGGTGCAAACTATGATATGGTATTAAATTAATTTGCAACTTTCTTTGA  
 AAAACATCATGGTTTAAATGTTAAATGGCAAGAATAATAGATAAAGAAG  
 TGAACCATCTACTGGCCTAATACAGCCCTACTAATCCCTCTTTAAAGCT  
 CATTCATCATAGTAAATTTAGAAGAAAATTCACAAGTTACTCAAGTATC  
 TATCTCTAAAAATGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAA  
 TGGCATATCAAAAAGCA

SEQ ID NO: 4803

Table 48: Comparative Sequences relating to SAG1474

## STRAIN A909

TACTACAAATACTATCGTTCAAACCTAATGACAGTAATCCTACCGCAAAAT  
 TTGTATCAGAATCAGGACAATCTGTAATAGGTCAAGTAAACAGATAAT  
 TCTGCGGCGCTTACAACAGTTGACACGCTCATCATATTTTCAGCTCCAGA  
 TGCTTTAAAAACAACCTCAATCAAGTCCTGTCTGTTGAGAGTACTTCTACTA  
 AGTTAATCGAAGAGACTTACAACAAAAAGATGGTCAAGATTAGCCAAC  
 ATGGTGAGAAAGTGGTCAAGTTACTAGTGAGGAACTCGTTAATATGGCATA  
 CGATATTATTGCTAAAGAAAACCCATCTTTAAATGCAGTCATTACTACTA  
 GACGCCAAGAAGCTATTGAAGAGGCTAGAAAACTTAAAGATACCAATCAG  
 CCGTTTTTAGGTGTTCCCTTGTAGTCAAGGGGTTAGGGCAGATATTAA  
 AGGTGGTGAACCAATAATGGCTTGATCTATGCAGATGGAAAAATTAGCA  
 CATTTGACAGTAGCTATGTCAAAAAATATAAGATTAGGATTATATTATT  
 TTAGGACAAACGAACCTTCCAGAGTATGGGTGGCGTAATATAACAGATT  
 TAAATTATACGGTCTAACGCATAATCCTTGGGATCTTGCTCATAATGCTG  
 GTGGCTCTTCTGGTGAAGTGACAGCCATTGCTAGCGGAATGACGCCA  
 ATTGCTAGCGGTAGTGATGCTGGTGGTTCTATCCGTATTCATCTTCTTG  
 GACGGGCTTGGTAGGTTTAAAAACCAACAGAGGATTGGTGAGTAATGAAA  
 AGCCAGATTCTATAGTACAGCAGTTTCTTTCCATTAACTAAGTCATCT  
 AGAGACCGAGAAACATTATTAACCTTATCTAAAGAAAAGCGATCAACGCT  
 AGTATCAGTTAATGATTAAAAATCTTTACCAATTGCTTATACCTTTGAAAT  
 CACCAATGGGAACAGAAAGTTAGTCAAGATGCTAAAAACGCTATTATGGAC  
 AAGCTCAGATTCTTAAAGAAAACAAGGATTCAAGTAACAGAGATAGACTT  
 ACCAATTGATGGTAGAGCATTATGCGTGATTATCAACCTTGGCTATTG  
 GCATGGGAGGAGCTTTTTCAACAATTGAAAAAGACTTAAAAAACATGGT  
 TTTACTAAAGAAGAGCTTGATCCTATTACTTGGGCAGTTTCATGTTATTTA  
 TCAAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTATGGAAGCCCAAA  
 AACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCACAAGCAATTT  
 CCTATTTCTTATCGCCAACGACCGCAAGTTTAGCCCTCTAATAACAGATA  
 TCCATATGTACAGAGGAAGATAAAAGAGCGATTATTAATATGAAAACT  
 TGAGCCAAAGAAGAAAGAAATGCTCTCTTTAATCGCCAGTGGGAGCCATG  
 TTGCGTAGAACACCTTTTACACAAATTGCTAATATGACAGGACTCCCAGC  
 TATCAGTATCCGACTTACTTATCTGAGTCTGGTTTACCCATAGGGACGA  
 TGTTAATGGCAGGTGCAAACTATGATATGTTAATTAAATTTGCAACT  
 TTCTTTGAAAAACATCATGGTTTTAATGTTAAATGGCAAAGAAATAATAGA  
 TAAAGAAGTGAAACCATCTACTGGCCCTAATACAGCTACTAATCCCTCT  
 TTAAGCTCATTTCATCATTAGTAAATTTAGAAGAAAATTCACAAGTTACT  
 CAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTTAAAAATAAACC  
 ATCCGTAATGCATATCAAAAAGCA

SEQ ID NO: 4804

## STRAIN COH1

AATAGTACTGAGACAAGTGCTTCAGTAGCTCCTACTACAAAT  
 ACTATCGTTCAAACCTAATGACAGTAATCCTACCGCAAAATTTGCATCAGA  
 ATCAGGCAAACTCTGTAATAGGTCAAGTAAACAGCTAATCTGCGGCGC  
 TTACAACAGTTGACACGCTCATATTTTCAGCTCCAGATGCTTTAAAAACA  
 ACTCAATCAAGTCCTGTCTGTTGAGAGTCTTCTACTAAGTTAACTGAAGA  
 GACATACAAACAAAAAGATGGTCAAGATTAGCCAACTGGTGAGAAAGTG  
 GTCAGGTTACTAGTGAGGAACCTCGTCAATATGGCATACGATATTATCGCT  
 AAAGAAAACCCATCTTTAAATGAGTCATTACTACTAGACGCCAAGAAGC  
 CATTGAAGAGGCTAGAAAACTTAAAGATACTAATCAGCCGTTTTTAGGTG  
 TTCCCTTGTAGTCAAGGGGTTAGGGCAGATATTAAAGGTGGTGAACCC  
 AATAATGGCTTGATCTATGCAGATGGAAAAATTAGCACATTTGACAGTAG  
 CTATGTCAAAAAATATAAGATTAGGATTATTTATTTTAGGACAAACGA  
 ATTTTCCAGATATGGGTGGCGTAATATAACAGACTCTAAATATATACGGT  
 CCAACGCATAATCCTTGAATCTTGTCTATAACGCTGGTGGCTCTTCTGG  
 TGGAAAGTGACAGCAGCTATTGCTAGCGGAATGACGCCAATTGCTAGCGGCA  
 GTGATGCTGGTGGTCTATCCGTATTCATCTTCTGGACGGGCTTAGTA  
 GGTTTAAACCAACAGAGGATTGGTGAGTAATGAAAAGCCAGATTGCTA  
 TAGTACAGCAGTTTCTTTCCATTAACTAAGTCATCTAGAGACGAGAAA  
 CATTGTTAACTTACCTAAAGAAAAGCGATCAACGCTAGTATCAGTTAAT  
 GATTTAAATCTTTACCAATTGCTTATACTTTGAAATCACCATTGGGAAC  
 AGAAGTTAGTCAAGATGCTAAAAATGCTATTATGGACAACGTCACATTTCT  
 TAAGAAAACAAGGATTCAAAGTGACAGAGATAGATTACCAATTGATGGT  
 AGAGCATTAATGCGTGATTATTCAACCTTGGCTATTGGCATGGGAGGAGC  
 TTTTTCAACAATTGAAAAAGACTTAAAAAACATGGTTTTACTTAAAGAAG  
 ACGTTGATCCCATTAATGCGGAGTTTATGTTATTTATCAAAATTCAGAT  
 AAGGCTGAACCTTAAGAAATCTATTGTGAAGCCCAAAACATATGGATGA  
 TTATCGTTAAGGCAATGGAGAAGCTTCACAAGCAATTTCTATTTCTTAT  
 CGCCAACGACCGCAAGTTTAGCCCTCTAATAACAGATCCATATGTAACA  
 GAGAAAGATAAAAGAGCGATTATTAATATGAAAACTTGAGCCAAGAAGA  
 AAGAATTGCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAGAACAC  
 CTTTACACCAATTGCTAATATGACAGGACTCCCAGCTATCAGTATCCCG  
 ACTTACTTATCTGAGTCTGGTTTACCCATAGGGACGATGTTAATGGCAGG  
 TGCAAACTATGATATGGTATTAAATTAATTTGCAACTTTCTTTGAAAAAC  
 ATCATGGTTTTAATGTTAATGGCAAAGAATAATAGATAAAGAAGTGAAA  
 CCATCTGCTGACCTAATACAGCCTACTAATCTCCCTCTTTAAAGCTCATT  
 ATCATTAGTAAATTTAGAAGAAAATTCACAAGTTACTCAAGTATCTATCT  
 CTAATAAATGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAATGGCA  
 TATCAAAAAGCA

SEQ ID NO: 4805

## STRAIN M732

TCAGTAGCTCCTACTACAAATACTATCGTTCAAACCTAATGACAGTAATCC

Table 48: Comparative Sequences relating to SAG1474

TACCGCAAAATTGTCATCAGAATCAGGACAACTCTGTAATAGGTCAAGTAA  
 AACCGAGCTAATCTGCGGCGCTTACAACAGTTGACACGCTCATATTTCA  
 GCTCCAGATGCTTTAAAAACAACCTCAATCAAGTCCTGTGCTTGAGAGTCC  
 TTCTACTAAGTTAACTGAAGAGACATACAAACAAAAAGATGGTCAAGATT  
 TAGCCAACATGGTGAGAAAGTGGTCAAGTTACTAGTGAGGAACCTGCTCAAT  
 ATGGCATACGATATTATCGCTAAAGAAAAACCATCTTTAAATGCAGTCAT  
 TACTACTAGACGCCAAGAGCCATTGAAGAGGCTAGAAAACTTAAAGATA  
 CTAATCAGCCGTTTTTAGGTGTTCCCTTGTTAGTCAAGGGGTTAGGGCAC  
 AGTATTAAGAGTGGTGAAACCAATAATGGCTTGATCTATGCAGATGGAAA  
 AATTAGCACATTGACAGTAGCTATGTCAAAAAATATAAAGATTAGGAT  
 TTATTATTTTAGGACAAACGAATTTTCCAGAGTATGGGTGGCGTAATATA  
 ACAGACTCTAAATTATACGGTCAACGCATATCTCTGGGATCTTGCTCA  
 TAACGCTGGTGGCTCTTCTGGTGGAGGTGACGACGCTATGCTAGCGGAA  
 TGACGCCAATTGCTAGCGGCGATGCTGGTGGTTCTATCCGTATTTCCA  
 TCTTCTTGGACGGGCTTAGTAGGTTTAAACCAACAAGAGGATTGGTGAG  
 TAATGAAAAGCCAGATTCTGTATAGTACAGCAGTTTCTTTCCATTAACTA  
 AGTCATCTAGAGACGCAGAAACATTGTTAACTTACCTAAAGAAAAGCGAT  
 CAAACGCTAGTATCAGTTAATGATTTAAAACTTTTACCAATTGCTTTATC  
 TTTGAAATCACCATTGGGAACAGAGTTAGTCAAGATGCTAAAAATGCTA  
 TTATGGACAACGTCACATTCTTAAGAAAAACAGGATTCAAAGTGACAGAG  
 ATAGATTTACCAATTGATGGTAGAGCATTAAATGCGTGATTATTCAACCTT  
 GGCTATTGGCATGGGAGGAGCTTTTCAACAATTGAAAAGACTTAAAAA  
 AACATGGTTTTTACTAAAGAAAGACGTTGATCCCATTTACTGGGCGATTCA  
 GTTATTTATCAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTGTGGA  
 AGCCCAAAACATATGGATGATTATCGTAAGCAATGGAGAAGCTTCCACA  
 AGCAATTTCTTATTTCTTATCGCCAAACGACCGCAAGTTTAGCCCTCTA  
 AATACAGATCCATATGTTACAGAGAAAGATAAAAGAGCGATTATATAAT  
 GGAAAACCTTGAGCCAAAGAAAGAAATGTCTCTTTAATCGCCAGTGGG  
 AGCTTATGTTGCGTAGAACACCTTTTACACCAATTGCTAATATGACAGGA  
 CTCCCGCTATCAGTATCCGACTTACTTATCTGAGTCTGGTTTACCCAT  
 AGGGACGATGTTAATGGCAGGTGCAACTATGATATGGTATTAAATTAAT  
 TTGCAACTTTCTTTGAAAACATCATGGTTTAAATGTTAAATGGCAAAGA  
 ATAATAGATAAAGAAAGTGAAACCATCTGCTGACCTAATACAGCCTACTAA  
 CTCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAATTCAC  
 AAGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTTAAA  
 AATAAACCATCCGTAATGGCATATCAAAAAGCA

SEQ ID NO: 4806

STRAIN 18RS21

AATAGTACTGAGACAAGTGCTTCAGTAGTTCCTACTACAAATACTATCGT  
 TCAAACTAATGACAGTAATCTTACCGCAAAATTTGTATCAGAATCAGGAC  
 AATCTGTAATAGGTCAAGTAAACCAGATAATCTGCGGCGCTTACAACA  
 GTTGACAGCCCTCATCATATTTAGCTCCAGATGCTTTAAAAACAACCTCA  
 ATCAAGTCTCTGTTGAGAGTACTTCTACTAAGTTAACTGAAGAGACTT  
 ACAACAAAAAGATGGTCAAGATTTAGCCAAACATGGTGAGAAGTGGTCAA  
 GTTACTAGTGAGGAACCTCGTTAATATGGCATACGATATTATTGCTAAAGA  
 AAACCCATCTTTAAATGCAGTCATTACTACTAGACGCCAAGAGCTATTG  
 AAGAGGCTAGAAAACTTAAAGATACCAATCAGCCGTTTTTAGGTGTTCC  
 TTGTTAGTCAAGGGTTAGGGCACAGTATTAAAGTGGTGAAACCAATAA  
 TGGCTTGATCTATGCAGATGGAAAAATTAGCACATTGACAGTAGCTATG  
 TCAAAAAATATAAAGATTAGGATTTATTTATTTTAGGACAAACGAACCTT  
 CCAGAGTATGGGTGGCGTAAATATAACAGATTCTAAATTATACGGTCTAAC  
 GCATAATCTTGGGATCTTGTCTATAATGCTGGTGGCTCTTCTGGTGGAA  
 GTGCAGCAGCCATTGCTAGCGGAATGACGCCAATTGCTAGCGGTAGTGAT  
 GCTGGTGGTTCTATCCGTATTCATCTTCTTGGACGGGCTTGGTAGGTTT  
 AAAACCAACAGAGGATTTGGTGAGTAATGAAAAGCCAGATTCTGATAGTA  
 CAGCAGTTCAATTTCCATTAACTAAGTCATCTAGAGACGCAGAAACATTA  
 TTAACCTATCTAAAGAAAAGCGATCAAACGCTAGTATCAGTTAATGATTT  
 AAAATCTTTACCAATTGCTTATCTTTGAAATCACCATTGGGAACAGAAG  
 TTAGTCAAGATGCTAAAAACGCTATTATGGACAAACGTCACATTCTTAAGA  
 AAACAAGGATTCAAAGTAACAGAGATAGACTTACCAATTGATGGTAGAGC  
 ATTAATGCGTGATTATTCAACCTTGGCTATTGGCATGGGAGGAGCTTTT  
 CAACAATTGAAAAGACTTAAAAAACATGGTTTTTACTAAAGAAAGCGTT  
 GATCCTATTACTTGGGCAGTTTATGTTATTTATCAAAATTCAGATAAGGC  
 TGAACCTTAAGAAATCTATTATGGAAGCCAAAAACATATGGATGATTATC  
 GTAAGGCAATGGAGAAGCTTCAACAAGCAATTTCTATTCTTTATCGCCA  
 ACGACCGCAAGTTTAGCCCTCTAAATACAGATCCATATGTAACAGAGGA  
 AGATAAAGAGCGATTATAATATGGAACCTTGAGCCAAGAAAGAAAGAA  
 TTGCTCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAGAACACCTTTT  
 ACACAAATTTGCTAATATGACAGGACTCCAGCTATCAGTATCCGACTTA  
 CTTATCTGAGTCTGGTTTACCCATAGGGACGATGTTAATGGCAGGTGCAA  
 ACTATGATATGGTATTAAATTAATTTGCAACTTTCTTTGAAAACATCAT  
 GGTTTTAATGTTAAATGGCAAAGAAATAATAGATAAAGAAAGTGAACCATC  
 TACTGGCCTAATACAGCCTACTAACTCCCTCTTTAAAGCTCATTCATCAT  
 TAGTAAATTTAGAAGAAAATTCACAAGTTACTCAAGTATCTATCTTAA  
 AATGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAATGGCATATCA  
 AAAAGCA

SEQ ID NO: 4807

STRAIN M781

TGCTTCAGTAGCTCTACTACAAATACTATCGTTCAAACCTAATGACAGTA  
 ATCTTACCGCAAAATTTGCATCAGAATCAGGACAACTCTGTAATAGGTCAA  
 GTAAACAGCTAATTTCTGCGGCGCTTACAACAGTTGACACGCTCATAT

Table 48: Comparative Sequences relating to SAG1474

TTCAGCTCCAGATGCTTTAAAAACAACCTCAATCAAGTCCTGTCGTTGAGA  
 GTCCTTCTACTAAGTTAACTGAAGAGACATACAAACAAAAGATGGTCAA  
 GATTAGCCAAACATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAATCGT  
 CAATATGGCATAACGATATTATCGCTAAAGAAAACCCATCTTTAAATGCAG  
 TCATTTACTACTAGACGCCAAGAAGCCATTGAAGAGGCTAGAAAACTTAAA  
 GATACTAATCAGCCGTTTCTAGGTGTTCCCTTGTGTAGTCAAGGGGTTAGG  
 GCACAGTATTAAGGTGGTGAAACCAATAATGGCTTGATCTATGCAGATG  
 GAAAAATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAAGATTTA  
 GGATTTATTATTTTAGGACAAACGAATTTCCAGAGTATGGGTGGCGTAA  
 TATAACAGACTCTAAATTATACGGTCCAACGCATAATCCTTGGAATCTTG  
 CTCATAACGCTGGTGGCTCTTCTGGTGGAAAGTGCAGCAGCTATGTCTAGC  
 GGAATGACGCCCAATTGCTAGCGGCAGTGTATGCTGGTGGTTCTATCCGTAT  
 TCCATCTTCTTGGACGGGCTTAGTAGGTTTAAAACCAACAGAGGATTGG  
 TGAGTAATGAAAAGCCAGATTCTGTATAGTACAGCAGTTCAITTTCCATTA  
 ACTAAGTCATCTAGAGACGCAGAAAACATTGTTAACTTACCTAAAGAAAAG  
 CGATCAACGCTAGTATCAGTTAATGATTTAAAACTTTACCAATGTCTT  
 ATACTTTGAAATCACCAATGGGAACAGAATAGTCAAGATGCTAAAAAT  
 GCTATTATGGACAACGCTCACATTTCTAAGAGAACAAGGATTCAAAGTGAC  
 AGAGATAGATTACCAATGTATGGTAGAGCATTAATGCGTGATTTATTCAA  
 CCTTGGCTATTGGCATGGGAGGAGCTTTTCAACAATTGAAAAGAGCTTA  
 AAAAAACATGGTTTACTAAAGAAAGCGTTGATCCCATTACTTGGGCAGT  
 TCACTGTATTATCAAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTG  
 TGGAAGCCCAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTT  
 CACAAGCAATTTCTTATTTCTTATCGCCAACGACCGCAAGTTAGCCCC  
 TCTAAATACAGATCCATATGTAAACAGAGAAAGATAAAAGAGCGATTATA  
 ATATGGAAAACCTTGAGCCAAAGAAAGAAATGTCTCTTAAATCGCCAG  
 TGGAGCGCTATGTTGGGTAGAACACCTTTACACCAATGTCTAATAAGAC  
 AGGACTCCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTAC  
 CCATAGGAGCAGTGTAAATGGCAGGTGCAAACTATGATATGGTATTAAAT  
 AAATTTGCAACTTTCTTTGAAAAACATCATGGTTTAAATGTTAAATGGCA  
 AAGAATATAGATAAAGAAAGTGAACCATCTGCTGACCTAATACAGCCTA  
 CTAATCCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAT  
 TCACAAGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGT  
 TAAAAATAAACCATCCGTAAATGGCATATCAAAAAGCA

SEQ ID NO: 4810

STRAIN CJB110

TAGTTCTTACTACAAATACTATCGTTCAAACCTAATGACAGTAATCCTACC  
 GCAAAATTTGTATCAGAAATCAGGACAATCTGTAATAGGTCAAGTAAACCC  
 AGATAATTTCTGCGCGCTTACAACAGTTGACACGCCTCATCATATTTAG  
 CTCCAGATGCTTTAAAAACAACCTCAATCAAGTCCTGTGCTTGAGAGTACT  
 TCTACTAAGTTAACTGAAGAGACTTACAAAACAAAAGATGGTAAAGATTT  
 AGCCAACATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAACCTCGTTAATA  
 TGGCATACGATATTATGCTAAAGAAAACCCATCTTTAAATGCAGTCATT  
 ACTACTAGACGCGCAAGAAGCTATTGAAGAGGCTAGAAAACCTTAAAGATA  
 CAATCAGCCGTTTCTAGGTGTTCCCTTGTGTAGTCAAGGGGTTAGGGCACA  
 GTATTAAAGGTGGTGAACCAATAATGGCTTGATCTATGCAGATGGAAAA  
 ATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAAGATTAGGATT  
 TATTATTTTAGGACAAACGAATTTCCAGAGTATGGGTGGCGTAAATATAA  
 CAGATTCTAAATTTATACGGTCTAACGCATAATCCTTGGGATCTTGCTCAT  
 AATGCTGGTGGCTCTTCTGGTGAAGTGCAGCAGCCATTGCTAGCGGAAT  
 GAGCCCAATGCTAGCGGTAGTGTGCTGGTGGTTCTATCCGTATTCCAT  
 CTTCTTGGACGGGCTTGGTAGGTTTAAAACCAACAGAGGATTGGTGAGT  
 CATGAAAAGCCAGATTCGTATAGTACAGCAGTTCAITTTCCATTAACATAA  
 GTCATCTAGAGACGCAGAAAACATTATTAACCTTATCTAAAGAAAAGCGATC  
 AAACGCTAGTATCAGTTAATGATTTAAATCTTTACCAATTGCTTATACT  
 TTGAAATCACCATGGGAACAGAAGTTAGTCAAGATGCTAAAAACGCTAT  
 TAGGACAAACGTCACATTCTTAAGAAAACAAGGATTCAAAGTAACAGAGA  
 TAGACTTACCAATTGATGGTAGAGCATTAATGCGGTGATTATTCAACCTTG  
 GCTATTGGCATGGGAGGAGCTTTTCAACAATTGAAAAAGACTTAAAAAA  
 AcATGGTTTTACTAAAGAAGACGTTGATCTTATTACTTGGGCAGTTCATG  
 TTATTTATCAAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTATGGAA  
 GCCCAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCACAA  
 GCAATTTCTATTTCTTATCGCCAACGACCGCAAGTTAGCCCCCTTAA  
 ATACAGATCCATATGTAACAGAGGAAGATAAAAGAGCGATTATAATATG  
 GAAAACCTTGAGCCAAGAAGAAAGAAATGCTCTCTTAAATCGCCAGTGGGA  
 GCCTATGTTGGGTAGAACACCTTTTACACAAATTGCTAATATGACAGGAC  
 TCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTACCCATA  
 gGGACgATGTTAATGGCAGGTGCAAACTATGATATGGTATTAAATTAAT  
 TTGCAACTTTCTTTGAAAAACATCATGGTTTAAATGTTAAATGGCAAGAA  
 TAATAGATAAAGAAAGTGAACCATCTACTGGCCTAATACAGCCTACTAAC  
 TCCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAATTCACA  
 AGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTTAAAA  
 ATAAACCATCCGTAAATGGCATATCAAAAAGCA

SEQ ID NO: 4811

STRAIN 1169NT

AATAGTACTGAGACAAGTGCTTCAGTAGCTCTACTACAAATACTATCGT  
 TCAAACTAATGACAGTAATCCTACCGCAAAATTTGCATCAGAAATCAGGAC  
 AATCTGTAATATGTCAAGTAAACAGAGATAATTTCTGCGGCGCTTACACAA  
 GTTGACACGCCTCATATTTAGCTCCAGATGATTAAAAACCAACTCAATC  
 AAGTCTGTGCTTGAGAGTACTTCTACTAAGTTAACTGAAGAGACATACA  
 AACAAAAAGATGGTCAAGATTAGCCACATGGTGAGAAGTGGTCAAGTT



Table 48: Comparative Sequences relating to SAG1474

ACTAGTGAGGAACTCGTCAATATGGCATACGATATTATTGCTAAAGAAAA  
 CCCCTCTTTAAATGCAGTCATTACTACTAGACGCCAAGAAGCCATTGAAG  
 AGGCTAGAAAACCTTAAAGATACTAATCAGCCATTTTGGTGTTCCTTGG  
 TTAGTCAAGGGGTTAGGGCACAGTATTAAAGGTGGTGAAACCAATAATGG  
 CTTGATCTATGCAGATGGAAAAATAGCACATTGACAGTAGCTATGTCA  
 AAAATATAAAGATTAGGATTTATTTTATAGGACAAACGAACCTTTCCA  
 GAGTATGGGTGGCGTAATATAACAGATTCTAATTATACGGTCCAACGCA  
 TAACCTCGGAATCTTGCTCATAATGCTGGTGGCTCTTCTGGTGGAAAGTG  
 CAGCAGCCATTGCTAGCGGATGACGCCAATTGCTAGCGGTAGTGATGCT  
 GGTGGTCTATCCGTATTCATCTTCTTGGACGGGCTTGGTAGGTTTAAA  
 ACCAACAGAGGATTGGTGAATTAAGAACCCAGATTTCGTATAGTACAG  
 CAGTTTCATTTTCCATTAACTAAGTCACTAGAGACGCAGAAACATTATTA  
 ACTTATCTAAAGAAAGCGATCAAAACGCTAGTATCAGTTAATGATTTAAA  
 ATCTTTACCAATTGCTTATACTTTGAAATCACCAATGGGAACAGAAGTTA  
 GTCAGAGTGTAAAAACGCTATTATGGACAAAGTCACTTCTTAAGAAAA  
 CAAGGATTCAAAGTAACAGAGATAGACTTACCAATTGATGGTAGAGCATT  
 AATGCGTGAATTATCAACCTTGGCTATTGGCATGGGAGGAGCTTTTCAA  
 CAATTGAAAAAGACTTAAAAAACATGGTTTACTAAAGAAGACGTTGAT  
 CCTATTACTTGGGCAGTTTATGTTATTTATCAAAATTGAGTAAGGCTGA  
 CCTAAGAAATCTATTATGGAGGCCAAAAACATATGGATGATTATCGTA  
 AGGCAATGGAGAGCTTCAACAGCAATTTCCTATTTCTTATCGCCAACG  
 ACGCAAGTTTGGCCCTCTAAATACAGATCCATATGTAACAGAGAAAGA  
 TAAAGAGCGATTATATATATGGAAACCTTGGCCAAAGAAAGAAAGATTG  
 CTCCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAGAACACCTTTTACA  
 CAAATTGCTAATATGACAGGACTCCAGCTATCAGTATCCGACTTACTT  
 ATCTGAGTCTGGTTTACCCTAGGGAGCATGTTAATGGCAGGTGCAAACT  
 ATGATATGGTATTAATTAATTTGCAACTTTCTTTGAAAAACATCATGGT  
 TTTAATGTTAAATGGCAAGAAATATAGATAAAGAAAGTGAACCATCTAC  
 TGGCCTAATACAGCCTACTAATCCCTCTTTAAAGCTCATTCATCATTAG  
 TAAATTTAGAGAAAAATTCACAGTTACTCAAGTATCTATCTCTAAAAAA  
 TGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAATGGCATATCAAAA  
 AGCA

SEQ ID NO: 4812

STRAIN JM9130013

TTTCAGTAGTCTCTACTACAAATACTATCGTTCAAACCTAATGACAGTAATC  
 CTACCGCAAAATTTTCATCAGAAATCAGGACAATCTGTAATAGGTCAAGTA  
 AAACCAGCTAATCTGTGGCGCTTACAAACAGTTGACACGCTCATATTTT  
 AGCTCCAGATGCTTTAAAAACAACCTCAATCAAGTCTGTGCTGAGAGTC  
 CTTCTACTAAGTTAACTGAAGAGACATACAAACAAAAAGATGGTCAAGAG  
 TTAGCCAAACATGGTGAGAGTGGTCAAGTTACTAGTGAGGAACCTCGTCAA  
 TATGGCATACGATATTATTGCTAAAGAAACCCATCTTTAAATGCAGTCA  
 TTACTACTAGACGCCAAGAAGCTATTGAAGAGGCTAGAAAACTTAAAGAT  
 ACCAATCAGCCGTTTTAGGTGTTCCCTTGTAGTCAAGGGGTTAGGGCA  
 CAGTATTAAAGGTGGTGAAACCAATAATGGCTTGATCTATGCAGGTGGAA  
 AAATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAGATTTAGGA  
 TTTATTATTTTAGGACAAACGAACCTTCCAGAGTATGGATGGCGCAATAT  
 AACAGATTCTAAATTATACGGTCCAACGCATAACCTTGGAACTCTTGCTC  
 ATAATGCTGGTGGCTCTTCTGGTGGAGTGACAGCAGTTATGCTAGCGGG  
 ATGACGCCAATGCTAGCGGTAGTGATGCTGGTGGTTCTATCGTATTTCC  
 ATCTTCTTGGACGGGCTTGGTAGGTTTAAACCAACAGAGGATTGGTGA  
 GTAATGAAAAGCCAGATTCTGTATAGTACAGCAGTTCAATTTCCATTAACT  
 AAGTCATCTAGAGACGCAGAAACATTATTAACCTTATCTAAAGAAAGCGA  
 TCAAACGCTAGTATCAGTTAATGATTTAAATCTTTTACCAATTTGCTTATA  
 CTTTGAATACCAATGGGAACAGAAAGTTAGTCAAGATGCTAAAAATGCT  
 ATTTAGGACACGTCATATTCTTAAGAAACCAAGGATTCAAAGTGACAGA  
 GATAGACTTACCAATTGATGGTAGAGCATTAAATGCGTGATTATTAACCT  
 TGGCTATTGGTATGGGAGGAGCTTTTCAACAATTGAAAAAGACTTAAAA  
 AAACATGGTTTACTAAAGAAAGACGTTGATCCCATTACTTGGGGAGTTCA  
 TGTATTATTATCAAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTATGG  
 AAGCCCAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCAC  
 AAGCAATTTCTATTTTCTTATCGCCAACGACCGCAAGTTTAGCCCTCT  
 AAATACAGATCCATATGTAACAGAGGAAGATAAAAGAGCGATTATAATA  
 TGGAAAACTTGAGCCAAAGAAAGAAATGCTCTCTTTAATCGCCAGTGG  
 GAGCCTATGTTGCGTAGAACACCTTTTACACAAATGCTAATATGACAGG  
 ACTCCAGCTATCAGTATCCGACTTACTTATCTGAGTCTGGTTTACCCA  
 TAGGACAGATGTTAATGGCAGGTGCAAACTATGATATGGTATTAAATAAA  
 TTTGCAACTTTCTTTGAAAAATATCATGGTTTAAATGTTAAATGGCAAG  
 AATAATAGATAAAGAGTGAACCATCTACTGGCCTAATACAGCCTACTA  
 ACTCCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAATTC  
 CAAGTTACTCAAGTATCTATCTCTTAAAAATGGATGAAATCGTCTGTTAA  
 AAATAAACCATCCGTAATGGCATAT

SEQ ID NO: 4813

STRAIN H36B

CTTCAGTAGTCTCTACTACAAATACTATCGTTCAAACCTAATGACAGTAAT  
 CCTACCGCAAAATTTTCATCAGAAATCAGGACAATCTGTAATAGGTCAAGT  
 AAAACAGCTAATCTGTGGCGCTTACAAACAGTTGACACGCTCATATTT  
 CAGCTCCAGATGCTTTAAAAACAACCTCAATCAAGTCTGTGCTGAGAGT  
 CTTCTACTAAGTTAACTGAAGAGACATACAAACAAAAAGATGGTCAAGA  
 TTTAGCCAAACATGGTGAGAGTGGTCAAGTTACTAGTGAGGAACCTCGTCA  
 ATATGGCATACGATATATTGCTAAAGAAACCCATCTTTAATGACAGTCA  
 ATTACTACTAGACGCCAAGAAGCTATTGAAGAGGCTAGAAAACTTAAAGA

Table 48: Comparative Sequences relating to SAG1474

TACCAATCAGCCGTTTTTAGGTGTTCCCTTGTAGTCAAGGGGTTAGGGC  
ACAGTATTAAAGGTGGTGAACCAATAATGGCTTGATCTATGCAGGTGGA  
AAAATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAGATTTAGG  
ATTTATTATTTTAGGACAAACGAACCTTCCAGAGTATGGATGGCGCAATA  
TAACAGATTCTAAATTATACGGTCCAACGCATAACCCCTGGAACTTTGCT  
CATAATGCTGGTGGCTCTTCTGGTGAAGTGACAGCAGTTATGCTAGCGG  
GATGACGCCAATTGCTAGCGGTAGTGATGCTGGTGGTTCTATCCGTATTC  
CATCTTCTTGGACGGGCTTGGTAGGTTTAAACCAACAAGAGGATTGGTG  
AGTAATGAAAAGCCAGATTTCGTATAGTACAGCAGTTCAATTTCCATTAAAC  
TAAGTCATCTAGAGACGCGAGAAACATTATTAACCTTATCTAAAGAAAAGCG  
ATCAAACGCTAGTATCAGTTAATGATTAAATCTTTACCAATTCGTATAT  
ACTTTGAATCACCAATGGGAACAGAAAGTTAGTCAAGATGCTAAAAATGC  
TATTATGGACAACGTCATATTCTTAAGAAAACAAGGATTCAAAGTGACAG  
AGATAGACTTACCAATTGATGGTAGAGCATTAAATGCGTGATTATTCACCC  
TTGGCTATTGGTATGGGAGGAGCTTTTCAACAATTGAAAAGAGCTTAA  
AAAACATGGTTTTACTAAAGAAGACGTTGATCCCATTACTTGGGCAGTTTC  
ATGTTATTATTAATAATTCAGATAAGGCTGAACCTTAAGAAATCTATTATG  
GAAGCCCCAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCA  
CAAGCAATTTCCATTCTTCTATCGCCAACGACCGCAAGTTAGCCCCCTC  
TAAATACAGATCCATATGTAAACAGAGGAAGATAAAAGAGCGATTATTAAT  
ATGGAAAACCTTGAGCCAAGAAGAAAGAAATTGCTCTCTTAAATCGCCAGTG  
GGAGCCTATGTTCCGTAGAACACCTTTTACACAAATGCTAATATGACAG  
GACTCCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTACCC  
ATAGGGACGATGTTAATGGCAGGTGCAAACTATGATATGTTAATTAATAA  
ATTTGCAACTTTCTTTGAAAAATATCATGGTTTAAATGTTAAATGGCAAA  
GAATAATAGATAAAGAGTGAACCATCTATGGCCCTAATACAGCCCTACT  
AACTCCCTCTTTAAAGCTCAITTCATCATAGTAAATTTAGAAGAAAATTC  
ACAAGTTACTCAAGTATCTATCTCTAAAAATGGATGAAATCGTCTGTTA  
AAAAATAA

PRETTY of: /biotcmp/msa71927.2{\*} January 22, 2003 07:23 ..

	1		50
msa71927.2{173_18RS21}	aatagtactg agacaagtgc ttcagtagtt ccTACTACAA ATACTATCGT		
msa71927.2{173_2603}	aatagtactg agacaagtgc ttcagtagtt ccTACTACAA ATACTATCGT		
msa71927.2{173_A909}	-----	-----	---TACTACAA ATACTATCGT
msa71927.2{173_090}	aatagtactg agacaagtgc ttcagtagtt ccTACTACAA ATACTATCGT		
msa71927.2{173_CJB110}	-----	-----tagtt	ccTACTACAA ATACTATCGT
msa71927.2{173_COH1}	aatagtactg agacaagtgc ttcagtagct ccTACTACAA ATACTATCGT		
msa71927.2{173_M781}	-----tgc	ttcagtagct	ccTACTACAA ATACTATCGT
msa71927.2{173_M732}	-----	-tcagtagct	ccTACTACAA ATACTATCGT
msa71927.2{173_H36B}	-----c	ttcagtagtt	ccTACTACAA ATACTATCGT
msa71927.2{173_JM9130013}	-----	ttcagtagct	ccTACTACAA ATACTATCGT
msa71927.2{173_1169NT}	aatagtactg agacaagtgc ttcagtagct ccTACTACAA ATACTATCGT		
Consensus	-----	-----	--***** *****

  

	51		100
msa71927.2{173_18RS21}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC		
msa71927.2{173_2603}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC		
msa71927.2{173_A909}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC		
msa71927.2{173_090}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC		
msa71927.2{173_CJB110}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC		
msa71927.2{173_COH1}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgcATCA GAATCAGGAC		
msa71927.2{173_M781}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgcATCA GAATCAGGAC		
msa71927.2{173_M732}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgcATCA GAATCAGGAC		
msa71927.2{173_H36B}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTtcATCA GAATCAGGAC		
msa71927.2{173_JM9130013}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTtcATCA GAATCAGGAC		
msa71927.2{173_1169NT}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgcATCA GAATCAGGAC		
Consensus	*****	*****	*****_--****

  

	101		150
msa71927.2{173_18RS21}	AATCTGTAAT AgGTCAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_2603}	AATCTGTAAT AgGTCAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_A909}	AATCTGTAAT AgGTCAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_090}	AATCTGTAAT AgGTCAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_CJB110}	AATCTGTAAT AgGTCAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_COH1}	AATCTGTAAT AgGTCAGTA AAACCAGcTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_M781}	AATCTGTAAT AgGTCAGTA AAACCAGcTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_M732}	AATCTGTAAT AgGTCAGTA AAACCAGcTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_H36B}	AATCTGTAAT AgGTCAGTA AAACCAGcTA ATTCTGtGGC GCTTACAACA		
msa71927.2{173_JM9130013}	AATCTGTAAT AgGTCAGTA AAACCAGcTA ATTCTGtGGC GCTTACAACA		
msa71927.2{173_1169NT}	AATCTGTAAT AtGTCAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA		
Consensus	*****	*_*****	*****_****

  

	151		200
msa71927.2{173_18RS21}	GTTGACACGC CtcacTCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_2603}	GTTGACACGC CtcacTCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_A909}	GTTGACACGC CtcacTCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_090}	GTTGACACGC CtcacTCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_CJB110}	GTTGACACGC CtcacTCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_COH1}	GTTGACACGC C...TCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_M781}	GTTGACACGC C...TCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_M732}	GTTGACACGC C...TCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_H36B}	GTTCACACGC	C...TCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACCTCA
msa71927.2{173_JM9130013}	GTTCACACGC	C...TCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACCTCA
msa71927.2{173_1169NT}	GTTCACACGC	C...TCATAT	TTCAGCTCCA	GATGaTTTAA	AAACAACCTCA
Consensus	*****	*-*****	*****	****-*****	*****
201					
msa71927.2{173_18RS21}	ATCAAGTCCT	GTCGTTGAGA	GtaCTTCTAC	TAAGTTAACT	GAAGAGACtT
msa71927.2{173_2603}	ATCAAGTCCT	GTCGTTGAGA	GtaCTTCTAC	TAAGTTAACT	GAAGAGACtT
msa71927.2{173_A909}	ATCAAGTCCT	GTCGTTGAGA	GtaCTTCTAC	TAAGTTAACT	GAAGAGACtT
msa71927.2{173_090}	ATCAAGTCCT	GTCGTTGAGA	GtaCTTCTAC	TAAGTTAACT	GAAGAGACtT
msa71927.2{173_CJB110}	ATCAAGTCCT	GTCGTTGAGA	GtaCTTCTAC	TAAGTTAACT	GAAGAGACtT
msa71927.2{173_COH1}	ATCAAGTCCT	GTCGTTGAGA	GtcCTTCTAC	TAAGTTAACT	GAAGAGACaT
msa71927.2{173_M781}	ATCAAGTCCT	GTCGTTGAGA	GtcCTTCTAC	TAAGTTAACT	GAAGAGACaT
msa71927.2{173_M732}	ATCAAGTCCT	GTCGTTGAGA	GtcCTTCTAC	TAAGTTAACT	GAAGAGACaT
msa71927.2{173_H36B}	ATCAAGTCCT	GTCGTTGAGA	GtcCTTCTAC	TAAGTTAACT	GAAGAGACaT
msa71927.2{173_JM9130013}	ATCAAGTCCT	GTCGTTGAGA	GtcCTTCTAC	TAAGTTAACT	GAAGAGACaT
msa71927.2{173_1169NT}	ATCAAGTCCT	GTCGTTGAGA	GtaCTTCTAC	TAAGTTAACT	GAAGAGACaT
Consensus	*****	*****	**-*****	*****	*****-*
251					
msa71927.2{173_18RS21}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_2603}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_A909}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_090}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_CJB110}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_COH1}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_M781}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_M732}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_H36B}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_JM9130013}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_1169NT}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
Consensus	*****	*****-*	**-*****	*****	*****
301					
msa71927.2{173_18RS21}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_2603}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_A909}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_090}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_CJB110}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_COH1}	GTTACTAGTG	AGGAACTCGT	cAATATGGCA	TACGATATTA	TcGCTAAAGA
msa71927.2{173_M781}	GTTACTAGTG	AGGAACTCGT	cAATATGGCA	TACGATATTA	TcGCTAAAGA
msa71927.2{173_M732}	GTTACTAGTG	AGGAACTCGT	cAATATGGCA	TACGATATTA	TcGCTAAAGA
msa71927.2{173_H36B}	GTTACTAGTG	AGGAACTCGT	cAATATGGCA	TACGATATTA	TcGCTAAAGA
msa71927.2{173_JM9130013}	GTTACTAGTG	AGGAACTCGT	cAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_1169NT}	GTTACTAGTG	AGGAACTCGT	cAATATGGCA	TACGATATTA	TtGCTAAAGA
Consensus	*****	*****	..*****	*****	*-*****
351					
msa71927.2{173_18RS21}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_2603}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_A909}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_090}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_CJB110}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_COH1}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCcATTG
msa71927.2{173_M781}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCcATTG
msa71927.2{173_M732}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCcATTG
msa71927.2{173_H36B}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCcATTG
msa71927.2{173_JM9130013}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_1169NT}	AAACCCtTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCcATTG
Consensus	*****-***	*****	*****	*****	*****-****
401					
msa71927.2{173_18RS21}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_2603}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_A909}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_090}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_CJB110}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_COH1}	AAGAGGCTAG	AAAACCTAAA	GATACtAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_M781}	AAGAGGCTAG	AAAACCTAAA	GATACtAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_M732}	AAGAGGCTAG	AAAACCTAAA	GATACtAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_H36B}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_JM9130013}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_1169NT}	AAGAGGCTAG	AAAACCTAAA	GATACtAATC	AGCCaTTTTT	AGGTGTTCCC
Consensus	*****	*****	*****-****	*****-****	*****
451					
msa71927.2{173_18RS21}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_2603}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_A909}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_090}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_CJB110}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_COH1}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_M781}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_M732}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_H36B}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_JM9130013}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_1169NT}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_2603}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_A909}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_090}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_CJB110}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_COH1}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_M781}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_M732}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_H36B}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_JM9130013}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_1169NT}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_2603}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_A909}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_090}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_CJB110}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_COH1}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_M781}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_M732}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_H36B}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_JM9130013}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_1169NT}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_2603}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_A909}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_090}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_CJB110}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_COH1}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_M781}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_M732}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_H36B}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_JM9130013}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_1169NT}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	GCATAAaCCT	tGGgATCtTG	CTCATAAaGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_2603}	GCATAAaCCT	tGGgATCtTG	CTCATAAaGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_A909}	GCATAAaCCT	tGGgATCtTG	CTCATAAaGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_090}	GCATAAaCCT	tGGgATCtTG	CTCATAAaGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_CJB110}	GCATAAaCCT	tGGgATCtTG	CTCATAAaGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_COH1}	GCATAAaCCT	tGGgATCtTG	CTCATAAaGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_M781}	GCATAAaCCT	tGGgATCtTG	CTCATAAaGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_M732}	GCATAAaCCT	tGGgATCtTG	CTCATAAaGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_H36B}	GCATAAaCCT	tGGgATCtTG	CTCATAAaGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_JM9130013}	GCATAAaCCT	tGGgATCtTG	CTCATAAaGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_1169NT}	GCATAAaCCT	tGGgATCtTG	CTCATAAaGC	TGGTGGCTCT	TCTGGTGGAA
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_2603}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_A909}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_090}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_CJB110}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_COH1}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_M781}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_M732}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_H36B}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_JM9130013}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_1169NT}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_2603}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_A909}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_090}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_CJB110}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_COH1}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_M781}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TaGTAGGTTT
msa71927.2{173_M732}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TaGTAGGTTT
msa71927.2{173_H36B}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_JM9130013}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_1169NT}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
Consensus	*****	*****	*****	*****	*_*****
801	850				
msa71927.2{173_18RS21}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_2603}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_A909}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_090}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_CJB110}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_COH1}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_M781}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_M732}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_H36B}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_JM9130013}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_1169NT}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
Consensus	*****	*****	*****	*****	*****
851	900				
msa71927.2{173_18RS21}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_2603}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_A909}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_090}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_CJB110}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_COH1}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTg
msa71927.2{173_M781}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTg
msa71927.2{173_M732}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTg
msa71927.2{173_H36B}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_JM9130013}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_1169NT}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
Consensus	*****	*****	*****	*****	*****
901	950				
msa71927.2{173_18RS21}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_2603}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_A909}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_090}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_CJB110}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_COH1}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_M781}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_M732}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_H36B}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_JM9130013}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
msa71927.2{173_1169NT}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTt
Consensus	*****	*****	*****	*****	*****
951	1000				
msa71927.2{173_18RS21}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_2603}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_A909}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_090}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_CJB110}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_COH1}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_M781}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_M732}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_H36B}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_JM9130013}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
msa71927.2{173_1169NT}	AAAATCTTTA	CCAATTGCTT	ATACITTGAA	ATCACCAGTG	GGAACAGAAG
Consensus	*****	*****	*****	*****	*****
1001	1050				
msa71927.2{173_18RS21}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCaC	ATTCTTAAGA
msa71927.2{173_2603}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCaC	ATTCTTAAGA
msa71927.2{173_A909}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCaC	ATTCTTAAGA
msa71927.2{173_090}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCaC	ATTCTTAAGA
msa71927.2{173_CJB110}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCaC	ATTCTTAAGA
msa71927.2{173_COH1}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCaC	ATTCTTAAGA
msa71927.2{173_M781}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCaC	ATTCTTAAGA
msa71927.2{173_M732}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCaC	ATTCTTAAGA
msa71927.2{173_H36B}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCaC	ATTCTTAAGA
msa71927.2{173_JM9130013}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCaC	ATTCTTAAGA
msa71927.2{173_1169NT}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCaC	ATTCTTAAGA
Consensus	*****	*****	*****	*****	*****
1051	1100				
msa71927.2{173_18RS21}	aAACAAGGAT	TCAAAGTaAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_2603}	aAACAAGGAT	TCAAAGTaAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_A909}	aAACAAGGAT	TCAAAGTaAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_090}	aAACAAGGAT	TCAAAGTaAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_CJB110}	aAACAAGGAT	TCAAAGTaAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_COH1}	aaACAAGGAT	TCAAAGTgAC	AGAGATAGAT	TTACCAATTG	ATGGTAGAGC		
msa71927.2{173_M781}	gAACAAGGAT	TCAAAGTgAC	AGAGATAGAT	TTACCAATTG	ATGGTAGAGC		
msa71927.2{173_M732}	aaACAAGGAT	TCAAAGTgAC	AGAGATAGAT	TTACCAATTG	ATGGTAGAGC		
msa71927.2{173_H36B}	aaACAAGGAT	TCAAAGTgAC	AGAGATAGAC	TTACCAATTG	ATGGTAGAGC		
msa71927.2{173_JM9130013}	aaACAAGGAT	TCAAAGTgAC	AGAGATAGAC	TTACCAATTG	ATGGTAGAGC		
msa71927.2{173_1169NT}	aaACAAGGAT	TCAAAGTgAC	AGAGATAGAC	TTACCAATTG	ATGGTAGAGC		
Consensus	*****	*****	*****	*****	*****		
msa71927.2{173_18RS21}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_2603}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_A909}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_090}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_CJB110}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_COH1}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_M781}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_M732}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_H36B}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_JM9130013}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_1169NT}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
Consensus	*****	*****	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_2603}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_A909}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_090}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_CJB110}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_COH1}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_M781}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_M732}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_H36B}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_JM9130013}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_1169NT}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
Consensus	*****	*****	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_2603}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_A909}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_090}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_CJB110}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_COH1}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_M781}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_M732}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_H36B}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_JM9130013}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_1169NT}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
Consensus	*****	*****	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_2603}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_A909}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_090}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_CJB110}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_COH1}	1251	TGAACCTTAAG	AAATCTATTg	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_M781}	1251	TGAACCTTAAG	AAATCTATTg	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_M732}	1251	TGAACCTTAAG	AAATCTATTg	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_H36B}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_JM9130013}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_1169NT}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
Consensus	*****	*****	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_2603}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_A909}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_090}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_CJB110}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_COH1}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_M781}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_M732}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_H36B}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_JM9130013}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_1169NT}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
Consensus	*****	*****	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	1351	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	1400	GATCCATATG	TaACAGAGgA
msa71927.2{173_2603}	1351	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	1400	GATCCATATG	TaACAGAGgA
msa71927.2{173_A909}	1351	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	1400	GATCCATATG	TaACAGAGgA
msa71927.2{173_090}	1351	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	1400	GATCCATATG	TaACAGAGgA

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_CJB110}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TaACAGAGgA
msa71927.2{173_COH1}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TaACAGAGaA
msa71927.2{173_M781}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TaACAGAGaA
msa71927.2{173_M732}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TtACAGAGaA
msa71927.2{173_H36B}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TaACAGAGgA
msa71927.2{173_JM9130013}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TaACAGAGgA
msa71927.2{173_1169NT}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TaACAGAGgA
Consensus	*****	*****	*****	*****	*-*****
msa71927.2{173_18RS21}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_2603}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_A909}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_090}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_CJB110}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_COH1}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_M781}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_M732}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_H36B}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_JM9130013}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_1169NT}	AGATAAAAGA	GCGATTTTATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_2603}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_A909}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_090}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_CJB110}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_COH1}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_M781}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_M732}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_H36B}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_JM9130013}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_1169NT}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_2603}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_A909}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_090}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_CJB110}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_COH1}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_M781}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_M732}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_H36B}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_JM9130013}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_1169NT}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_2603}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_A909}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_090}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_CJB110}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_COH1}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_M781}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_M732}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_H36B}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_JM9130013}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_1169NT}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_2603}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_A909}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_090}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_CJB110}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_COH1}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_M781}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_M732}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_H36B}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_JM9130013}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_1169NT}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	GGTTTTAATG	TAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAACCATC
msa71927.2{173_2603}	GGTTTTAATG	TAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAACCATC
msa71927.2{173_A909}	GGTTTTAATG	TAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAACCATC

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_090}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC						
msa71927.2{173_CJB110}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC						
msa71927.2{173_COH1}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC						
msa71927.2{173_M781}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC						
msa71927.2{173_M732}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC						
msa71927.2{173_H36B}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC						
msa71927.2{173_JM9130013}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC						
msa71927.2{173_1169NT}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC						
Consensus	*****	*****	*****	*****	*****						
1701						1750					
msa71927.2{173_18RS21}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT						
msa71927.2{173_2603}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT						
msa71927.2{173_A909}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT						
msa71927.2{173_090}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT						
msa71927.2{173_CJB110}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT						
msa71927.2{173_COH1}	TgCTGaCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT						
msa71927.2{173_M781}	TgCTGaCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT						
msa71927.2{173_M732}	TgCTGaCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT						
msa71927.2{173_H36B}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT						
msa71927.2{173_JM9130013}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT						
msa71927.2{173_1169NT}	TaCTGgCCTA	ATACAGCCTA	CTAACTCCCT	CTTTAAAGCT	CATTTCATCAT						
Consensus	*-***-****	*****	*****	*****	*****						
1751						1800					
msa71927.2{173_18RS21}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA						
msa71927.2{173_2603}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA						
msa71927.2{173_A909}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA						
msa71927.2{173_090}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA						
msa71927.2{173_CJB110}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA						
msa71927.2{173_COH1}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA						
msa71927.2{173_M781}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA						
msa71927.2{173_M732}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA						
msa71927.2{173_H36B}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA						
msa71927.2{173_JM9130013}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA						
msa71927.2{173_1169NT}	TAGTAAATTT	AGAAGAAAAT	TCACAAGTTA	CTCAAGTATC	TATCTCTAAA						
Consensus	*****	*****	*****	*****	*****						
1801						1850					
msa71927.2{173_18RS21}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca						
msa71927.2{173_2603}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca						
msa71927.2{173_A909}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca						
msa71927.2{173_090}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca						
msa71927.2{173_CJB110}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca						
msa71927.2{173_COH1}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca						
msa71927.2{173_M781}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca						
msa71927.2{173_M732}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca						
msa71927.2{173_H36B}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca						
msa71927.2{173_JM9130013}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca						
msa71927.2{173_1169NT}	AAATGGATGA	AATCGTCTGT	TAAAAATAAA	ccatccgtaa	tggcatatca						
Consensus	*****	*****	*****	-----	-----						
1851											
msa71927.2{173_18RS21}	aaaagca										
msa71927.2{173_2603}	aaaagca										
msa71927.2{173_A909}	aaaagca										
msa71927.2{173_090}	aaaagca										
msa71927.2{173_CJB110}	aaaagca										
msa71927.2{173_COH1}	aaaagca										
msa71927.2{173_M781}	aaaagca										
msa71927.2{173_M732}	aaaagca										
msa71927.2{173_H36B}	-----										
msa71927.2{173_JM9130013}	-----										
msa71927.2{173_1169NT}	aaaagca										
Consensus	-----										
SEQ ID NO: 4814											
STRAIN 2603 frame: 1											
NSTETSASVVTINTIVQINDSNPTAKFVSESGQSVIGQVKPDNSAALTIVDTPHHISAP											
DALKTTQSSPVVESTSTKLTEETYKQKQDLANMVRSGQVTEELVNMAVDIIAKENPS											
LNAVITTRRQEAIEEARLKLKDTNQPLGVPLLVKGLGHSIKGETNNGLIYADGKISTFD											
SSYVVKYKDLGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGSGSAAAIAS											
GMTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPKDSYSTAVHPLTKSSRDAETL											
LTYLKKSDQTLVSVNDLSKSLPIATYTKSPMGTEVSQDAKNALMDNVTFLRKQGFVKTEID											
LPIDGRALMRDYSFLAIGMGGAFFSTIEKDLKKGFTKEDVDPITWAVHVIYQNSDKAELK											
KSIMEAQKHMDYRKAMEKLHKQFPPIFLSPITASLAPLNTDPYVTEEDKRAIYNMENLSQ											
EERIALFNRRQWEPMLRRTPFTQIANMTGLPAISIPYLSSEGLPIGTMLMAGANYDMVLI											
KFATFFEKHHGFNVKQRIIDKEVKPSTGLIQPTNSLFAHSSLVNLENSQVTQVSISK											
KWKSSVKNKPSVMAYQKA											
SEQ ID NO: 4815											
STRAIN_090 frame: 1											
NSTETSASVVPITNTIVQINDSNPTAKFVSESGQSVIGQVKPDNSAALTIVDTPHHISAP											



Table 48: Comparative Sequences relating to SAG1474

DALKTTQSSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAFYDIIAKENPS  
 LNAVITTRRQEAIEEARKLKDTNQPFLLVGLVPLLVKGLGHSIKGGETNNGLIYADGKISTFD  
 SSVYKVKYKDLGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGGSSAAAIAS  
 GMTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETL  
 LTYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVTEID  
 LPIDGRALMRDYSTLAIGMGGAFFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELK  
 KSIMEAQKHMDYRKAMEKLHKQFPFIPLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ  
 EERIALFNRQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLI  
 KFATFFEKHHGFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSISK  
 KMKSSVKNKPSVMAYQKA

SEQ ID NO: 4816

STRAIN A909 frame: 2

TTNTIVQTNDSNPTAKFVSESGQSVIGQVKPDNSAALTVDTPHISAPDALKTTQSSPV  
 VESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAFYDIIAKENPSLNAVITTRRQ  
 AIEEARKLKDTNQPFLLVGLVPLLVKGLGHSIKGGETNNGLIYADGKISTFSSSVYKVKYKDLG  
 FIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGGSSAAAIASGMTPIASGSDA  
 GGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETLLTYLKKSDQTL  
 VSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVTEIDLPIDGRALMRD  
 YSTLAIGMGGAFFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELKKSIMEAQKHMD  
 DYRKAMEKLHKQFPFIPLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQERIALFNRQW  
 EPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATFFEKHHG  
 FNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSISKKMKSSVKNKPS  
 VMAYQKA

SEQ ID NO: 4817

STRAIN COH1 frame: 1

NSTETSASVAFTTNTIVQTNDSNPTAKFVSESGQSVIGQVKPANSAAALTVDTPHISAPD  
 ALKTTQSSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAFYDIIAKENPSL  
 NAVITTRRQEAIEEARKLKDTNQPFLLVGLVPLLVKGLGHSIKGGETNNGLIYADGKISTFDS  
 SSVYKVKYKDLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGGSSAAAIASG  
 MTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETLL  
 TYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVTEIDLP  
 PIDGRALMRDYSTLAIGMGGAFFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELKK  
 SIVEAQKHMDYRKAMEKLHKQFPFIPLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ  
 EERIALFNRQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIK  
 FATFFEKHHGFNVKQRIIDKEVKPSADLIQPTNSLFKAHSSLVNLEENSQVTQVSISKK  
 WMKSSVKNKPSVMAYQKA

SEQ ID NO: 4818

STRAIN M732 frame: 1

SVAPTNTNTIVQTNDSNPTAKFVSESGQSVIGQVKPANSAAALTVDTPHISAPDALKTTQ  
 SPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAFYDIIAKENPSLNAVITTR  
 RQEAIEEARKLKDTNQPFLLVGLVPLLVKGLGHSIKGGETNNGLIYADGKISTFSSSVYKVKY  
 KDLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGGSSAAAIASGMTPIASG  
 SDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETLLTYLKKSD  
 QTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVTEIDLPIDGRAL  
 MRDYSTLAIGMGGAFFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELKKSIVEAQ  
 KHMDYRKAMEKLHKQFPFIPLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQERIALFN  
 RQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATFEK  
 HHGFNVKQRIIDKEVKPSADLIQPTNSLFKAHSSLVNLEENSQVTQVSISKKMKSSSVK  
 NKPSVMAYQKA

SEQ ID NO: 4819

STRAIN 18RS21 frame: 1

NSTETSASVPTNTNTIVQTNDSNPTAKFVSESGQSVIGQVKPDNSAALTVDTPHISAP  
 DALKTTQSSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAFYDIIAKENPS  
 LNAVITTRRQEAIEEARKLKDTNQPFLLVGLVPLLVKGLGHSIKGGETNNGLIYADGKISTFD  
 SSVYKVKYKDLGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGGSSAAAIAS  
 GMTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETL  
 LTYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVTEID  
 LPIDGRALMRDYSTLAIGMGGAFFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELK  
 KSIMEAQKHMDYRKAMEKLHKQFPFIPLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ  
 EERIALFNRQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLI  
 KFATFFEKHHGFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSISK  
 KMKSSVKNKPSVMAYQKA

SEQ ID NO: 4820

STRAIN M781 frame: 2

ASVAPTNTNTIVQTNDSNPTAKFVSESGQSVIGQVKPANSAAALTVDTPHISAPDALKTTQ  
 SSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAFYDIIAKENPSLNAVITTR  
 RQEAIEEARKLKDTNQPFLLVGLVPLLVKGLGHSIKGGETNNGLIYADGKISTFSSSVYKVKY  
 KDLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGGSSAAAIASGMTPIAS  
 GSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETLLTYLKKSD  
 QTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVTEIDLPIDGRA  
 LMRDYSTLAIGMGGAFFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELKKSIVEAQ  
 KHMDYRKAMEKLHKQFPFIPLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQERIALF  
 NRQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATFFE  
 KHHGFNVKQRIIDKEVKPSADLIQPTNSLFKAHSSLVNLEENSQVTQVSISKKMKSSSV  
 KNKPSVMAYQKA

SEQ ID NO: 4821

STRAIN CJB110 frame: 3

Table 48: Comparative Sequences relating to SAG1474

VPTTNTIVQTNDSNPTAKFVSESGQSVIGQVKPDNSAALTVDTPHHISAPDALKTTQSS  
 PVVESTSTKLTEETKYKQDGLANMVRSGQVTSEELVNMAVDIIAKENPSLNAVITTRR  
 QEAIIEARKLKDNTQNPFLGVPLLVKGLGHSIKGGETNNGLIYADGKIISTFDSYVKKYK  
 LGFIILGQTNFPPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGGSSAAAIASGMTPIASG  
 DAGGSIRIPSSWTGLVGLKPTRGLVSHKPDYSYSTAVHFPPLTKSSRDAETLLTYLKKSDQ  
 TLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVKVTEIDLPIDGRAL  
 RDYSTLAIGMGGAFTSTIEKDLKKGFTKEDVDPIWAVHVIYQNSDKAELKKSIMAQKH  
 MDDYRKAMEKLHKQFPFIPLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEBERIALFNR  
 QWEPMLRRTPTFTQIANMTGLPAISIPTYLSSEGLPIGTMLMAGANYDMVLIKPFATPFEEKH  
 HGFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVVSISKKWMKSSVK  
 KPSPMAYQKA

## SEQ ID NO: 4822

STRAIN 1169NT frame: 1

NSTETSASVAPTNTNTIVQTNDSNPTAKFSESGQSVIGQVKPDNSAALTVDTPHHISAPD  
 DLKTTQSSPVVESTSTKLTEETKYKQDGLANMVRSGQVTSEELVNMAVDIIAKENPSL  
 NAVITTRRQEAIIEARKLKDNTQNPFLGVPLLVKGLGHSIKGGETNNGLIYADGKIISTFDS  
 SYVKKYKDLGFIILGQTNFPPEYGWRNITDSKLYGPTHNPRLAHNAGSSGGSSAAAIASG  
 MTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSHKPDYSYSTAVHFPPLTKSSRDAETLL  
 TYLKKSDQTLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVKVTEIDL  
 PIDGRALMRDYSTLAIGMGGAFTSTIEKDLKKGFTKEDVDPIWAVHVIYQNSDKAELKK  
 SIMAQKHMDYRKAMEKLHKQFPFIPLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEB  
 ERIALFNRQWEPMLRRTPTFTQIANMTGLPAISIPTYLSSEGLPIGTMLMAGANYDMVLIK  
 FATPFEEKHGFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVVSISKK  
 WMKSSVKNPSPMAYQKA

## SEQ ID NO: 4823

STRAIN JM9130013 frame: 2

SVAPTNTNTIVQTNDSNPTAKFSESGQSVIGQVKPANSVALTTVDTPHHISAPDALKTTQSS  
 SPVVESTSTKLTEETKYKQDGLANMVRSGQVTSEELVNMAVDIIAKENPSLNAVITTR  
 RQEAIIEARKLKDNTQNPFLGVPLLVKGLGHSIKGGETNNGLIYAGGKIISTFDSYVKKYK  
 DLGFIILGQTNFPPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGGSSAAAIASGMTPIASG  
 SDAGGSIRIPSSWTGLVGLKPTRGLVSHKPDYSYSTAVHFPPLTKSSRDAETLLTYLKKSD  
 QTLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVKVTEIDLPIDGRAL  
 MRDYSTLAIGMGGAFTSTIEKDLKKGFTKEDVDPIWAVHVIYQNSDKAELKKSIMAQKH  
 HMDYRKAMEKLHKQFPFIPLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEBERIALFN  
 RQWEPMLRRTPTFTQIANMTGLPAISIPTYLSSEGLPIGTMLMAGANYDMVLIKPFATPFEEK  
 YHGFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVVSISKKWMKSSVK  
 NKPSVMAY

## SEQ ID NO: 4824

STRAIN H36B frame: 3

SVVPTTNTIVQTNDSNPTAKFSESGQSVIGQVKPANSVALTTVDTPHHISAPDALKTTQSS  
 SPVVESTSTKLTEETKYKQDGLANMVRSGQVTSEELVNMAVDIIAKENPSLNAVITTR  
 RQEAIIEARKLKDNTQNPFLGVPLLVKGLGHSIKGGETNNGLIYAGGKIISTFDSYVKKYK  
 DLGFIILGQTNFPPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGGSSAAAIASGMTPIASG  
 SDAGGSIRIPSSWTGLVGLKPTRGLVSHKPDYSYSTAVHFPPLTKSSRDAETLLTYLKKSD  
 QTLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVKVTEIDLPIDGRAL  
 MRDYSTLAIGMGGAFTSTIEKDLKKGFTKEDVDPIWAVHVIYQNSDKAELKKSIMAQKH  
 HMDYRKAMEKLHKQFPFIPLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEBERIALFN  
 RQWEPMLRRTPTFTQIANMTGLPAISIPTYLSSEGLPIGTMLMAGANYDMVLIKPFATPFEEK  
 YHGFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVVSISKKWMKSSVK  
 NK

PRETTY of: /biotmp/msa72034.2{\*} January 22, 2003 07:25 ..

	1		50
msa72034.2{173_090}	nstetsasvv	pTTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_18RS21}	nstetsasvv	pTTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_2603}	nstetsasvv	pTTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_A909}	-----	-TTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_CJB110}	-----	pTTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_COH1}	nstetsasva	pTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSaALTT
msa72034.2{173_M732}	-----	-sva pTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSaALTT
msa72034.2{173_M781}	-----	-asva pTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSaALTT
msa72034.2{173_1169NT}	nstetsasva	pTTNTIVQTN DSNPTAKFaS	ESGQSVicQV KpDnSaALTT
msa72034.2{173_H36B}	-----	-svv pTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSvALTT
msa72034.2{173_JM9130013}	-----	-sva pTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSvALTT
Consensus	-----	-*****	*****
	51		100
msa72034.2{173_090}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGk dLANMVRSGQ
msa72034.2{173_18RS21}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_2603}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_A909}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_CJB110}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGk dLANMVRSGQ
msa72034.2{173_COH1}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGk dLANMVRSGQ
msa72034.2{173_M732}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_M781}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_1169NT}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_H36B}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_JM9130013}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ

Table 48: Comparative Sequences relating to SAG1474

Consensus	***--*****	*-*****	*****	*****	*****	*****
msa72034.2{173_090}	101	150				
msa72034.2{173_18RS21}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_2603}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_A909}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_CJB110}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_COH1}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_M732}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_M781}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_1169NT}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_H36B}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
msa72034.2{173_JM9130013}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP	
Consensus	*****	*****	*****	*****	*****	*****
msa72034.2{173_090}	151	200				
msa72034.2{173_18RS21}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_2603}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_A909}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_CJB110}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_COH1}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_M732}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_M781}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_1169NT}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_H36B}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
msa72034.2{173_JM9130013}	LLVKGLGHSI	KGGETNNGLI	YAGKISTFD	SSYVKKYKDL	GFIILGQTNF	
Consensus	*****	*****	*****	*****	*****	*****
msa72034.2{173_090}	201	250				
msa72034.2{173_18RS21}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
msa72034.2{173_2603}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
msa72034.2{173_A909}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
msa72034.2{173_CJB110}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
msa72034.2{173_COH1}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
msa72034.2{173_M732}	PEYGWRNITD	SKLYGxTHNP	wdLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
msa72034.2{173_M781}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
msa72034.2{173_1169NT}	PEYGWRNITD	SKLYGpTHNP	rnLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
msa72034.2{173_H36B}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
msa72034.2{173_JM9130013}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAaAIAS	GMPPIASGSD	
Consensus	*****	*****	*****	*****	*****	*****
msa72034.2{173_090}	251	300				
msa72034.2{173_18RS21}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_2603}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_A909}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_CJB110}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_COH1}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_M732}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_M781}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_1169NT}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_H36B}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
msa72034.2{173_JM9130013}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL	
Consensus	*****	*****	*****	*****	*****	*****
msa72034.2{173_090}	301	350				
msa72034.2{173_18RS21}	LTLYLKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
msa72034.2{173_2603}	LTLYLKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
msa72034.2{173_A909}	LTLYLKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
msa72034.2{173_CJB110}	LTLYLKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
msa72034.2{173_COH1}	LTLYLKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
msa72034.2{173_M732}	LTLYLKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
msa72034.2{173_M781}	LTLYLKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
msa72034.2{173_1169NT}	LTLYLKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
msa72034.2{173_H36B}	LTLYLKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
msa72034.2{173_JM9130013}	LTLYLKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR	
Consensus	*****	*****	*****	*****	*****	*****
msa72034.2{173_090}	351	400				
msa72034.2{173_18RS21}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	
msa72034.2{173_2603}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	
msa72034.2{173_A909}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	
msa72034.2{173_CJB110}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	
msa72034.2{173_COH1}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	
msa72034.2{173_M732}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	
msa72034.2{173_M781}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	
msa72034.2{173_1169NT}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	
msa72034.2{173_H36B}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	
msa72034.2{173_JM9130013}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFTSTIEKDL	KKHGFTKEDV	

Table 48: Comparative Sequences relating to SAG1474

msa72034.2{173_JM9130013}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV
Consensus	*****	*****	*****	*****	*****
	401				450
msa72034.2{173_090}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_18RS21}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_2603}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_A909}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_CJB110}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_COH1}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_M732}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_M781}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_1169NT}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_H36B}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_JM9130013}	DPITWgVHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
Consensus	*****	*****	*****	*****	*****
	451				500
msa72034.2{173_090}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_18RS21}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_2603}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_A909}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_CJB110}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_COH1}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_M732}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_M781}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_1169NT}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_H36B}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_JM9130013}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
Consensus	*****	*****	*****	*****	*****
	501				550
msa72034.2{173_090}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_18RS21}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_2603}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_A909}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_CJB110}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_COH1}	TpIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_M732}	TpIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_M781}	TpIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_1169NT}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_H36B}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKyh
msa72034.2{173_JM9130013}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKyh
Consensus	*..*****	*****	*****	*****	*****_*
	551				600
msa72034.2{173_090}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_18RS21}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_2603}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_A909}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_CJB110}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_COH1}	GFNVKQRII	DKEVKPSadL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_M732}	GFNVKQRII	DKEVKPSadL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_M781}	GFNVKQRII	DKEVKPSadL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_1169NT}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_H36B}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_JM9130013}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
Consensus	*****	*****	*****	*****	*****
	601				619
msa72034.2{173_090}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_18RS21}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_2603}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_A909}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_CJB110}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_COH1}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_M732}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_M781}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_1169NT}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_H36B}	KWMKSSVKNK	~~~~~			
msa72034.2{173_JM9130013}	KWMKSSVKNK	psvmay---			
Consensus	*****	~~~~~			

Table 49: Comparative Sequences related to SAG1502

SEQ ID NO: 4901

STRAIN 2603

aaacatccgatacttaatgatcaaaaatccttagcaattgttgaacagat  
 agaatatgatttttgataaattcgataattcagaagcttctttttatgcaa  
 cattagctagawttcgcggttatggatagagaaatcaaaaatttattaga  
 gaaaatccaaatagtc aaatcctttcaattgggtgtggacttgatacaag  
 gtttgaaagagtcgataatggacaaattaggtggatataaccttgatttgc  
 cagaggttatggagataagaaaattatttttgaagagcatgaaagagtt  
 actaatatagcaaaaatcagccctagatgaaacttggacacgggaggtaaa  
 tccccaaaatgcccccttttctaactcgtgtcagaagggtgttttaattgtttc  
 taaaagaagatgacgttagagacttttcttcatatcctgacaaattcattt  
 agccaattttatggcacaatttgatttgggtcataaggaaatgattaataa  
 aggaaagcaacatgatagcaagtaagtatatggatagacaatttcagtttg  
 gtatcacagatgggtcatgagatttgggttagaccctaaattaaagcaa  
 ataaatctgatttaactttacagatgagatgagcaaatgtgagttaggcac  
 acttcgctcttacttccaacaattcgtaaatataaattgttttaggtg  
 tgtacgaatataaagcatc

SEQ ID NO: 4902

STRAIN 090

TAATGATCAAAAATCCTTAGCAATTGTTGAACAGATAGAATATGATTTTG  
 ATAAATTGCGATAAATTGAGAAGCTTCTTTTATGCAACATTAGCTAGAATT  
 CGCGTTATGGATAGAGAAATCAAAAATTTATTAGAGAAAATCCAATAG  
 TCAAAATCCTTTCAATTGGTGTGGACTTGATACAAGGTTTGAAAGAGTCG  
 ATAAATGGACAAAATTAGGTGGTATAACCTTGATTGGCAGAGGTTATGGAG  
 ATAGAGAAAATTTATTTTGAAGAGCATGAAGAGTTACTAATATAGCAAAA  
 ATCAGCCATAGATGAAACTTGGACACGGGAGGTAAATCCCCAAAATGCCC  
 CTMTTCTAATCGTGTGAGAAGGTGTTTAAATGTTTCTAAAAGAAGATGAC  
 GTAGAGACTTTTCTTCATATCTTGACAAAATTCATTAGCCAATTTATGGC  
 ACAATTTGATTGTGTGATAAGGAAATGATTAAATAAGGAAAGCAACATG  
 ATACAGTAAAGTATATGGATACAGAATTTCAAGTTTGGTATCAGATGGT  
 CATGAGATTGTGGATTAGACCCTAAATTAAGCAAAATAAATCTGATTAA  
 CTTCACAGATGAGATGAGCAAAATTTGAGTTAGGCACACTTCGCTCTTTAC  
 TTCCAACAATTCGTAATTTAATAATTGTTTAGGTGTGTACGAATATAAA  
 GCATC

SEQ ID NO: 4903

STRAIN A909

AAACATCCGATACTTAATGA

TCAAAAATCCTTAGCAATTGTTGAACAGATAGAATATGATTTTGATAAAAT  
 TCGATAAATTGAGAAGCTTCTTTTATGCAACATTAGCTAGAATTGCGGTT  
 ATGGATAGAGAAATCAAAAATTTATTAGAGAAAATCCAATAGTCAAAAT  
 CcTTTCaATTGGTGTGGACTTGATACAAGGTTTGAAAGAGTCGATAATG  
 GACAAATTAGGTGGTATAACCTTGATTGGCAGAGGTTATGGAGATAAGA  
 AAATTaTTTTTGAAGAGCATGAAAGAGTTACTAATATAGCAAAAATCAGC  
 CCTAGATGAaACTTGGACACGGGAGGTAAATCCCCAAAATGCCCCCTTTTC  
 TAATCGGTGTGAGAAGGTGTTTAAATGTTTCTAAAAGAAGATGACGTAGAG  
 ACTTTTCTTCATATCTTGACAAAATTCATTAGCCAATTTATGGCACAATT  
 TGATTGTGTGATAAGGAAATGATTAAATAAGGAAAGCAACATGATACAG  
 TAAAGTATATGGATACAGAATTTCAAGTTTGGTATCAGATGGTCTAGAG  
 ATTTGTGATTAGACCCTAAATTAAGCAAAATAAATCTGATTAACTTTAC  
 AGATGAGATGAGCAAAATTTGAGTTAGGCACACTTCGCTCTTTACTTCCAA  
 CAATTCGTAAATTTAATAATTGTTTAGGTGTGTACGAATATAAGCATC

SEQ ID NO: 4904

STRAIN H36B

AAACATCCGATACTTAATGATCAAAAATCCTTAGCA

ATTGTTGAACAGATAGAATATGATTTTGATAAAATTCGATAATTCAGAAGC  
 TTCTTTTATGCAaCATTAGCTAGAATTGCGGTTATGGATAGAGAAATCA  
 AAAAAATTATTAGAGAAAATCCAATAGTCATATCCTTTCAATTGGCTGT  
 GgACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTA  
 TAACCTTGATTGGCAGAGGTTATGGAGATAAGAAAATTATTTTTGAAG  
 AGCATGAAAGAGTTACTAATATAGCAAAAATCAGCCcTAGATGAAACTTGG  
 ACACGGGAGGTAAATCCCCAAAATGCCCCCTTTCTAATCGTGTGAGAAG  
 TGTTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTCTTCATATCC  
 TGACAAAATTCATTAGCCAATTTATGGCACAATTGATTGTGTGcAGAG  
 GAAATGATTAAATAAGGAAAGCAACATGATACAGTAAAGTATATGGATAC  
 AGAATTTCAAGTTGGGTATCAGATGGTCAAGAAATTGTGGATTTAGACC  
 CTAAATTAAGCAAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAA  
 TTTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAATTTAA  
 TAATTGTTTAGGTGTGTACGAATATAAGCATC

SEQ ID NO: 4905

STRAIN 18RS21

AACATCCGATACTTAATGATCAAAAATCCTTAGCAAT

TGTTGAACAGATAGAATATGATTTTGATAAAATTCGATAATTCAGAAGCTT  
 CTTTTATGCAACATTAGCTAGAATTGCGGTTATGGATAGAGAAAATCAAA  
 AAATTTATTAGAGAAAATCCAATAGTCaAATCCTTTCAATTGGTGTGG  
 ACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTATA  
 ACCTTGATTGGCAGAGGTTATGGAGATAAGAAAATTATTTTTGAAGAG  
 CATGAAAGAGTTACTAATATAGCAAAAATCAGCCCTAGATGAAACTTGGAC  
 ACCGGAGGTAAATCCCCAAAATGCCCCCTTTCTAATCGTGTGcAGAGGTG  
 TTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTCTTCATATCCTG

Table 49: Comparative Sequences related to SAG1502

ACAAATTCATTTAGCCAAATTTATGGCACaATTTGATTGTGTGCATaAGGA  
AATGATTAAATAAGGAAAGCAACATGATACAGTAAAGTATATGGATACAG  
AATTTCAAGTTTGGTATCACAGATGGTCATGAGATTGTGGATTAGACCCT  
AAATTAAGCAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAATT  
TGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTGTAATTTAATA  
ATTGTTTAGGTGTGTACGAATATAaGCAATC

SEQ ID NO: 4906

STRAIN M732

AAACATCCGATACCTTAATGATCAAAAATCCTTAGCAATTGTTGAACA  
GATAGAAATATGATTGGATAAATTCGATAATTCAGAAGCTTCTTTTATG  
CAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAAAAATTTATT  
AGAGAAAATCCAAATAGTCAAAATCCTTTCAATTGGTTGTGGACTTGATC  
AAGGTTTGAAGAGTTCGATAATGGACAAATTAGGTGGTATAACCTTGATT  
TGCCAGAGGTTATGGAGATAAGAAAATTTATTTTGAAGAGCATGAAAGA  
GTTACTAATATAGCAAAATCAGCCCTAGATGAACTTGACACGGGAGGT  
AAATCCCCAAAATGCCCCCTTTCTAATCGTGTGAGAAGGTGTTTAAATGT  
TTCTAAAAGAAAGATGACGTAGAGACTTTCTTCATATCCTGACAAATTC  
TTTAGCCAAATTTATGGGCAAAATTTGATTGTGTGCATAGGAAATGATTAA  
TAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACAGAAATTTCAAT  
TTGGTATCACAGATGGTCATGAGATTGTGGATTAGACCCTAAATTAAG  
CAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAATTTGAGTTAGG  
CACACTTCGCTCTTTACTTCCAACAATTGTAATTTAATAATTTGTTAG  
GtGTGTACGAATATAAAGCATC

SEQ ID NO: 4907

STRAIN COH1

AAACATCCGATACCTTAATGATCAAAAATCCTTAGCAA  
TTGTTGAACAGATAGAATATGATTGGATAAATTCGATAATTCAGAAGCT  
TCCTTTTATGCAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAA  
AAAATTTATTAGAGAAAATCCAAATAGTCAAAATCCTTTCAATTGGTTGTG  
GACTTGATACAAGGTTTGAAGAGTTCGATAATGGACAAATTAGGTGGTAT  
AACCTTGATTGCGCAGAGTTATGGAGATAAGAAAATTTATTTTGAAGA  
GCATGAAGAGTTACTAATATAGCAAAATCAGCCCTAGATGAACTTGGA  
CACGGGAGGTAAATCCCCAAAATGCCCCCTTTCTAATCGTGTGAGAAGGT  
GTTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTTCTTCATATCCT  
GACAAATTCATTTAGCCAAATTTATGGCACAATTTGATTGTGTGCATAAGG  
AAATGATTAAATAAGGAAAGCAACATGATACAGTAAAGTATATGGATACA  
GAATTTCAAGTTTGGTATCACAGATGGTCATGAGATTGTGGATTAGACCC  
TAAATTAAGCAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAAT  
TTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTGTAATTTAAT  
AATTGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4908

STRAIN M781

AAACATCCGATACCTTAATGATCA  
AAAATCCTTAGCAATTTGTAACAGATAGAATATGATTGGATAAATTCG  
ATAATTCAGAAGCTTCTTTTATGCAACATTAGCTAGAATTCGCGTTATG  
GATAGAGAAATCAAAAATTTATTAGAGAAAATCCAAATAGTCAAATCCT  
TTCAATTGGTTGTGGACTTGATACAAGGTTTGAAGAGTCGATAATGGAC  
AAATTAGGTGGTATAACCTTGATTGCGCAGAGTTATGGAGATAAGAAAA  
TTATTTTGAAGAGCATGAAAGAGTTACTAATATAGCAAAATCAGCCCT  
AGATGAAACTTGGACACGGGAGGTAAATCCCCAAAATGCCCCCTTTTCTAA  
TCGTGTGAGAAGGTGTTTTAATGTTTCTAAAAGAAAGTACGTAGAGACT  
TTTCTTCATATCCTGACAAATTCATTAGCCAAATTTATGGCACAATTTGA  
TTGTGTGCATAGGAAATGATTAAATAAGGAAAGCAACATGATACAGTAA  
AGTATATGGATACAGAAATTCAGTTTGGTATCACAGATGGTCATGAGATT  
GTGGATTAGACCCCTAAATTAAGCAAATAAATCTGATTAACTTTACAGA  
TGAGATGAGCAAATTTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAA  
TTCGTAATTTAATAATGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4909

STRAIN CJB110

AAACATCCGATACCTTAATGATCAAAAATCCTTAGCAA  
TTGTTGAACAGATAGAATATGATTGGATAAATTCGATAATTCAGAAGCT  
TCCTTTTATGCAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAA  
AAAATTTATTAGAGAAAATCCAAATAGTCAAAATCCTTTCAATTGGTTGTG  
GACTTGATACAAGGTTTGAAGAGTTCGATAATGGACAAATTAGGTGGTAT  
AACCTTGATTGCGCAGAGTTATGGAGATAAGAAAATTTATTTTGAAGA  
GCATGAAGAGTTACTAATATAGCAAAATCAGCCCTAGATGAACTTGGA  
CACGGGAGGTAAATCCCCAAAATGCCCCCTTTCTAATCGTGTGAGAAGGT  
GTTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTTCTTCATATCCT  
GACAAATTCATTTAGCCAAATTTATGGCACAATTTGATTGTGTGCATAAGG  
AAATGATTAAATAAGGAAAGCAACATGATACAGTAAAGTATATGGATACA  
GAATTTCAAGTTTGGTATCACAGATGGTCATGAGATTGTGGATTAGACCC  
TAAATTAAGCAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAAT  
TTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTGTAATTTAAT  
AATTGTTTAGGTGTGTACGAATATAAAGCATC

SEQ ID NO: 4910

STRAIN 1169NT

AAACATCCGATACCTTAATGATCAAAAATCCTTAGCAAT  
TGTTGAACAGATAGAATATGATTGGATAAATTCGATAATTCAGAAGCTT

Table 49: Comparative Sequences related to SAG1502

CTTTTATGCAACATTAGCTAGAAATTCGCGTTATGGATAGAGAAATCAAA AAATTTATTAGAGAAAAATCCAAATAGTCATATCCTTTCTATTGGTTGTGG ACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATAGGTGGTATA ACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAATTATTTTGAAGAG CATGAAAGAGTTACTAATATAGCAAAATCAGCCCTAGATGAACTTGGAC ACAGGAGGTAATCCCCAAATGCCCTTTTCTGATCGTGTGAGAGGTG TTTAAATGTTTCTAAAGAGATGACGTAGAGACTTTTCTCATATCCTG ACAAATTCATTTAGCCAATTTATGGCACATTTGATTGTGTGAGAAAGGA AATGATTAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACAG AATTTAGTTTGGTATCACAGATGGTCATGAAATTTGGGATTAGACCCCT AAATTAAGCAAAATAATCTGATTAACTTTACAGATGAGATGAGCAAAAT TGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCTGTAATTTAATA ATTGTTAGGTGTGTACGAATATAAGCATC									
SEQ ID NO: 4911 STRAIN JM9130013 AGCAATGTGTGAACAGATAGAAATGATT TTGATAAATTCGATAATTCAGAAGCTTCTTTTATGCAACATTAGCTAGA ATTTCGCGTTATGGATAGAGAAATCAAAAAATTTATTAGAGAAAAATCCAAA TAGTCATATCCTTTCAATTGGCTGTGGACTTGATACAAGGTTTGAAAGAG TCGATAATGGACAAATAGGTGGTATAACCTTGATTGGCCAGAGGTTATG GAGATAAGAAAAATTATTTTGAAGAGCATGAAAGAGTTACTAATATAGC AAAATCAGCCCTAGATGAACTTGGACACGGGAGGTAAATCCCCAAATG CCCCTTTCTAATCGTGTGAGAAGGTGTTTAAATGTTTCTAAAGAAAGAT GACGTAGAGACTTTTCTCATATCCTGACAAATTCATTAGCCAATTTAT GGCACAAATTTGATTGTGTGAGAAGGAAATGATTAAATAAGGAAAGCAAC ATGATACAGTAAAGTATATGGATACAGAAATTTAGTTTGGTATCACAGAT GGTCATGAAATTTGGATTATAGACCCCTAAATTAAGCAAAATAAATCTGAT TAACTTTACAGATGAGATGAGCAAAATTTAGTTAGGCACACTTCGCTCTT TACTTCCAACAATTCGTAAATTTAATAATTTGTTAGGTGTGTACGAATAT AAAGCATC									
PRETTY of: /biotmp/msa42193.2{*}    January 21, 2003 05:04 ..									
msa42193.2{176_090}	1	-----	-----	taatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT	50	
msa42193.2{176_CJB110}		AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT			
msa42193.2{176_18RS21}		-AACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT			
msa42193.2{176_2603}		AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT			
msa42193.2{176_A909}		AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT			
msa42193.2{176_COH1}		AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT			
msa42193.2{176_M732}		AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT			
msa42193.2{176_M781}		AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT			
msa42193.2{176_H36B}		AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT			
msa42193.2{176_JM9130013}		-----	-----	-----	-----	-----			
msa42193.2{176_1169NT}		AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT			
Consensus		*****	*****	-----	-----	*****	*****		
msa42193.2{176_090}	51	AGAATATGAT	TTtGATAAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA	100		
msa42193.2{176_CJB110}		AGAATATGAT	TTtGATAAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
msa42193.2{176_18RS21}		AGAATATGAT	TTtGATAAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
msa42193.2{176_2603}		AGAATATGAT	TTtGATAAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
msa42193.2{176_A909}		AGAATATGAT	TTtGATAAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
msa42193.2{176_COH1}		AGAATATGAT	TTtGATAAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
msa42193.2{176_M732}		AGAATATGAT	TTtGATAAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
msa42193.2{176_M781}		AGAATATGAT	TTtGATAAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
msa42193.2{176_H36B}		AGAATATGAT	TTtGATAAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
msa42193.2{176_JM9130013}		AGAATATGAT	TTtGATAAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
msa42193.2{176_1169NT}		AGAATATGAT	TTtGATAAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA			
Consensus		*****	***-*****	*****	*****	*****	*****		
msa42193.2{176_090}	101	CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA	150		
msa42193.2{176_CJB110}		CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
msa42193.2{176_18RS21}		CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
msa42193.2{176_2603}		CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
msa42193.2{176_A909}		CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
msa42193.2{176_COH1}		CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
msa42193.2{176_M732}		CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
msa42193.2{176_M781}		CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
msa42193.2{176_H36B}		CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
msa42193.2{176_JM9130013}		CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
msa42193.2{176_1169NT}		CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA			
Consensus		*****	*-*****	*****	*****	*****	*****		
msa42193.2{176_090}	151	GAAAAATCCAA	ATAGTCaAaT	CCITTCaATT	GGtTGTGGAC	TTGATACAAG	200		
msa42193.2{176_CJB110}		GAAAAATCCAA	ATAGTCaAaT	CCITTCaATT	GGtTGTGGAC	TTGATACAAG			
msa42193.2{176_18RS21}		GAAAAATCCAA	ATAGTCaAaT	CCITTCaATT	GGtTGTGGAC	TTGATACAAG			
msa42193.2{176_2603}		GAAAAATCCAA	ATAGTCaAaT	CCITTCaATT	GGtTGTGGAC	TTGATACAAG			
msa42193.2{176_A909}		GAAAAATCCAA	ATAGTCaAaT	CCITTCaATT	GGtTGTGGAC	TTGATACAAG			
msa42193.2{176_COH1}		GAAAAATCCAA	ATAGTCaAaT	CCITTCaATT	GGtTGTGGAC	TTGATACAAG			

Table 49: Comparative Sequences related to SAG1502

msa42193.2{176_M732}	GAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_M781}	GAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_H36B}	GAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_JM9130013}	GAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_1169NT}	GAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	201	250			
msa42193.2{176_CJB110}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_18RS21}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_2603}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_A909}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_COH1}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_M732}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_M781}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_H36B}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_JM9130013}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_1169NT}	GTTTGAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	251	300			
msa42193.2{176_CJB110}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_18RS21}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_2603}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_A909}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_COH1}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_M732}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_M781}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_H36B}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_JM9130013}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_1169NT}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	301	350			
msa42193.2{176_CJB110}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_18RS21}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_2603}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_A909}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_COH1}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_M732}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_M781}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_H36B}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_JM9130013}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_1169NT}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	351	400			
msa42193.2{176_CJB110}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_18RS21}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_2603}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_A909}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_COH1}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_M732}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_M781}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_H36B}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_JM9130013}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_1169NT}	TCCCCAAAAT	GCCCCCTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	401	450			
msa42193.2{176_CJB110}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_18RS21}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_2603}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_A909}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_COH1}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_M732}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_M781}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_H36B}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_JM9130013}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_1169NT}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	451	500			
msa42193.2{176_CJB110}	AGCCAATTTA	TGGCACAATT	TGATTGTGTG	CaTAAGGAAA	TGATTAATAA
msa42193.2{176_18RS21}	AGCCAATTTA	TGGCACAATT	TGATTGTGTG	CaTAAGGAAA	TGATTAATAA
msa42193.2{176_2603}	AGCCAATTTA	TGGCACAATT	TGATTGTGTG	CaTAAGGAAA	TGATTAATAA
msa42193.2{176_A909}	AGCCAATTTA	TGGCACAATT	TGATTGTGTG	CaTAAGGAAA	TGATTAATAA



Table 49: Comparative Sequences related to SAG1502

msa42193.2{176_COH1}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CATaAGGAAA	TGATTAATAA
msa42193.2{176_M732}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CATaAGGAAA	TGATTAATAA
msa42193.2{176_M781}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CATaAGGAAA	TGATTAATAA
msa42193.2{176_H36B}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CAGaAGGAAA	TGATTAATAA
msa42193.2{176_JM9130013}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CAGaAGGAAA	TGATTAATAA
msa42193.2{176_1169NT}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CAGaAGGAAA	TGATTAATAA
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_CJB110}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_18RS21}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_2603}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_A909}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_COH1}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_M732}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_M781}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_H36B}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_JM9130013}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_1169NT}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_CJB110}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_18RS21}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_2603}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_A909}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_COH1}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_M732}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_M781}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_H36B}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_JM9130013}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_1169NT}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_CJB110}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_18RS21}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_2603}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_A909}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_COH1}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_M732}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_M781}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_H36B}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_JM9130013}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_1169NT}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_CJB110}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_18RS21}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_2603}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_A909}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_COH1}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_M732}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_M781}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_H36B}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_JM9130013}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_1169NT}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_CJB110}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_18RS21}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_2603}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_A909}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_COH1}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_M732}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_M781}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_H36B}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_JM9130013}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_1169NT}	TGTACGAATA	TAAAGCATC			
Consensus	*****	*****			

SEQ ID NO: 4912

STRAIN 2603 frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARKXRVMDREIKKFIRENPNSQILSI  
 CGGLDTRFRVNDNGQIRWYNLDLFEVMEIRKLFFEEHERVTNIAKSALDETWTRVNPQN  
 APPLIVSEGVLMFLKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKHQDITVKYMDTE

Table 49: Comparative Sequences related to SAG1502

FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVY EYKA

**SEQ ID NO: 4913**

STRAIN 090 frame: 2

NDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSIGCGLD  
TRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSAIDETWTREVPQNAPFLI  
VSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTEFQFGI  
TDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVY EYKA

**SEQ ID NO: 4914**

STRAIN A909 frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI  
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVPQN  
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTE  
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVY EYKA

**SEQ ID NO: 4915**

STRAIN H36B frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSHILSI  
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVPQN  
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTE  
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVY EYKA

**SEQ ID NO: 4916**

STRAIN 18RS21 frame: 3

HPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSIG  
CGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVPQNA  
PFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTEF  
QFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVY EYKA

**SEQ ID NO: 4917**

STRAIN M732 frame: 1

KHPILNDQKSLAIVEQIEYDLDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI  
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVPQN  
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTE  
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVY EYKA

**SEQ ID NO: 4918**

STRAIN COH1 frame: 1

KHPILNDQKSLAIVEQIEYDLDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI  
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVPQN  
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTE  
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVY EYKA

**SEQ ID NO: 4919**

STRAIN M781 frame: 1

KHPILNDQKSLAIVEQIEYDLDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI  
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVPQN  
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTE  
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVY EYKA

**SEQ ID NO: 4920**

STRAIN CJB110 frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI  
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSAIDETWTREVPQN  
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTE  
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVY EYKA

**SEQ ID NO: 4921**

STRAIN 1169NT frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSHILSI  
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTQEVNPQN  
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTE  
FQFGITDGHEIVDLDPKPKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVY EYKA

**SEQ ID NO: 4922**

STRAIN JM9130013 frame: 2

AIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSHILSIGCGLDTRFERV  
DNGQIRWYNLDLPEVMEIRKLFEEHERVTNIAKSALDETWTREVPQNAPFLIVSEGVL  
MLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGQHDVTKYMDTEFQFGITDGHEI  
VDLDPKPKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVY EYKA

PRETTY of: /biotmp/msa42204.2{\*} January 21, 2003 05:05 ..

	1		50
msa42204.2{176_H36B}	khpilndqks	LAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR	
msa42204.2{176_JM9130013}	-----	-AIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR	
msa42204.2{176_090}	-----ndqks	LAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR	
msa42204.2{176_18RS21}	-hpiilndqks	LAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR	
msa42204.2{176_2603}	khpilndqks	LAIVEQIEYD fDKFDNSEAS FYATLARxRV MDREIKKFIR	
msa42204.2{176_A909}	khpilndqks	LAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR	
msa42204.2{176_CJB110}	khpilndqks	LAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR	

Table 49: Comparative Sequences related to SAG1502

msa42204.2{176_COH1}	khpilndqks	laIVEQIEYD	ldKFDNSEAS	FYATLARiRV	MDREIKKFIR
msa42204.2{176_M732}	khpilndqks	laIVEQIEYD	ldKFDNSEAS	FYATLARiRV	MDREIKKFIR
msa42204.2{176_M781}	khpilndqks	laIVEQIEYD	ldKFDNSEAS	FYATLARiRV	MDREIKKFIR
msa42204.2{176_1169NT}	khpilndqks	laIVEQIEYD	fdKFDNSEAS	FYATLARiRV	MDREIKKFIR
Consensus	-----	*****	*****	*****	*****
51					
msa42204.2{176_H36B}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_JM9130013}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_090}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_18RS21}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_2603}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_A909}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_CJB110}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_COH1}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_M732}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_M781}	ENPNsqILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_1169NT}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
Consensus	*****	*****	*****	*****	*****
101					
msa42204.2{176_H36B}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_JM9130013}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_090}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_18RS21}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_2603}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_A909}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_CJB110}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_COH1}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_M732}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_M781}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_1169NT}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
Consensus	*****	***-*****	*****	*****	*****
151					
msa42204.2{176_H36B}	SQFMAQFDLC	qKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_JM9130013}	SQFMAQFDLC	qKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_090}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_18RS21}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_2603}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_A909}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_CJB110}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_COH1}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_M732}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_M781}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
msa42204.2{176_1169NT}	SQFMAQFDLC	qKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLKQ
Consensus	*****	-*****	*****	***-*****	*****
201					
msa42204.2{176_H36B}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_JM9130013}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_090}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_18RS21}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_2603}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_A909}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_CJB110}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_COH1}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_M732}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_M781}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_1169NT}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
Consensus	*****	*****	*****	*****	
239					

Table 50: Comparative Sequences relating to SAG 1024

## SEQ ID NO. 5001

## STRAIN 2603

ATGAAAAACAAAACTATTACTGCTTATTGGAGGCTTATTAATAATGATAATGATGACA  
 GCATGTAAGGATTCAAAAATCCAGAAAACCGCACAAAGGAAGAGTACCAAGCTGAACAA  
 AATTTTAAACCGTTTTTTGAGTTTGTAGCAGAAAAGATAAGATTGAGCAAAATACAA  
 AAATACTTACTATTAGTATCGGATTCAGGTGATGCATTAGATTAGAAATATTTCTATAGT  
 ATTCAAGATTTAAAAAAAATAAGGATTTAGGGAAGTTTGAACAAGAAAAGTCAAATA  
 GAAAAGCCGGTGGCTATAATGAGTTAGAAAATAAGAGGTCCCAITTTGAATATTTTAA  
 AATAATATAGTTTATCCAAAAGGAAAACCGAATATTACATTTGATGACTTTATTATCGGA  
 GCAATGGATACTAAAGAATTAAAGAATTAAAAAATTAAAAAGTAAAAAGTTATTATTA  
 AAACATCCGGAACCTGAGTTGAAGATATAACATATGAATTGCCGACACAGTCAAGCTT  
 ATTAATAAA

## SEQ ID NO. 5002

## STRAIN 090

TAAGGATTCAAAAATCCAGAAAACCGCACAAAG  
 GAAGAGTACCAAGCTGAACAAAATTTTAACTGTTTTTGGAGTTTTTGTAGC  
 ACAAATATATAAGATTGAAACAAAATACAAAATACCTTACTATTAGTAT  
 CGGATTCAGGTGATGCATTAGATTAGAAATATTTCTATAGTATTCAGAT  
 TTAATAAAAAATAAGGATTTAGGGAAGTTTGAACAAGAAAAGTCAAAAT  
 AGAAAAGCCGGTGGCTATAATGAGTTAGAAAATAAGAGGTCCCATTTG  
 AATATTTTAAAAATAATATAGTTTATCCAAAAGGAAAACCGAATATTACA  
 TTTGATGACTTTATTATCGGAGCAATGGATACAAAGAATTAAAAAATT  
 AAAAGTAAAAAGTTATTTATTAACATCCGGAACCTGAGTTGAAAGATA  
 TAACATATGAATTGCCGACACAGTCAAGCTTATTAATAAA

## SEQ ID NO. 5003

## STRAIN 18RS21

TAAGGATTCAAAAATCCAGAAAACCGCACAAAGGAAG  
 AGTACCAAGCTGAACAAAATTTTAAACCGTTTTTGGAGTTTTTGTAGCAGAA  
 AAGATATAAGATTGAGCAAAATACAAAATACCTTACTATTAGTATTCGGA  
 TTCAGGTGATGCATTAGATTAGAAATATTTCTATAGTATTCAGATTTAA  
 AAAAAATAAGGATTTAGGGAAGTTTGAACAAGAAAAGTCAAAATAGAA  
 AAGCCGGTGGCTATAATGAGTTAGAAAATAAGAGGTCCCATTTGAATA  
 TTTTAAAAATAATATAGTTTATCCAAAAGGAAAACCGAATATTACATTTG  
 ATGACTTTATTATCGGAGCAATGGATACAAAGAATTAAAGAATTAAAA  
 GAATTAATAAAATTAAAGTAAAAAGTTATTTATTAACATCCGGAAC  
 TGAGTTGAAAGATATAACATATGAATTGCCGACACAGTCAAGCTTATTA  
 AAAAA

PRETTY of: /biotmp/msa212269.2{\*} February 10, 2003 05:07 ..

msa212269.2{184_090}	1	50
msa212269.2{184_2603}	atgaaaaaac aaaaaactatt actgcttatt ggaggcttat taataatgat	
msa212269.2{184_18RS21}	*****	
Consensus	*****	
msa212269.2{184_090}	51	100
msa212269.2{184_2603}	-----TAAGG ATTCAAAAAT CCCAGAAAAC CGCACAAAGG	
msa212269.2{184_18RS21}	aatgatgaca gcatgTAAGG ATTCAAAAAT CCCAGAAAAC CGCACAAAGG	
Consensus	*****	
msa212269.2{184_090}	101	150
msa212269.2{184_2603}	AAGAGTACCA AGCTGAACAA AATTTTAAAC tGTTTTTTGA GTTTTTAGCA	
msa212269.2{184_18RS21}	AAGAGTACCA AGCTGAACAA AATTTTAAAC cGTTTTTTGA GTTTTTAGCA	
Consensus	*****	
msa212269.2{184_090}	151	200
msa212269.2{184_2603}	CAAAAAtATA AAGATTTGaa CAAAATACAA AAATACTTAC TATTAGTATC	
msa212269.2{184_18RS21}	CAAAAAGATA AAGATTTGag CAAAATACAA AAATACTTAC TATTAGTATC	
Consensus	*****	
msa212269.2{184_090}	201	250
msa212269.2{184_2603}	GGATTTCAGGT GATGCATTAG ATTAGAAATA TTTCTATAGT ATTCAAGATT	
msa212269.2{184_18RS21}	GGATTTCAGGT GATGCATTAG ATTAGAAATA TTTCTATAGT ATTCAAGATT	
Consensus	*****	
msa212269.2{184_090}	251	300
msa212269.2{184_2603}	TAAAAAATAA TAAGGATTTA GGAAGTTTG AAACAAGAAA AAGTCAAATA	
msa212269.2{184_18RS21}	TAAAAAATAA TAAGGATTTA GGAAGTTTG AAACAAGAAA AAGTCAAATA	
Consensus	*****	
msa212269.2{184_090}	301	350
msa212269.2{184_2603}	GAAAAGCCGG GTGGCTATAA TGAGTTAGAA AATAAAGAGG TCCCATTGGA	
msa212269.2{184_18RS21}	GAAAAGCCGG GTGGCTATAA TGAGTTAGAA AATAAAGAGG TCCCATTGGA	
Consensus	*****	

Table 50: Comparative Sequences relating to SAG 1024

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msa212269.2{184_090} 351
msa212269.2{184_2603} 400
msa212269.2{184_18RS21}
Consensus *****

msa212269.2{184_090} 401
msa212269.2{184_2603} 450
msa212269.2{184_18RS21}
Consensus *****

msa212269.2{184_090} 451
msa212269.2{184_2603} 500
msa212269.2{184_18RS21}
Consensus *****

msa212269.2{184_090} 501
msa212269.2{184_2603} 550
msa212269.2{184_18RS21}
Consensus *****

msa212269.2{184_090} 551
msa212269.2{184_2603}
msa212269.2{184_18RS21}
Consensus *****

SEQ ID NO. 5004
STRAIN 2603 frame: 1
MKKQKLLLLIGLLIMIMMTACKDSKIPENRTKEEYQAEQNFKPFFFFLAQKDKDLSKIQ
KYL LVSDSGDALDLEYFYISIQDLKKNKDLGKFETRKSQIEKPGGYNELENKEVPFPEYFK
NNIVYPKGKPNITFDDFIIGAMDTKELKELKELKLVKSYLLKHPETELKDITYELPTQSKL
IKK

SEQ ID NO. 5005
STRAIN 090 frame: 2
KDSKIPENRTKEEYQAEQNFKPFFFFLAQKYKDLNKIQKYL LVSDSGDALDLEYFYISIQ
DLKKNKDLGKFETRKSQIEKPGGYNELENKEVPFPEYFKNNIVYPKGKPNITFDDFIIGAM
DTKELKELKELKLVKSYLLKHPETELKDITYELPTQSKLIKK

SEQ ID NO. 5006
STRAIN 18RS21 frame: 2
KDSKIPENRTKEEYQAEQNFKPFFFFLAQKDKDLSKIQKYL LVSDSGDALDLEYFYISIQ
DLKKNKDLGKFETRKSQIEKPGGYNELENKEVPFPEYFKNNIVYPKGKPNITFDDFIIGAM
DTKELKELKELKLVKSYLLKHPETELKDITYELPAQSKLIKK

PRETTY of: /biotmp/msa212547.2{*} February 10, 2003 05:11 ..

msa212547.2{184_18RS21} 1
msa212547.2{184_2603} 50
msa212547.2{184_090}
Consensus *****

msa212547.2{184_18RS21} 51
msa212547.2{184_2603} 100
msa212547.2{184_090}
Consensus *****

msa212547.2{184_18RS21} 101
msa212547.2{184_2603} 150
msa212547.2{184_090}
Consensus *****

msa212547.2{184_18RS21} 151
msa212547.2{184_2603} 186
msa212547.2{184_090}
Consensus *****

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Table 51: Comparative Sequences relating to SAG0677

SEQ ID NO. 5101

STRAIN 2603

ttgaataataaagggtgtcggtggcgatgggtgtccaaatttatcaatacta  
tatcaaaatggacaacaataaaccttacttaagtcccaaagataagacta  
ctgtagagaagttagaagatcgctggaaaaaatctcttcaaagttcag  
gatactggcattgggtttgaaagacgtttatcttcaatctgttaagtatgt  
tggtgggtggcaataataatttagacctatcacacctccaggatttaaaa  
aagaagataaaaaagttgaaaaaccaaatttagacctccaccagggaatt  
gatttaccagcaccaacttcaatgagaagttttgattattcaacccacc  
gggaactaagccaagcaaacccaaagatagtttatcaactcctccagggt  
tcccagatttaaacacgcccggatgaagcaccacaaaggatagtaaaaa  
gacgctattgaagataaatcaggagcaatataatagctaaagtctctca  
acttagctttgtgatggccctatttttagctagcaaaagtaaatggcaaaa  
tattcaagtcgaatctgatggcaaattagtcatctcctagaatgctttg  
tcagctaataatcaatttgatgacactagtcttaaaatttatcgtaataata  
tcgcaataaagaaattactatcacacagattatttgcagatacaaaat  
atgtcaatatcacagcgggtgactatttgagcaatactacttttgagcaa  
ttagctactgggtgaaacagtagattaccatgccattgtattttcaagct  
tgctgctatttaagacaaggggtggaagatttatgttaacgataaattgc  
aagaaactctcgtatagcgtttaaagataaatctgttaagattgggtatt  
gaattaccaaattgatgtcagacatatgtatgtttatctgttctcgtttt  
gaatgaggttaaaactgttgataaatcttgaaaaatgatgaacaagaca  
ttaatctcagcaaaaacttaccatttaaaatacaacccgacaaatcgtcgt  
ctagagtttactatataaacttaactcaagttcagaatcatgaccac  
tttcaagatggaaagatgccagaattgggtgaacaaaaagatgtttctt  
tggatataaacgatattggacatgagtaagtttaaaactattcgaacttgg  
cgaaggattctgaatttaaggggacaacttattgcaaaaactggaacagt  
tgaattagatatgtttttcaacaatctcaagaccagcttcaattatta  
aaaaatataccttatccaaatgggtgttccaaatgaattgaaaaaattt  
gactctgattttgggttaactgaaagttagatagatggatactatatta  
taagatgcaattaaccttaatttaaatcaaccagtggtgcaagctctta  
aagttgtttataaagggcaagaagatccatatagtcacagaagaagat  
atgactaaaaaaggtgaacagctcagtcattcaactcaagccaatgaaaa  
tacagcaaaagtaacctttgctaatatgactgggtcacattatagtaagg  
ttactgtgaatggaaaagaagttgttaaggttagtgagtacctttaact  
aaaggatggacaacatttgtattacataaaacagaaaaattcatataatgt  
taaaagtttgattatggagacgggttagtgtaagtaagaaagtcaacaac  
ttcctttaagtcctagatttatctaaaaatagcatatgagggatatgcta  
cttactatgcaaaaagattcagcgtatcacgaaacagtgacagctcagtc  
ccttcgaattaatctcactgcagatactaaacttaattttaatgctgtta  
aaggagcagtgctcttactgaaaatgatgatgagacagtttgagtt  
gctggaccacaagatgactcctgttagtgaaacataaatacccatcagttt  
tctcttaactcctgccttatggaaactgctagtgaggcaactcctaaatg  
gtaaggaatcacagcatctggtattatcggtcacatcaaggatgggtgat  
aaaagcaagcatgttgaagtcaaaatgggtgaatgaaaaatggagacatgct  
aggaacccctgttatttcaaggttaagacttgactaatcgacacaaac  
cattatagtgaggcagtagagtagtcttattgcccgttaacaatatgagttc  
cgggctaaattaccacttagtcgttttaacacttggattagggttgaagt  
ggtaacagaagcaggagagaagcaagtagttgtcgtcgcatgttctttg  
accaatcagttccagagcttaacacagcagtttgctaaacgtgatttgact  
tctgatactgctcttatccacatcggtgccaagatgactctctaaact  
aaaattatatcaagatgattcattacttgaatctgttgataaaacccggtc  
tttatagtttttagaaatgggttagaaatcactaaagatatgacagtacca  
ctagaatttggagataatatatttaagttatctgctgttgacttatcaaa  
ttatcgtcgttaatgagacccttatatctatagaacccgttttgatgtta  
aagcaagcccaatgacagctgacaaaggagctaaagttaactgtggatag  
ttgatgaagcacttagttgttccagaatggcaggagcttatacattaac  
aatcgacgaagctccaaacacaaatgaatcaggaatgttaacaaacgcta  
aagtatcgattcattatgtaaatgggtgttgataaagttgatgttccg  
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agctgaagaagcagctaaagctgaagaagcagtaaaagctgaagaggac  
ataaaacccaagaagcactatagttgaagaaggctacaaggttaataac  
gttcatcaaaactgatactacagttaaagcgtctgatttaccaaagactaa  
gacagtttccgagttcatatggctagaacagacaataaacagataaactt  
cacatcagacacatgttgaaaaacaaatataaatacattgccatccact  
ggtagacagcaaacgtgggttattatctactgggaatggctatcgttatgct  
gagtgattatttttagtttagctaaaaagtttaaaagcaaatat

SEQ ID NO. 5102

STRAIN A909

TTGAATAATAAAGGTGTCGGTGGCGAT

GGTGTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAACCTTA  
CTTAAGTCCCAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGA  
AAAAAATTACTTTCAAAGTTCAAGATATCGGCATTGGTTTGAAGACGTT  
TATCTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCT  
TATCACACCTCCAGGATTTAAAAAAGAGATAAAAAAGTTGAAAAACCAA  
AATTAGACCGTCCACCAGGAATTGATTACCAACCAACTTCAATGAGA  
AGTTTGTATTATCAACCCACCGGGAAGTAAGCCAAGCAAAACCAAGA  
TAGTTTATCAACTCCTCCAGGTTTCCAGATTTAACACGCCGCCGGATG  
AAGCACTAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGCA  
ATTAAATATGCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCTATTTT  
AGCTAGCAAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAT  
TAGTCATTCCTAGAAATGCTTTGTGAGTAATCAATTTGATGACACTAGT

Table 51: Comparative Sequences relating to SAG0677

CTTAAATTTTATCGTAATAATAATCGCAATAAGAAATTACTATCACAAC  
 AGATTATTTTGCAGATACAAAATATGTCAATATCACAGCGGTGACTATT  
 TGAGCAATACACTTTTGAGCAATTAGCTACTGGTGAACAGTAGATTAC  
 CATGCCATTGTATTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAA  
 GATTTATGTTAAAGATAAATGCAAGAACTTCTCGTATAGCGCTTAAAG  
 ATAAATCTGTTAAGATTGGTATTGAATTACCAATGATGTGAGACATATT  
 GATAGTTTATCTGTTCTGTTGAATGAGGTTAAACTGTTGATAATAT  
 CTTGAAAAATGATGAACAAGACATTAACTCTCAGCAAACTTACCAATTAA  
 AATACAAACCCGACAAATCGTCTAGAGTTTACTATTAAATAACATTAAAC  
 TCAAGTTTCAGAAATCATGACCACTTCAAAGATGGAAAGATGCCAGAATT  
 GGTGTAaCAAAAAGATGTTCTTTGGATATAaCGATATGGACATGAGTA  
 AGTTTAAAACTATTGCACTTGGACGAAAGGATTCTGAATTTAAGGACAA  
 CTTATTGCAAAAACCTGGAACAGTTGAATTAGATATGTTTTCAAACAATC  
 TCAAGACCCAGCTTCAATTATTTAAAAAATATACCTTATCCAAAATGGTG  
 TTCCAAATGAATTGAAAAAATTGACTCTAGTTTGGTTTAACTGAAAGT  
 CAGATAGTGGATATATATTTATAAAGATGCAATTAACTTAAATTTAA  
 ATTAACAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGCAAGAAGATC  
 CATATAGTCATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAGT  
 CATTTCACTCAAGCCAATGAAATACAGCAAAAGTAACTTTGCTAATAT  
 TGAATGCTGACATTATAGTAAGTTACTGTGAATGGAAAGAAGTTGGTA  
 AAGGTAGTGAGTTACTTTAACTAAAGGATGGACAACATTTGATTACAT  
 AAAAAAGAAATTCATTAAATGTTAAAGTTGATTATGGAGACGGGTAG  
 TGTAAAGTAAGAAAGTTCAACAACCTTCTTTAAGTCTTAGATTATCTAAAA  
 ATAAAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGGTAT  
 TACGAaaCAAGTGAAGTCTAGTCTCGAATTAACTCTCACTGCAGATAC  
 TAACTTAAATTTAATGCTGTTAAAGGAGCGAGTCTCTTACTGAAAATA  
 TGATGATGAGACAGTTTGCAGTTGCTGGACCAAGATGATCCTGTTAGT  
 GAACATAAATACCCATCAGTATTTCTCTTAACTCTGCTTATTGGAAAC  
 TGCTAGTGAGGCACTCTaAATGGTAAGGAATCACAGCATCTGGTATTA  
 TCCGTACATCAAGGATGGTGAATAAAGCAAGCATGTTGAAGTCAAAATG  
 GTGAATGAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAA  
 AGACTTGACTAATCGAACAAAACCAATTAATGAGTGGACGTAGAGTACTTT  
 ATGCCGGTAAACAATATGAGTTCCGGGCTAAATTACCCTTAGTCTGTTTT  
 AACACTTGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAG  
 TATTGTTGCTCGCATGTTCTTTGACCAATCAGTCCAGAGCTTAAACAG  
 CAGTTGCTAAACGATTTGACTTCTGATCTGCTCTTATCCACATCGTT  
 GCCAAGATGACTCTCTAAAACTAAATTTATCAAGATGATTCTTACT  
 TGAATCTGTTGATAAAACCGGTCTTTATAGTTTTAGAAATGGTGTAGAAA  
 TCACTAAAGATATGACAGTACCACTAGAATTTGGAGATAATATTATTAAG  
 TTATCTGCTGTTGACTTATCAAAATATCGTCTGTAATGAGACCCCTTCATAT  
 CTATAGAAACCGTTTTGATGTTAAAGCAAGCCAATGACAGCTGACAAAG  
 GAGCTAAAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAA  
 ATGGCAGGAGCTTATACATTAAATCGACGAAGATCCAACACAAATGA  
 ATCAGGAATGTTAAACAAACGCTAAAGTATCGATTCAATTATGTAATGGTG  
 GTGTTGATAAAGTTGATGTTCCGATTAAAGTGAAGTTGACTTGAAGCTTAT  
 CGTAAAGCTGAAGAAGCACATAAGCTGACGAAGCACGTAAAGCTGAAGA  
 AGCAGCTAAAGCTGAAGAAGCACGTAAAGCTGAAGAAGCACGTAAAGCTG  
 AAGAGGGACATaAAACCCAAAGAACCTTATAGTTGAAGAAGGCTACAAG  
 GTTAATAACGTTTCATCAAACTGATCTACAGTTAAAGCGTCTGATTAC  
 AAAGACTAAGACAGTTTCCGAGTTTCATATGGCTAGAACAGACAATAAAC  
 AGATAACTTCATCAGACATGTTGAAAAACAATTTAAAAATA

SEQ ID NO. 5103

STRAIN H3B

TGGTGTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAACCTT  
 ACTTAAGTCCCAAGATAAGACTACTGTAGAGAAGTTAGaaGATCGCTGG  
 AAAAAAATTACTTTCAAAGTTCCAGGATACTGGCATTGGTTTGAAGACGT  
 TTATCTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACC  
 TTATCACACCTCCAGGATTAAAAAAGAAGATAAAAAAGTTGAAAAACCA  
 AAATTAGACCGTCCACCAGGAATTGATTTACCAGCACCAACTTCAATGAG  
 AAGTTTGTATTATCAACCCACCGGGAACCTAAGCCAAGCAACCCAAAG  
 ATAGTTTATCAACTCTCCAGGTTTCCAGATTTTAAACAGCCGCGCGGAT  
 GAAGCACTAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGC  
 AATTAAATATGCTAAGTCTCTTCAACTAGCTTTGTTGATGACCCCTATTT  
 TAGCTAGCAAAAGTAAATGGCAAAATATTACAAGTCAATCTGATGGCAAA  
 TTAGTCATTCTTGAATATGCTTTGTGAGCTAATCAATTTGATGACACTAG  
 TCTTAAAAATTTATCGTAATAATAATCGCAATAAAGAAATTAATATCACAA  
 CAGATTATTTTGCAGATACAAAATATGTCAATATCACAGCGGTGACTAT  
 TTGAGCAATACTACTTTTGAAGCAATTAGCTACTGGTGAaaCAGTAGATTA  
 CCATGCCATTGTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTA  
 AGATTTATGTCAACGATAAATTGCAAGAACTTCTCGTATAGCGCTTAAAG  
 GATAAATCTGTTAAGATTGGTATTGAATTACCAATGATGTGAGACATAT  
 TGATAGTTTATCTGTTCTGTTGAATGAGGTTAAACTGTTGATAATA  
 TCTTGAAAAATGATGAACAAGACATTAACTCTCAGCAAACTTACCAATTA  
 AAATACAACCCGACAAATCGTCTAGAGTTTACTATTAAATAACATTAA  
 CTAAGTTTCAGAAATCATGACCACTTCAAAGATGGAAAGATGCCGAAT  
 TGGTTGAACAAAAGATGTTCTTTGGATATAAACGATATGGACATGAGT  
 AAGTTTAAACTATTGCACTTGGACGAAAGGATTCTGAATTTAAGGGACA  
 ACTTATTGCAAAAACCTGGAACAGTTGAATTAGATATGTTTTCAAACAAT  
 CTCAAGACCCAGCTTCAATTATTTAAAAAATATACCTTATCCAAAATGGT  
 GTTCCAAATGAATTGAAAAAATTGACTCTAGTTTGGTTTAACTGAAAG  
 TCAGATAGATGGATCTATATTTATAAAGATGCAATTAACTTAAATTTA  
 AATTAACAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGAT

Table 51: Comparative Sequences relating to SAG0677

CCATATAGTCATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAG  
TCATTCAACTCAAGCCAATGAAATACAGCAAAAGTAACCTTTGCTAATA  
TTGACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAAAGAAGTTGGT  
AAAGGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACA  
TAAACAGAAAAATTCATTAAATGTTAAAGTTTGATTATGGAGACGGGTA  
GTGTAAGTAAGAAAGTTCAACAACCTCCCTTAAAGTCTTAGATTATCTAAA  
AATAAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTA  
TTACGAAACAAGTGACAGTCTAGTCTTCCGAATTAATCTCACTGCAGATA  
CTAAACTTAATTTTAATGCTGTTAAAGGAGCGAGTGTCTTACTGAAAAAT  
ATGATGATGAGACAGTTTGCAAGTTGCTGGACCACAAGATGATCCTGTTAG  
TGAACATAAATACCCATCAGTATTTCTCTTAACCTCCTGCCTTATTGGAAA  
CTGCTAGTGAGGCACTCTAAATGGTAAGGAAATCACAGCATCTGGTATT  
ATCGGTCACATCAAGGATGGTGATAAAGCAAGCATGTTGAAGTCAAAAT  
GGTGAATGAAATGGAGACATGCTAGGAACCCCTGTTATTATCAAGGTA  
AAGACTTGACTAATCGAACAAAACCATTAATGAGTGGACGTAGAGTACTT  
TATGCCGGTAAACAATATGAGTTCGGGGCTAAATTACCACCTAGTCGTTT  
TAAcAaCTTGGATTAGGGTTGAAGTGGTAACAGAGCAGGAGAGAAAGCAA  
GTATTGTTTCGTCGCGATGTTCTTTGACCAATCAGTTCAGAGCTTAACACA  
GCAGTTGCTAAACGTTGATTGACTTCTGATAGTCTCTTATCCACATCGT  
TGCCAAAGATGACTCTCTAAAACTAAAAATTATATCAAGATGATTCAATAC  
TTGAATCTGTGATAAAACCGGCTTTTATAGTTTGAAGATGGGTAGAA  
ATCACTAAAGATATGACAGTACCCTAGAAATTTGGAGATAATATTACTAA  
GTTATCTGCTGTTGACTTATCAAATTTATCGTCGTAATGAGACCCCTTCATA  
TCTATAGAAACCGTTTGTATGTTAAAGCAAGCCAAATGACAGCTGACAAA  
GGAGCTAAAGTAAGTCTGAGGATATGTTGATGAAGCACTAGTTGTTCCAGA  
AATGGCAGGAGCTTATACATTAACTCGACGAAGCTCCAAACACAAATG  
AATCAGGAATGTTAACAACCGCTAAAGTATCGATTCAATTATGTAATGGT  
GGTGTGATAAAGTtGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTAT  
TCGTTAAAGCTGAAGAAGCACATAAAGCTGACGAAGCAGTAAAGCTGAAG  
AAGCAGTAAAGCTGACGAAGCACATAAAGCTGAAGAAGTACGTAAGCT  
GAAGAAGCACATAAAGCTGAAGAAGCAGTAAAGCTGAAGAAGGACATAA  
AACCCAAGAAGCACCTATAGTTGAAGAAGGCTACAAGTTAATAACGTTT  
ATCAAACTGATACTACAGTTAAAGCGTCTGATTACCAAGACTAAGACA  
GTTTCCGAGTTTATATGGCTAGAACAGACAATAAACAGATAAATTCACA  
TCAGACACATG

SEQ ID NO. 5104

STRAIN 18RS21

TTGAATAATAAGGTGTGCGTGGCGATGGTGTCCAA  
ATTTATCAATACTATATCAAAATGGACAACAATAAACCTTACTTAAGTCC  
CAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAAAATTA  
CTTTCAAAGTTTCAAGATACTGGCATTGGTTTGAAGACGTTTATCTTCAA  
TCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTATCACACC  
TCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAACCAAATTAGACC  
GTCCACCAGGAATTGATTACCAGCACCACTCAATGAGAAGTTTGTAT  
TATTCACCCCAACCGGAACTAAGCCAGCAACCCAAAGATAGTTTATC  
AACTCCTCCAGGTTTCCAGATTAAACACGCGCGCGGATGAAGCACCAA  
AGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGCAATTAATAT  
GCTAAGTCTCTCAACTTAGCTTTGTTGATGACCCATTTTAGCTAGCAA  
AGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAAATTAGTCATTC  
CTAGAAATGCTTTGTCAGCTAATCAATTTGATGACACTAGTCTTAAATTT  
TATCGTAATAATAATCGCAATAAAGAAATTACTATCACACAGATTATTT  
TGAGATACAAAATATGTCATATACAGCGTTGACTATTTGAGCAATA  
CTACTTTTGAAGCAATTAGCTACTGGTGAACAGTAGATTACCATGCCATT  
GTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGATTTATGT  
TAACGATAAATTGCAAGAACTTCTCGTATAGCGCTTAAAGATAAATCTG  
TTAAGATTGGTATTGAATTAACCAATGATGTCAGACATATTGATAGTTTA  
TCTGTTCTGTCGTTTGAATGAGGTTAAACTGTGATAATATCTTGAAAAA  
TGATGAACAAGCATTAAATCTCAGCAAaACTTACCAATTAATAACAACC  
CGACAATCGTCGTCTAGAGTTTACTATTAATAACATTAACTCAAGTTCA  
GAAATCATGACCACTTTCAAAGATGGAAGATGCCAGAAATGGTTGAACA  
AAAAGATGTTCTTTGGATATaAACGATATGGACATGAGTAAGTTTAAAA  
CTATTGCACTTGACGAAAGGATTCTGAATTTAAGGGACAACCTTATTGCA  
AAAACCTGGAACAGTTGAATTAGATATGTTTTCAACAATCTCAAGACCC  
AGCTTCAATTTATAAAAAAATATACCTTATCCAAATGGTGTTCCAAATG  
AATTGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGTCAGATAGAT  
GGATACTATATTATAAAGATGCAATTAACCTTAATTTAAATTAACAGG  
TGGTCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCATATAGTC  
ATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAGTCATTCAACT  
CAAGCCAATGAAATACAGCAAAAGTAACCTTTGCTAATATTGACTGGTC  
ACATTATAGTAAGGTTACTGTGAATGGAAGAAGTTGTTAAAGGTAGTG  
AGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACATAAAACAGAA  
AATTCAATTAATGTTAAAGTTTGTATTATGGAGACGGGTAGTGAAGTAA  
GAAAGTTCAACAACCTCCTTTAAGTCTTAGATTATCTAAAAATTAAGCATA  
TGAGGGATATGCTACTTACTATGCAAAAAGATTGACGCTATTACGAAACA  
AGTGACAGTCTAGTCTTTCGAATTAATCTCACTGCAGATACTAACTTAA  
TTTTAATGCTGTTAAAGGAGCGAGTGTCTTACTGAAAAATATGATGATGA  
GACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGTTAGTGAACATAAA  
TACCCATCAGTATTTCTTAACTCCTGCCTTATTGGAACCTGCTAGTGA  
GGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATCGGTCA  
TCAAGGATGGTGATAAAGCAAGCATGTTGAAGTCAAAATGGTGAATGAA  
AATGGAGACATGCTAGGAACCCCTGTTATTATCAAGGTAAAGACTTGAC  
TAATCGAACAAAACCATTAATGAGTGGACGTAGAGTACTTTATGCCGGTA



Table 51: Comparative Sequences relating to SAG0677

AACAATATGAGTTCCGGGCTAAATTACCACTTAGTCGTTTAACTTGG  
 ATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAGTATTGTTCC  
 TCGCATGTTCTTTGACCAATCAGTTCCAGAGCTTAACACAGCAGTTGCTA  
 AACGTGATTTGACTTCIGATACTGCTCTTATCCACATCGTTGCCAAAGAT  
 GACTCTCTAAAACCTAAAATTATATCAAGATGATTCAATACCTGAATCTGT  
 TGATAAAACCGGTCCTTATAGTTTGAAGATGGTGTAGAAATCACTAAAG  
 ATATGACAGTACCCTAGAAATTGGAGATAATATATTAAGTTATCTGCT  
 GTTGACTTATCAAATTATCGTCGTAATGAGACCCCTTCATATCTATAGAAA  
 CCGTTTGTGATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGAGCTAAAG  
 TAACTGTGGaTATGTTGATGAAGCACTTAGTTGTTCCAGAAATGGCAGGA  
 GCTTATACATTAACAATCGACGAAGCTCCAAACACAAATGAATCAGGAAT  
 GTTAACAAACCGCTAAAGTATCGATTCAATTATGTAATGGTGGTGTGATA  
 AAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTTCGTAAGCT  
 GAAGAAGCACGTAAGCTGAAGAAGCACGTAAGCTGAAGAGGGACATAA  
 AACCCAAAGACCTATAGTTGAAGAAGGCTACAAGGTTAATAACGTTT  
 ATCAAACCTGATACATGATTAAAGCGTCTGATTACCAAAGACTAAGACA  
 GTTTCCGAGTTTATATGGCTAGAACAGACAATAACAGATAACTTCACA  
 TCAGACACATGTTGAA

SEQ ID NO. 5105

STRAIN M732

TTGAATAATAAAGGTGTCGGTGGCGATGGTGTCC

AAATTTATCAATACTATATCAAAATGGACAACAATAAACCTTACTTAAGT  
 CCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAAAAT  
 TACCTTCAAAGTTCAGGATACTGGCATTGGTTTGAAGACGTTTATCTTC  
 AATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTATCACA  
 CCTCCAGGATTTAAAAAGAAAGATAAAAAAGTTGAAAAACCAAAATTAGA  
 CCGTCCaCAGGAATTGATTTACCAGCACCAACTCAATGAGAAGTTTGTG  
 ATTATTCAACCCACCGGGAACCTAAGCCAAAGCAACCCAAAGATAGTTTA  
 TCAACTCTCCAGGTTTCCAGATTTAACACAGCCGCGGATGAAGCCAC  
 CAAAGGATAGTAAAAAGACGCTATTGAAGATAAATCAGGAGCAATTAAA  
 TATGCTAAGTCTCTCAACTTAGCTTTGTTGATGACCCATTTTAGCTAG  
 CAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAAATTAGTCA  
 TTCTTAGAAATGCTTTGTGAGCTAATCAATTTGATGACACTAGTCTTAAA  
 ATTTATCGTAATAATAATCGCAATAAAGAAATTACTATCACACAGATTA  
 TTTTGCAGATACAAAATATGTCAATATCACAGCGGTTGACTATTTGAGCA  
 ATACTACTTTTGGAGCAATAGCTACTGGTGAACAGTAGATTACCATGCC  
 ATTGTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGATTTA  
 TGTTAACGATAAAATGCAAGAACTTCTCGTATAGCGCTTAAAGATAAAT  
 CTGTTAAGATTGGTATTGAATTACCAATGATGTCAGACATATTGATAGT  
 TTATCTGTTCTCGTTTGAATGAGGTTAAACTGTTGATAATATCTTGAA  
 AAATGATGAACAAGACATTAATCTCAGCAAACTTACCAATTAATAATACA  
 ACCGACAAATCGTCTGCTAGAGTTTACTATTAATAACATTAACTCAAGT  
 TCAGAAATCATGACCACTTTCAAAGATGGAAGATGCCAGAAATGGTTGA  
 ACAAAGATAGTTTCTTTGGATATAAAGATATGGACATGAGTAAGTTTA  
 AAACCTATTGCACTTGGACGAAAGGATTCTGAATTTAAGGACAACTTATT  
 GCAAAACTGGAAACAGTTGAATTAGATATGTTTTCAAACAACTCAAGA  
 CCCAGCTTCAATTTAATAAAAAATATACCTTATCCAAATGGTGTTCCTAA  
 ATGAATGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGTCAGATA  
 GATGATACTATATTTATAAAGATGCAATTAACTTAAaTTTAAATTAAC  
 CAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCATATA  
 GTCATCAGAAAGAAATATGACTAAAAAAGGTGAACAGCTCAGTCATTCA  
 ACTCAAGCCAATGAAAATACAGCAAAAGTAACCTTTGCTAATATTGACTG  
 GTCACATTATAGTAAGGTTACTGTGAATGGAAGAAAGTTGGTAAAGGTA  
 GTGAGTTACCTTTAACTAAGGATGGACAACTTTGTATTACATAAAACA  
 GAAAATTCAATTAATGTTAAAGTTTGAATTATGGAGACGGTAGTGTAAAG  
 TAAGAAAGTTCAACAACTTCTTTAAGTCTTAGATTATCTAAAAATAAGC  
 ATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTATTACGAA  
 ACAAGTGACAGTCTAGTCTTCGAATTAATCTCACTGCAGATACTAACT  
 TAATTTAATGCTGTTAAAGGAGCGAGTCTCTTACTGAAAATATGATGA  
 TGAGACAGTTTGCAAGTTGCTGGACCAAGATGATCCTGTTaGTGAACAT  
 AAATACCCATCAGTaTTCTCTTAACTCCTGCCCTATTGGAAaCTGCTAG  
 TGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATCGGTC  
 ACATCAAGGATGGTGATAAAGCAAGCATGTGAAGTCAAAATGGTGAAT  
 GAAAATGGAGACATGCTAGAACCCCTGTTATTATTCAAGGTAAGACTT  
 GACTAATCGAACAAAACCAATTAAAGAGTGGACGTAGAGTACTTTATGCCG  
 GTAAACAAATATGAGTTCCGGGCTAAATTACCACCTAGTCTGTTTAACT  
 TGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAGTATTGT  
 TCGTGCATGTTCTTTGACCAATCAGTCCAGAGCTTAACACAGCAGTTG  
 CTAAACGTGATTTGACTTCTGATACTGCTCTTATCCACATCGTTGCCAAA  
 GATGACTCTCTAAAACCTAAAATTATATCAAGATGATTCAATCTTGAATC  
 TGTGTATAAAACCGGTCCTTATAGTTTGAAGATGGTGTAGAAATCACTA  
 AAGATATGACAGTACCCTAGAAATTGGAGATAATATTTAAGTTATCT  
 GCTGTTGACTTATCAAATTATCGTCGTAATGAGACCCCTTCATATCTATAG  
 AAACCGTTTGTGATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGAGCTA  
 AAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAATGGCA  
 GGAGCTTATACATTAACAATCGACGAAGCTCCAAACACAAATGAATCAGG  
 AATGTTAACAAACGCTAAAGTATCGATTCAATTATGTAATGGTGGTGTG  
 ATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTTCGTAA  
 GCTGAAGAGACATAAAGCTGACGAAGCACGTAAGCTGAAGAAGCACG  
 TAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAGCTGAAGAAG  
 CACATAAAGTGAAGAAGCACGTAAGCTGAAGAAGGACATAAACCACAA  
 GAAGCACCTATAGTTGAAGAAGGCTACAAAGTTAATAACGTTTATCAAC

Table 51: Comparative Sequences relating to SAG0677

TGATACTACAGTTAAAGCGTCTGATTACCAAAGACTAAGACAGTTTCCG  
CAGTTTCATATGGCTAGAACAGACAATAAACAGATAACTTCACATCAGACA  
CATGTTGAAAA

SEQ ID NO. 5106

STRAIN COH1

TTGAATAATAAAGGTGTCCGGTGGCGATGGT  
GTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAACCTTACTT  
AAGTCCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAA  
AAATTACTTTCAAAGTTCAGGATACTGGCATTGGTTTGAAAGACGTTTAT  
CTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTAT  
CACACCTCCAGGATTAAAAAAGAAGATAAAAAAGTTGAAAAACCAAAAT  
TAGACCGTCCACCAGGAATTGATTTACCAGCACCAACTTCAATGAGAAGT  
TTTGATTATTCAACCCACCGGGAAGTAAGCCAAGCAACCCAAAGATAG  
TTTATCAACTCCTCCAGGTTCCAGATTAAACACGCCGCCGGATGAAG  
CCaCCAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGCAAT  
TAAATATGCTAAGTCTTCAACTTAGCTTGTGTGATGACCTATTATTAG  
CTAGCAAGATAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAAATTA  
GTCAATCTAGAAATGCTTGTGAGCTAATCAATTTGATGACACTAGTCT  
TAAATTTTATCGTAATAATAATCGCAATAAAGAAATTACTATCACAACAG  
ATTATTTTGCAGATACAAATATGTCAATATCAGACGGTTGACTATTGT  
AGCAATACTACTTTTGAGCAATTAGCTACTGGTGAAACAGTAGATTACCA  
TGCCATTGTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGA  
TTTATGTTAAGCATAAATGCAAGAACTTCTCGTATAGCGCTTAAAGAT  
AAATCTGTTAAGATTGCTATTGAATTACCAATGATGTCAGACATATTGA  
TAGTTTATCTGTTTCGTCGTTTGAATGAGGTTAAACTGTTGATAATATCT  
TGAAAAATGATGAACAAGACATTAACTCTAGCAAACTTACCAATTAAAA  
TACAACCCGACAAATCGTCTGCTAGAGTTTACTATTAATAACATTAACTC  
AAGTTTCAAGAAATCATGACCACTTTCAAAGATGGAAGATGCCAGAATTGG  
TTGAACAAAAAGATGTTCTTTGGATATAAACGATATGGACATGAGTAAG  
TTTAAACTATTTCGACTTGGACGAAAGGATTCTGAATTTAAGGGCACACT  
TATTTGCAAAAACCTGGAACAGTTGAATTAGATATGTTTTCAAACAACTCTC  
AAGACCCAGCTTCAATTATTAATAAATATACCTTATCCAAATGGTGT  
CCAAATGAATTGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGTCA  
GATAGATGGATACTATATTATAAAGATGCAATTAACTTAAATTTAAAT  
TAACCAAGTGGTCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCA  
TATAGTATCATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAGTCA  
TTCAACTCAAGCCAATGAAATACAGCAAAAGTAACCTTTGCTTAATATTG  
ACTGGTCACTTATAGTAAGGTTACTGTGAATGGAAGAAGTTGGTAAA  
GGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACATAA  
AACAGAAAAATTCATTAAATGTTAAAGTTTGATTATGGAGACGGGTAGTG  
TAAGTAAGAAAGTTCAACAACTTCTTTAAGTCTTGAATTATCTAAAAAT  
AAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTATTA  
CGAAACAAGTGACAGTCTAGTCTTCAATTAATCTCACTGCAGATACTA  
AACTTAATTTAATGCTGTTAAAGGAGCGAGTGTCTTACTGAAAAATATG  
ATGATGAGACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGTTAGTGA  
ACATAAATACCCATCAGTATTTCTTAACTCCTGCCTTATTGGAAGTCT  
CTAGTGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATC  
GGTCACATCAAGGATGGTGATAAAGCAAGCATGTTGAAGTCAAAATGGT  
GAATGAAAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAAAG  
ACTTGACTAATCGAACAAAACCAATTAATGAGTGGACGTAGAGTACTTTAT  
GCCGGTAAACAAATATGAGTTCCGGGCTAAATTACCCTTAGTCTGTTTAA  
CACTTGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAGTA  
TTGTTCTGTCGATGTTCTTTGACCAATCAGTTCCAGAGCTTAAACAGCA  
GTTGCTAAACGTGATTGACTTCTGATATGCTCTTATCCACATCGTTGTC  
CAAGATGACTCTCTAAACCTAAATTTATATCAAGATGATTCAATTACTTG  
AATCTGTTGATAAAACCGGTCTTTATAGTTTGAAGATGGTGTAGAAATC  
ACTAAAGATATGACAGTACCCTAGAAATTTGGAGATAATAATTATTAAAGTT  
ATCTGCTGTTGACTTATCAAATTATCGTCTGAATGAGACCTTCATATCT  
ATAGAAACCGTTTGTATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGA  
GCTAAAGTAACGTGGATATGTTGATGAAGCACTAGTTGTTCCAGAAAT  
GGCAGGAGCTTATACATTAACTCGACGAAGCTCCAAACACAAATGAAT  
CAGGAATGTTAAACAAACGCTAAAGTATCGATTCTATTATGTAATGGTGGT  
GTTGATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTTCG  
TAAAGCTGAAGAAGCACATAAAGCTGACGAAGCAGTAAAGCTGAAGAAG  
CAGTAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAAGCTGAA  
GAAGCACATAAAGCTGAAGAAGCAGTAAAGCTGAAGAAGGACATAAAAC  
CCAAGAAGCACCTATAGTTGAAGAAGGCTACAAAGTTAATAAGGTTTATC  
AACTGATACTACAGTTTAAAGCGTCTGATTACCAAGACTAAGACAGTT  
TCCGCGATTCTATGCTAGAACAGACAATAAACAGATAACTTCACATCA  
GACACATGT

SEQ ID NO. 5107

STRAIN M781

TTGAATAATAAAGGTGTCCGGTGGCGATGGT  
GTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAACCTTACTT  
AAGTCCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAA  
AAATTACTTTCAAAGTTCAGGATACTGGCATTGGTTTGAAAGACGTTTAT  
CTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTAT  
CACACCTCCAGGATTAAAAAAGAAGATAAAAAAGTTGAAAAACCAAAAT  
TAGACCGTCCACCAGGAATTGATTTACCAGCACCAACTTCAATGAGAAGT  
TTTGATTATTCAACCCACCGGGAAGTAAGCCAAGCAACCCAAAGATAG  
TTTATCAACTCCTCCAGGTTTCCAGATTAAACACGCCGCCGGATGAAG

Table 51: Comparative Sequences relating to SAG0677

CCaCCAAAGGATAGTAAAAAGACGCTATTGAAGATAAATCAGGAGCAAT  
TAAATATGCTAAGTCTCTTCAACTAGCTTTGTTGATGACCCATATTTAG  
CTAGCAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAAATTA  
GTCAATTCCTAGAAATGCTTTGTGACGTAATCAATTTGATGACACTAGTCT  
TAAaATTATCGTAATAATAATCGCAATAAAGAAATTaCTATCACAACAG  
ATTATTTTGCAGATACAAAATATGTCAATATCACAGCGGTTGACTATTG  
AGCAATTAATACTTTTGTAGCAATTAGCTACTGGTGAAACAGTAGATTACCA  
TGCCATTTGATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGA  
TTTATGTTAAGATAAATTCGAAGAACTTCTCGTATAGCGCTTAAAGAT  
AAATCTGTTAAGATTGGTATTGAATTACCAATGATGTCAGACATATTGA  
TAGTTTATCTGTTCTGTTGAAATGAGGTTAAACTGTTGATAATATCT  
TGAAAAATGATGAACAAGACATTAATCTCAGCAAACTTACCAATTAAAA  
TACAACCCGACAAATCGTCTGCTAGAGTTTACTATTAAATACATTAACTC  
AAGTTCAGAAATCATGACCCTTTCAAAGATGGAAGATGCCAGAAATGG  
TTGAACAAAAAGATGTTTCTTTGGATATAACGATATGACATGAGTAAG  
TTTAAAACTATTGCACTTGGACGAAAGGATTCTGAATTAAGGGCAAACT  
TATTGCAAAACTGGAACAGTTGAATTAGATATGTTTTCAAACCAATCTC  
AAGACCCAGCTTCAATTATTAAAAAATATACCTTATCCAAATGGTGT  
CCAAATGAATTAAGAAATTTGACTCTAGTTTGGTTTAACTGAAAGTCA  
GATAGATGGATACATATAATTATAAAGATGCAATTAACCTTAAATTTAAAT  
TAACCAAGTGGTCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCA  
TATAGTCATCAGAAAGAAGATATGACTAAAAAGGTGAACAGCTCAGTCA  
TTCAACTCAAGCCCAATGAAAATACAGCAAAAGTAACCTTTGCTAATATTG  
ACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAGAAGTGGTAAAG  
GGTAGTGAGTTACCTTAACTAAAGGATGGACAACATTGTTATTACATAA  
AACAGAAATTCATTAAATGTTAAAGTTGATTTATGAGAGCGGGTAGTG  
TAAGTAAGAAAGTTCAACCACTTCTTAAAGTCTTAGATTATCTAAAAAT  
AAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTATTA  
CGAAACAGTGACAGTCTAGTCTTGAATTAATCTCAGTCAGATACTA  
AACTTAAATTTAATGCTGTTAAAGGAGCGAGTGTCTTACTGAAAATATG  
ATGATGAGACAGTTGCAAGTGTCTGGACCAAGATGATCCTGTTAGTGA  
ACATAAATACCCATCAGTATTTCTTAACTCCTGCTTATTGGAACCTG  
CTAGTGAGGCAACTCTAATGTTAAGGAAATCACAGCATCTGGTATTATC  
GGTCACATCAAGGATGGTGATAAAGCAAGCATGTTGAAGTCAAAATGGT  
GAATGAAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAAAG  
ACTTGACTAATCGAACAAACCAATTAATGAGTGGACGTAGAGTACTTTAT  
GCCGGTAAACCAATATGAGTTCCGGGCTAAATTACCACTTAGTCGTTTAA  
CACTTGGATTAGGGTTGAAGTGGTAAACAGAGCAGGAGAGAAAGCAAGTA  
TTGTTCTGTCGATGTTCTTTGACCAATCAGTTCAGAGCTTAAACAGCA  
GTTGCTAAACGTTGATTTGACTTCTGATACTGCTCTTATCCACATCGTTG  
CAAAGATGACTCTCTAAACTAAAATTTATATCAAGATGATTCACTACTTG  
AATCTGTTGATAAAACCGGTCTTTATAGTTTGAAGTGGTGTAGAAATC  
ACTAAAGATATGACAGTACCCTAGAAATTTGGAGATAATATTATTAGTT  
ATCTGCTGTTGACTTATCAAAATATCGTCTGAATGAGACCCCTCATATCT  
ATAGAAAACCGTTTGTATGTTAAAGCAAGCAAAATGACAGCTGACAAAGGA  
GCTTAAAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAAT  
GGCAGGAGCTTATACATTAAACCAATCGACGAAGCTCCAAACCAAAATGAAT  
CAGGAATGTTTAAACAAAGCTAAGTATCGATTCAATTATGTAATGGTGGT  
GTTGATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTCG  
TAAAGCTGAAGAAGCACATAAAGCTGACGAAGCAGTAAAGCTGAAGAAG  
CAGCTAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAAGCTGAA  
GAAGCACATAAAGCTGAAGAAGCACCGTAAAGCTGAAGAGGGACATAAAA  
CCCAAGAGCACCTATAGTTGAAGAAGGCTACAAAGTTAATAACGTTTAT  
CAAACTGATACATAGTTAAAGCGTCTGATTACCAAGACTAAGACAGT  
TTCCGCAAGTTATATGGCTAGAACAGACAATAAACAGATAAATTCATC  
AGACACATGTTG

SEQ ID NO. 5109

STRAIN JM9130013

TGGTGTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAAC  
CTTACTTAAAGTCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGC  
TGGAAAAAATTTACTTTCAAAGTTTCAAGATCTGGCATTGGTTTGAAGA  
CGTTTATCTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTAG  
ACCTTATCACACCTCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAA  
CCAAAAATTAGACCGTCCACCAGGAATTGATTACCAGCACCAACTTCAAT  
GAGAAGTTTGTATTATCAACCCACCGGGAATTAAGCCAAGCAACCCA  
AAGTAGTTTATCAACTCTTCCAGGTTTCCAGATTAAACACGCGCGCG  
GATGAAGCACCAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGG  
AGCAATTAATATGCTAAGTCTCTTCAACTAGCTTTGTTGATGACCCCTA  
TTTTAGCTAGCAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGC  
AAATTAGTCATTCTTAGAAATGCTTTGTGAGCTAATCAATTTGATGACAC  
TAGTCTTAAATTTATCGTAATAATAATCGCAATTAAGAAATTAATATCA  
CAACAGATTATTGTCAGATACAAAATATGTCAATATCACAGCGGTTGAC  
TATTTGAGCAaTACTACTTTTGTAGCAATTAGCTACTGGTGAAACAGTAGA  
TTACCATGCCATTGTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTG  
GTAAGATTATGTTAAGGATAAATTGCAAGAACTTCTCGTATAGCGCTT  
AAAGATAAATCTGTTAAGATTGGTATTGAATTACCAATGATGTCAGACA  
TATTGATAGTTTATCTGTTGCTGTTGAATGAGGTTAAACTGTTGATA  
ATATCTTGAATAATGATGAACAAGACATTAACTCAGCAAACTTACCAA  
TTAAATACAAACCCGACAAATCGTCTGCTAGAGTTTACTATTAAATACAT  
TAATCTAAGTTTCAAAATCATGACCACTTCAAAGATGGAAGATGCCAG  
AATTGGTTGAACAAAAAGATGTTTCTTTGGATATAAACGATATGGACATG  
AGTAAGTTTAAACTATTGCACTTGGACGAAGGATTCTGAATTTAAGGG

Table 51: Comparative Sequences relating to SAG0677

ACAACCTTATTGCAAAACTGGAACAGTTGAATTAGATATGTTTTTCAAAC  
 AATCTCAAGACCCAGCTTCAATTATTAATAAATATACCTTATCCAAAT  
 GGTGTTCCAAATGAATTGAAAAAATTTGACTCTAGTTTGGTTAACTGA  
 AAGTCAGATAGATGGATACATATTTATAAAGATGCAATTAACTTAAAT  
 TTAAATTAAACAGTGGTGCAGTCTTAAAGTTGTTTATAAGGGCAAGAA  
 GATCCATATAGTCATCAGAAAGAGATATGACTAAAAAGGTGAACAGCT  
 CAGTCATTCAACTCAAGCCATGAAAAATACAGCAAAAGTAACCTTTGCTA  
 ATATTGACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAAAGAGTT  
 GGTAAAGGTAGTGAGTTACCTTTAACTAAAGGATGGCAACATTGTATT  
 ACATAAAACAGAAAAATTCATTAAATGTTAAAGTTTGATTATGGAGACGG  
 GTAGTGAAGTAAGAAAGTTCAACAACTTCCCTTAAAGTCCAGATTATCT  
 AAAAAATAAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAG  
 GTATTACGAAACAAGTGACAGTCTAGTCCTTCGAATTAACTCTACTGCAG  
 ATACTAAACTTAATTTTAATGCTGTTAAAGGAGCGAGTCTCTTACTGAA  
 AATATGATGATGAGACAGTTTGCAAGTTGCTGGACCAAGATGATCCTGT  
 TAGTGAACATAAATCCCATCAGTATTTCTCTTAACTCCTGCCTTATTGG  
 AAACCTGCTAGTGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGT  
 ATTATCGGTACATCAAGGATGGTGATAAAAGCAAGCATGTTGAAGTCAA  
 AATGGTGAATGAAATGGAGACATGCTAGGAACCCCTGTTTATTATCAAG  
 GTAAGACTTGACTAATCGAACAACCATTAATGAGTGGAGCTAGAGTA  
 CTTTATGCCGGTAAACAATATGAGTTCCGGGCTAAATTACCCTTAGTCG  
 TTTTAACTTTGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGaGaaag  
 cAaGTATTGTTCTGCGCATGTTCTTTGACCAATCAGTTCAGAGCTTAAC  
 ACAGCAGTTGCTAAACGTGATTGACTTCTGATAGTCTCTTATCCACAT  
 CGTTGCCAAGATGACTCTCTAAACTAAAATTATATCAAGATGATTCTAT  
 TACTTGAATCTGTGATAAAACCGGCTTTTATAGTTTGAAGATGGTGA  
 GAAATCACTAAAGATATGACAGTACCACTAGAAATTTGGAGATAATATTAT  
 TAAGTTATCTGCTGTTGACTTATCAAATTATCGTCGTAATGAGACCCCTC  
 ATATCTATAGAAACCGTTTGTATGTTAAAGCAAGCCAAATGACAGCTGAC  
 AAAGGAGCTAAAGTAACGTGTGATATGTTGATGAAGCACTTAGTTGTTCC  
 AGAAATGGCAGGAGCTTATACATTAAACAATCGACGAAGCTCCAAACACAA  
 ATGAATCAGGAATGTTAAACAACGCTAAAGTATCGATTCAATTATGTAAT  
 GGTGGTGTGATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGC  
 TATTTCGTAAAGCTGAAGAAGCACATAAAGCTGACGAAGCAGTAAAGCTG  
 AAGAAGCACGTAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAA  
 GCTGAAGAAGCACATAAAGCTGAAGAAGCACCGTAAAGCTGAAGAGGGAC  
 ATAAAACCCGAAGCACCTATAGTTGAAGAAGCTACAAGTTAATAAC  
 GTTCATCAAACTGATACACTACAGTTAAAGCGTCTGATTACCAAAGACTAA  
 GACAGTTTCGCGAGTTCATATGGCTAGAACAGACAATAAACAGATAAAT  
 CATATCAGACACATGTTG

## MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa235280.2{\*} December 10, 2002 05:12 ..

	1		50
msa235280.2{195_COH1}	ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA		
msa235280.2{195_M732}	ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA		
msa235280.2{195_M781}	ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA		
msa235280.2{195_H36B}	-----TGGT GTCCAAATTT ATCAATACTA		
msa235280.2{195_JM9130013}	-----TGGT GTCCAAATTT ATCAATACTA		
msa235280.2{195_18RS21}	ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA		
msa235280.2{195_2603}	ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA		
msa235280.2{195_A909}	ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA		
Consensus	-----*****		
	51		100
msa235280.2{195_COH1}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA		
msa235280.2{195_M732}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA		
msa235280.2{195_M781}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA		
msa235280.2{195_H36B}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA		
msa235280.2{195_JM9130013}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA		
msa235280.2{195_18RS21}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA		
msa235280.2{195_2603}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA		
msa235280.2{195_A909}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA		
Consensus	*****		
	101		150
msa235280.2{195_COH1}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG		
msa235280.2{195_M732}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG		
msa235280.2{195_M781}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG		
msa235280.2{195_H36B}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG		
msa235280.2{195_JM9130013}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG		
msa235280.2{195_18RS21}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG		
msa235280.2{195_2603}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG		
msa235280.2{195_A909}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG		
Consensus	*****		
	151		200
msa235280.2{195_COH1}	GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT		
msa235280.2{195_M732}	GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT		
msa235280.2{195_M781}	GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT		
msa235280.2{195_H36B}	GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT		

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_JM9130013}	GATACTGGCA	TTGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
msa235280.2{195_18RS21}	GATACTGGCA	TTGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
msa235280.2{195_2603}	GATACTGGCA	TTGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
msa235280.2{195_A909}	GATACTGGCA	TTGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
Consensus	*****	*****	*****	*****	*****
201					
msa235280.2{195_COH1}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_M732}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_M781}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_H36B}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_JM9130013}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_18RS21}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_2603}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_A909}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
Consensus	*****	*****	*****	*****	*****
250					
251					
msa235280.2{195_COH1}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_M732}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_M781}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_H36B}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_JM9130013}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_18RS21}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_2603}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_A909}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
Consensus	*****	*****	*****	*****	*****
300					
301					
msa235280.2{195_COH1}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCCAACC
msa235280.2{195_M732}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCCAACC
msa235280.2{195_M781}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCCAACC
msa235280.2{195_H36B}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCCAACC
msa235280.2{195_JM9130013}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCCAACC
msa235280.2{195_18RS21}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCCAACC
msa235280.2{195_2603}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCCAACC
msa235280.2{195_A909}	GATTTACCAg	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCCAACC
Consensus	*****	*****	*****	*****	*****
350					
351					
msa235280.2{195_COH1}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_M732}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_M781}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_H36B}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_JM9130013}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_18RS21}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_2603}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_A909}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
Consensus	*****	*****	*****	*****	*****
400					
401					
msa235280.2{195_COH1}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	cCACcAAAGG	ATAGTAAAAA
msa235280.2{195_M732}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	cCACcAAAGG	ATAGTAAAAA
msa235280.2{195_M781}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	cCACcAAAGG	ATAGTAAAAA
msa235280.2{195_H36B}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	.CACTAAAGG	ATAGTAAAAA
msa235280.2{195_JM9130013}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	.CACcAAAGG	ATAGTAAAAA
msa235280.2{195_18RS21}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	.CACcAAAGG	ATAGTAAAAA
msa235280.2{195_2603}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	.CACcAAAGG	ATAGTAAAAA
msa235280.2{195_A909}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	.CACTAAAGG	ATAGTAAAAA
Consensus	*****	*****	*****	*****	*****
450					
451					
msa235280.2{195_COH1}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_M732}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_M781}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_H36B}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_JM9130013}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_18RS21}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_2603}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_A909}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
Consensus	*****	*****	*****	*****	*****
500					
501					
msa235280.2{195_COH1}	AACCTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_M732}	AACCTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_M781}	AACCTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_H36B}	AACCTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_JM9130013}	AACCTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_18RS21}	AACCTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_2603}	AACCTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_A909}	AACCTAGCCT	TGTTGATGac	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
Consensus	*****	*****	*****	*****	*****
550					

Table 51: Comparative Sequences relating to SAG0677

		551			600
msa235280.2{195_COH1}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_M732}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_M781}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_H36B}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_JM9130013}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_18RS21}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_2603}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_A909}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
Consensus	*****	*****	*****	*****	*****
		601			650
msa235280.2{195_COH1}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_M732}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_M781}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_H36B}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_JM9130013}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_18RS21}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_2603}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_A909}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
Consensus	*****	*****	*****	*****	*****
		651			700
msa235280.2{195_COH1}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_M732}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_M781}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_H36B}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_JM9130013}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_18RS21}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_2603}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_A909}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
Consensus	*****	*****	*****	*****	*****
		701			750
msa235280.2{195_COH1}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_M732}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_M781}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_H36B}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_JM9130013}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_18RS21}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_2603}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_A909}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
Consensus	*****	*****	*****	*****	*****
		751			800
msa235280.2{195_COH1}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_M732}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_M781}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_H36B}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_JM9130013}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_18RS21}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_2603}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_A909}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
Consensus	*****	*****	*****	*****	*****
		801			850
msa235280.2{195_COH1}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_M732}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_M781}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_H36B}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_JM9130013}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_18RS21}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_2603}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_A909}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
Consensus	*****	*****	*****	*****	*****
		851			900
msa235280.2{195_COH1}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_M732}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_M781}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_H36B}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_JM9130013}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_18RS21}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_2603}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_A909}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
Consensus	*****	*****	*****	*****	*****
		901			950
msa235280.2{195_COH1}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2{195_M732}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2{195_M781}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2{195_H36B}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2{195_JM9130013}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_18RS21}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2{195_2603}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2{195_A909}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
Consensus	*****	*****	*****	*****	*****
951					
msa235280.2{195_COH1}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_M732}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_M781}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_H36B}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_JM9130013}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_18RS21}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_2603}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_A909}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
Consensus	*****	*****	*****	*****	*****
1001					
msa235280.2{195_COH1}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_M732}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_M781}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_H36B}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_JM9130013}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_18RS21}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_2603}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_A909}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
Consensus	*****	*****	*****	*****	*****
1051					
msa235280.2{195_COH1}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_M732}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_M781}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_H36B}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_JM9130013}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_18RS21}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_2603}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_A909}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
Consensus	*****	*****	*****	*****	*****
1101					
msa235280.2{195_COH1}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_M732}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_M781}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_H36B}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_JM9130013}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_18RS21}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_2603}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_A909}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
Consensus	*****	*****	*****	*****	*****
1151					
msa235280.2{195_COH1}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACTA	TTCGACTTGG
msa235280.2{195_M732}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACTA	TTCGACTTGG
msa235280.2{195_M781}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACTA	TTCGACTTGG
msa235280.2{195_H36B}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACTA	TTCGACTTGG
msa235280.2{195_JM9130013}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACTA	TTCGACTTGG
msa235280.2{195_18RS21}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACTA	TTCGACTTGG
msa235280.2{195_2603}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACTA	TTCGACTTGG
msa235280.2{195_A909}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAAACTA	TTCGACTTGG
Consensus	*****	*****	*****	*****	*****
1201					
msa235280.2{195_COH1}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_M732}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_M781}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_H36B}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_JM9130013}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_18RS21}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_2603}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_A909}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
Consensus	*****	*****	*****	*****	*****
1251					
msa235280.2{195_COH1}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_M732}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_M781}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_H36B}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_JM9130013}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_18RS21}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_2603}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_A909}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
Consensus	*****	*****	*****	*****	*****
1301					
1350					

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_COH1}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_M732}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_M781}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_H36B}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_JM9130013}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_18RS21}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_2603}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_A909}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
Consensus	*****	*****	*****	*****	*****	
1351						1400
msa235280.2{195_COH1}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_M732}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_M781}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_H36B}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_JM9130013}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_18RS21}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_2603}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_A909}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
Consensus	*****	*****	*****	*****	*****	
1401						1450
msa235280.2{195_COH1}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_M732}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_M781}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_H36B}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_JM9130013}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_18RS21}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_2603}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_A909}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
Consensus	*****	*****	*****	*****	*****	
1451						1500
msa235280.2{195_COH1}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_M732}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_M781}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_H36B}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_JM9130013}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_18RS21}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_2603}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_A909}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
Consensus	*****	*****	*****	*****	*****	
1501						1550
msa235280.2{195_COH1}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_M732}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_M781}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_H36B}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_JM9130013}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_18RS21}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_2603}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_A909}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
Consensus	*****	*-*****	*****	*****	*****	
1551						1600
msa235280.2{195_COH1}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_M732}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_M781}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_H36B}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_JM9130013}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_18RS21}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_2603}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_A909}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
Consensus	*****	*****	*****	*****	*****	
1601						1650
msa235280.2{195_COH1}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_M732}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_M781}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_H36B}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_JM9130013}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_18RS21}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_2603}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_A909}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
Consensus	*****	*****	*****-****	*****	*****	
1651						1700
msa235280.2{195_COH1}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG	
msa235280.2{195_M732}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG	
msa235280.2{195_M781}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG	
msa235280.2{195_H36B}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG	
msa235280.2{195_JM9130013}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG	
msa235280.2{195_18RS21}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG	



Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_2603}	TAAAGGATGG	ACAACATTGG	TATTACATAA	AACAGAAAAT	TCATTAAATG
msa235280.2{195_A909}	TAAAGGATGG	ACAACATTGG	TATTACATAA	AACAGAAAAT	TCATTAAATG
Consensus	*****	*****	*****	*****	*****
1701					
msa235280.2{195_COH1}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCAACAA
msa235280.2{195_M732}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCAACAA
msa235280.2{195_M781}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCAACAA
msa235280.2{195_H36B}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCAACAA
msa235280.2{195_JM9130013}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCAACAA
msa235280.2{195_18RS21}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCAACAA
msa235280.2{195_2603}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCAACAA
msa235280.2{195_A909}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCAACAA
Consensus	*****	*****	*****	*****	*****
1750					
1751					
msa235280.2{195_COH1}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_M732}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_M781}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_H36B}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_JM9130013}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_18RS21}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_2603}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_A909}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
Consensus	*****	*****	*****	*****	*****
1800					
1801					
msa235280.2{195_COH1}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_M732}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_M781}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_H36B}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_JM9130013}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_18RS21}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_2603}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_A909}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
Consensus	*****	*****	*****	*****	*****
1850					
1851					
msa235280.2{195_COH1}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_M732}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_M781}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_H36B}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_JM9130013}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_18RS21}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_2603}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_A909}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
Consensus	*****	*****	*****	*****	*****
1900					
1901					
msa235280.2{195_COH1}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_M732}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_M781}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_H36B}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_JM9130013}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_18RS21}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_2603}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_A909}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
Consensus	*****	*****	*****	*****	*****
1950					
1951					
msa235280.2{195_COH1}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_M732}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_M781}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_H36B}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_JM9130013}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_18RS21}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_2603}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_A909}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
Consensus	*****	*****	*****	*****	*****
2000					
2001					
msa235280.2{195_COH1}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_M732}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_M781}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_H36B}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_JM9130013}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_18RS21}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_2603}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_A909}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
Consensus	*****	*****	*****	*****	*****
2050					
2051					
msa235280.2{195_COH1}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
2100					

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_M732}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_M781}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_H36B}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_JM9130013}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_18RS21}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_2603}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_A909}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_M732}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_M781}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_H36B}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_JM9130013}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_18RS21}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_2603}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_A909}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_M732}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_M781}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_H36B}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_JM9130013}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_18RS21}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_2603}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_A909}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_M732}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_M781}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_H36B}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_JM9130013}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_18RS21}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_2603}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_A909}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_M732}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_M781}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_H36B}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_JM9130013}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_18RS21}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_2603}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_A909}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_M732}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_M781}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_H36B}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_JM9130013}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_18RS21}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_2603}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_A909}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_M732}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_M781}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_H36B}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_JM9130013}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_18RS21}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_2603}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_A909}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_M732}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_M781}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_H36B}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_JM9130013}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_18RS21}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_2603}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_A909}	TTCTGTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAC	
Consensus	*****	*****	*****	*****	*****	
msa235280.2{195_COH1}	2451	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_M732}		TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_M781}		TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_H36B}		TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_JM9130013}		TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_18RS21}		TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_2603}		TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
msa235280.2{195_A909}		TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT
Consensus		*****	*****	*****	*****	*****
msa235280.2{195_COH1}	2501	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_M732}		CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_M781}		CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_H36B}		CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_JM9130013}		CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_18RS21}		CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_2603}		CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
msa235280.2{195_A909}		CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC
Consensus		*****	*****	*****	*****	*****
msa235280.2{195_COH1}	2551	ACTAGAAITTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_M732}		ACTAGAAITTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_M781}		ACTAGAAITTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_H36B}		ACTAGAAITTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_JM9130013}		ACTAGAAITTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_18RS21}		ACTAGAAITTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_2603}		ACTAGAAITTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA
msa235280.2{195_A909}		ACTAGAAITTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA
Consensus		*****	*****	***_*****	*****	*****
msa235280.2{195_COH1}	2601	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_M732}		ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_M781}		ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_H36B}		ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_JM9130013}		ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_18RS21}		ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_2603}		ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
msa235280.2{195_A909}		ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT
Consensus		*****	*****	*****	*****	*****
msa235280.2{195_COH1}	2651	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_M732}		AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_M781}		AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_H36B}		AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_JM9130013}		AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_18RS21}		AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_2603}		AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
msa235280.2{195_A909}		AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT
Consensus		*****	*****	*****	*****	*****
msa235280.2{195_COH1}	2701	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_M732}		GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_M781}		GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_H36B}		GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_JM9130013}		GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_18RS21}		GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_2603}		GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
msa235280.2{195_A909}		GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA
Consensus		*****	*****	*****	*****	*****
msa235280.2{195_COH1}	2751	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_M732}		CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_M781}		CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_H36B}		CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_JM9130013}		CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_18RS21}		CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_2603}		CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT
msa235280.2{195_A909}		CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT
Consensus		*****	**_*****	*****	*****	*****
msa235280.2{195_COH1}	2801	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_M732}		AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_M781}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_H36B}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_JM9130013}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_18RS21}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_2603}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_A909}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_M732}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_M781}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_H36B}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_JM9130013}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_18RS21}	GATTAAAGTA	GTTGACTTAG	AAGCTATT..	.....	.....
msa235280.2{195_2603}	GATTAAAGTA	GTTGACTTAG	AAGCTATT..	.....	.....
msa235280.2{195_A909}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_M732}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_M781}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_H36B}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_JM9130013}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_18RS21}	.....	.....	.....	..CGTAAAGC	TGAaGAAGCA
msa235280.2{195_2603}	.....	....cgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_A909}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
Consensus	-----	-----	-----	-----	-----
msa235280.2{195_COH1}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_M732}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_M781}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_H36B}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_JM9130013}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_18RS21}	CgTAAAGCTG	AAGAAGcA..	.....	.....	.....
msa235280.2{195_2603}	CgTAAAGCTG	AAGAAGcA..	.....	.....	.....
msa235280.2{195_A909}	CgTAAAGCTG	AAGAAGcA..	.....	.....	.....
Consensus	*-*****	*****-*	-----	-----	-----
msa235280.2{195_COH1}	agca.CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_M732}	agca.CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_M781}	agcacCGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_H36B}	agca.CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_JM9130013}	agcacCGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_18RS21}	....CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_2603}	....CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_A909}	....CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
Consensus	-----	*****	*****	*****	*****
msa235280.2{195_COH1}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_M732}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_M781}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_H36B}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_JM9130013}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_18RS21}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_2603}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_A909}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_M732}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_M781}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_H36B}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_JM9130013}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_18RS21}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_2603}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_A909}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	-----
msa235280.2{195_M732}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TGAAAA----
msa235280.2{195_M781}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TG-----
msa235280.2{195_H36B}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATG~	-----
msa235280.2{195_JM9130013}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TG-----
msa235280.2{195_18RS21}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TGAA-----
msa235280.2{195_2603}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TGAAAAACAA
msa235280.2{195_A909}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TGAAAAACAA

Table 51: Comparative Sequences relating to SAG0677

Consensus	*****	*****	*****	*****	*****
	3201				3250
msa235280.2{195_COH1}	-----	-----	-----	-----	-----
msa235280.2{195_M732}	-----	-----	-----	-----	-----
msa235280.2{195_M781}	-----	-----	-----	-----	-----
msa235280.2{195_H36B}	-----	-----	-----	-----	-----
msa235280.2{195_JM9130013}	-----	-----	-----	-----	-----
msa235280.2{195_18RS21}	-----	-----	-----	-----	-----
msa235280.2{195_2603}	ATTAAAAATA	cattgccatc	cactgggtgac	agcaaacgtg	gttattatat
msa235280.2{195_A909}	ATTAAAAATA	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	3251				3300
msa235280.2{195_COH1}	-----	-----	-----	-----	-----
msa235280.2{195_M732}	-----	-----	-----	-----	-----
msa235280.2{195_M781}	-----	-----	-----	-----	-----
msa235280.2{195_H36B}	-----	-----	-----	-----	-----
msa235280.2{195_JM9130013}	-----	-----	-----	-----	-----
msa235280.2{195_18RS21}	-----	-----	-----	-----	-----
msa235280.2{195_2603}	cactggaatg	gctatcgta	tgctgagtgt	attatttagt	ttagctaaaa
msa235280.2{195_A909}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	3301	3317			
msa235280.2{195_COH1}	-----	-----			
msa235280.2{195_M732}	-----	-----			
msa235280.2{195_M781}	-----	-----			
msa235280.2{195_H36B}	-----	-----			
msa235280.2{195_JM9130013}	-----	-----			
msa235280.2{195_18RS21}	-----	-----			
msa235280.2{195_2603}	agtttaaaag	caaatat			
msa235280.2{195_A909}	-----	-----			
Consensus	*****	*****			

## SEQ ID NO. 5110

STRAIN 2603 frame: 1

LNKGVGGDGVQIYQYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKD VY  
 LQSVKYVGGGNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPG TK  
 PSKPKDSLSTPPGFPDLNTPPDEAPKDSKDAIEDKSGAIKYAKSLQLSFVDDPILASKV  
 NGKILQVESDGLVI PRNALSANQFDDTSLKIYRNNRNKEITITTDYFADTKYVNI TAV  
 DYLSNTTPEQLATGETVDYHAI VFSSFAAIKDKGGKIYVNDKLQETSRIALKDKSVKIGI  
 ELPNDVRHIDLSVRLNEVKTVDNILKNDEQDINLSKTYQLKYNPTNRRLEFTINNINS  
 SSEIMTTFKDGMPPELVEQKDVSLDINDMDSKFKTIRLGRKDSEFKGQLIAKTGTVELD  
 MFFKQSQDPASI IKKIYLIQNGVPNELKKFDSSFGLTESQIDGYIYKDAINLKFKLTS G  
 ASLKVYVYKGQEDPYSHQKEDMTKKGEQLSHSTQANENTAKVT FANIDWSHYSKVTVNGKE  
 VVGKSELPLTKGWTTFVLHKTENSLNVKSLIMETGSVSKKVQQLPLSPRLSKNKHMRDML  
 LTMQKDSAYYETSDSLVLRINLTADTKLNFNAVGASALTENMMMRQFAVAGPQDDPVSE  
 HKYPSVFLLTTPALLETASEATLNGKEITASGIIGHIKDGDKSKHVEVKMVNENGDM LGTP  
 VI IQGKDLTNRTKPLMSGRRVL YAGKQYEFRAKLPLSRFNTWIRVEVVTEAGEKASI VRR  
 MFFDQSVPELNTAVAKRDLTSDTALIHIVAKDDSLKLKLYQDDSLLESVDKTGLYSFRNG  
 VEITKDMTVPLEFGDNI IKLSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAKVTVD M  
 LMKHLVVP EMAGAYTLTIDEAPNTNESGMLTNAKVSIIHYVNGGVDKVDVPIKVVDLEAIR  
 KAEEARKAEEARKAEEARKAEEGHKTQEAPIVEEGYKVN NVHQDTTIVKASDLPKTKTVS  
 AVHMARTDNKQITSHQTHVEKQIKNTLPSTGDSKRGYITGMAIVMLSVLFLSLAKKFKSK  
 Y

## SEQ ID NO. 5111

STRAIN A909 frame: 1

LNKGVGGDGVQIYQYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKD VY  
 LQSVKYVGGGNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPG TK  
 PSKPKDSLSTPPGFPDLNTPPDEALKDSKDAIEDKSGAIKYAKSLQLSFVDDPILASKV  
 NGKILQVESDGLVI PRNALSANQFDDTSLKIYRNNRNKEITITTDYFADTKYVNI TAV  
 DYLSNTTPEQLATGETVDYHAI VFSSFAAIKDKGGKIYVNDKLQETSRIALKDKSVKIGI  
 ELPNDVRHIDLSVRLNEVKTVDNILKNDEQDINLSKTYQLKYNPTNRRLEFTINNINS  
 SSEIMTTFKDGMPPELVEQKDVSLDINDMDSKFKTIRLGRKDSEFKGQLIAKTGTVELD  
 MFFKQSQDPASI IKKIYLIQNGVPNELKKFDSSFGLTESQIDGYIYKDAINLKFKLTS G  
 ASLKVYVYKGQEDPYSHQKEDMTKKGEQLSHSTQANENTAKVT FANIDWSHYSKVTVNGKE  
 VVGKSELPLTKGWTTFVLHKTENSLNVKSLIMETGSVSKKVQQLPLSPRLSKNKHMRDML  
 LTMQKDSAYYETSDSLVLRINLTADTKLNFNAVGASALTENMMMRQFAVAGPQDDPVSE  
 HKYPSVFLLTTPALLETASEATLNGKEITASGIIGHIKDGDKSKHVEVKMVNENGDM LGTP  
 VI IQGKDLTNRTKPLMSGRRVL YAGKQYEFRAKLPLSRFNTWIRVEVVTEAGEKASI VRR  
 MFFDQSVPELNTAVAKRDLTSDTALIHIVAKDDSLKLKLYQDDSLLESVDKTGLYSFRNG  
 VEITKDMTVPLEFGDNI IKLSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAKVTVD M  
 LMKHLVVP EMAGAYTLTIDEAPNTNESGMLTNAKVSIIHYVNGGVDKVDVPIKVVDLEAIR  
 KAEEAHKADAEARKAEEARKAEEARKAEEGHKTQEAPIVEEGYKVN NVHQDTTIVKASDLPKTKTVS  
 AVHMARTDNKQITSHQTHVEKQIKNTLPSTGDSKRGYITGMAIVMLSVLFLSLAKKFKSK  
 Y

## SEQ ID NO. 5112

STRAIN H36B frame: 2

GVQIYQYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKD VY  
 LQSVKYVGGGNNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPG TK  
 PSKPKDSLSTPPGFPDLNTPPDEALKDSKDAIEDKSGAIKYAKSLQLSFVDDPILASKV  
 NGKILQVESDGLVI PRNALSANQFDDTSLKIYRNNRNKEITITTDYFADTKYVNI TAV

DGKLVIPRNALSANQFDDTSLKIRYNNNRNKEITITDDYFADTKYVNITAVDYLNSNTFFE  
QLATQETVDYSHAIVSSFAAIKDKGGKIIYVNDLKQETSRIALKDKSVKIGELPNVDVRHI  
DLSVRRILNEVKTVDNLINKNDEQDINLSKTYQLKYNTRNRLEFTINNINSSEIMTTFY  
DGKMPLEVBQKVSLDINDMDSKFPTILRLRGDKSEFGQLAKTQETVELDMFFKQSQDDP  
ASIIKKIYLIQNGVPNELKFPDSSGFLTESQIDGYYIKYDAILNKFKPLSGASLQVNVYVK  
QEDPVSQHKEDMTKKGEQLSHSTQANENTAKVTFANIDSHYSKTVNKGVBKGGSELPL  
TKGWITFVLHKTENSLNVKSLMINTQETSVSXKVVQQLPLSPSRKKNHMRDMLTMQKDSAY  
YETSDSLVRILNLTADTKLNFNAVKGASALTNNMMMRQFAVAGPQDDPVSEHKYPSVFLL  
TPALTEASEATINGEKIITASIGIHGIDKDGSKHVEYKVMNNGMDLGTVPVIOGKDLT  
NRTKPLMSGRRLVYAGQKYEFRAKPLSRFNTWIRVEVUTEAGEAKSIVRMFPDQSVPE  
LNTAVAKRDLTSDTALIKHIVAKDDSLKLQLYQDSSLSDSVKDTKGSYFRNGVETITKMTV  
PLEFGDNITKLSAVDLSNYRRNETLHYYRNRFDVKASQMTADGKAKVTVDMLMKHLVUPE  
MAGAYTLTIDEAPNTNESGMLTNAKVS IHYVNGGVDKVDVPKIVVDLEAIRKAEAAHKAD  
EARKAEARKADAEAKAEVRKAEAAHKVEEARKAEABGHKTQEAPIVEEGYKVNNVHQT  
TVKASDLPKTKTYSVHMARTDNQKIQTSQTH

LNKKGVGGDGVQIYQYYIMKDNKNPKYLPSPDKTITVEKLEDRWKKITFKVQSDTQIGLKDQV  
LQSQVYVGGGNLNDLITPFGKEDKKVEKPLDRPPGIDLAPTSMSRFDYSYTPPGTK  
SPKPKDLSLTSPGFPDLNTPPDEAPKDSKKDAIEDKSGAIKYAKSLQLSFVDDPILASKY  
NGKTLQVBESDGLKVIERNALSANQFDDTSLKITRNNNNKAIITITDYFADTKYVNIAT  
DYLNTLPEQLATGETVDYHAIVFSSFAAIKDKGGIKYVNDKLQETSRIALDKDSVKIGI  
ELPNDVRHIDLSLVRRLNEVQTVDNILKNDEQDILNSKTYQLKYNPNTNRRLPETINNIS  
SEEMITTFDKGKQVNVKQDVSLDINDMDSKPKTIRLGRKDSFBFGKQIAGTKGTVELD  
MFFKQSQDPASIIKKYLIQNGVNELKFKDSFSGLTESQIDGYYIYKDAINLKFKLTSG  
ASLKVVYQGDSPYSHQKEDMTKKEGLSHSTQANENTAKTVYKIDANDWSHYSKVTNGKE  
VVGKSELPLTKGWTTFVLHKTEINSNVKSLIMETGVSXKVKVQDLSPRLSKNKHMRDML  
LTKQKDSAYYTESDLSLVRLNLATDTKLNFNAVKGASALTENNMMRQFVAGQDPMVSE  
HKYPSVFLTLPALLETASEATLNGKEITASGIHGIKQDKSKHVEVKVMNENGLMGTPE  
VIIOGKDLTNRTKPLMSGRRLVYAGKYQVEFRAKLPLSRFNTYIRVEVVTENGEBKASIVR  
MFFQDSVPELNTAVAKRDLSDTALIHIVAKDDSLKLKLYQDSSLSESQMTADKGAKVTVDM  
LMKHLVPEMAGAYTLTIKSAVDLNTSYRNETLHIYRNRFDVKASQMTADKGAKVTVDM  
KAEARKAEAEARKAEEGHKTKQEAPIVEEGYKVNNVHQITDTTVKASDLPKTKTVAHVHAR  
TNDQKITSHQTHVE

LNKKVGVGDDGVQIQYIQQYIKKNNKKPYLSPDKTKTVEKLEDRWKTKTFVKQVDITGLGKDQVY  
LQSVKQYVGGGNNLNDLITPKPFKKDKBKVEPKLDRPGDILEDAPMTSRMSFSDYSTPGTK  
SPKPKDYLSDGFGFPDLNTPDEATKG. .KRRY. R. IRSN. IC. VSTL. LC. .PYFS. QS  
KQWNTISRI. WQISHS. KCFVS. SI. .H. S. NLS. .SC. RNYHYNRLPFCRYKICQYHS  
.LFQYQYF. AISWY. NSRLPCHCIPFGLCCY. RGOW. DLR. R. IARNFSYSR. R. IC. DWY.  
.ITK. CQTY. .FICSSPE. G. NC. .YLEK. .TRH. SQONLPKIQDPKSSSRVY. .H. L  
KFRNHDFHQRWDKARDIG. TKRCFFGYKRYGHE. V. NYSTWTKGF. I. GTTYCKWNNS. IR  
VYFQITSRPSFN. KNIPYKPKWSC. IEKI. L. L. FWFN. KSDRWILY. RCN. P. I. INQW  
CKS. SCL. RARRSI. SGERRYD. KR. TAQSFNSQ. KYSKNCL. Y. LVTL. .GYCEWKR  
SW. R. VTFN. RMDNICIT. NRKFKIC. KFDYGDG. CK. ESSTSFKS. II. K. AYEGBA  
TYYAKRFSVLNRK. QSPFSN. SHCRY. T. P. CC. RSECYG. KYDDTBSCWITR. SC. .  
T. IPISISLNSCLIGNC. .GNSKW. GNHSWYWRSHQGW. .KOAC. SONGE. KWRHARNP  
CYYSR. RLD. SNTKINETW. STLCTR. IT. VPG. ITT. SF. HLD. G. SGNRSRESKCYSS  
HVL. PISSRA. HSSC. T. DDF. YCSPHRCQR. LSKTKIISR. FIT. IC. .NRSL. F. KW  
CRNH. RYDSTNRILY. YV. VTIC. LKILKS. .DPSYL. KPF. C. SKPNDS. QRS. SNGCY  
VDEALCSNRNGRIYNNRRSSKIK. IRNVNKR. SIDSLCKWVC. .S. CSD. SS. LRSYS  
.S. RST. S. RST. S. RST. S. RST. S. RST. S. RST. SRST. S. RGT. NPRSTYS. RRL  
QS. .RSSN. YYS. SV. FTKD. DSFRSSYG. NRQ. TDNFTSDTC. K

LNKKVGVGGDGVQYIQYYIKMDNNKPYLSPKDKITVEKLEDRWKKITFKVKQDGTIGLKDQVY  
LQSVKVVGGGNNLLDITPPGFGKDDKKEVKPKLDRPPGIDLPAPTSMRSFDDYSTTPPGTK  
PSPKKDSLSTPPGFDPLNTPPDEATKG. KRRY. R. IRSN. I. VST. LC. . PYFS. QS  
KWONITSRI. WQISHS. KCFVS. SI. . H. S. NLS. . SQ. RNYHNYSFLCRYKICQVHSG  
. LFEQYTF. AISYW. NSRLPCHPICFLCCY. RQGW. DLR. R. IARNFSYA. R. IC. DWY  
. ITK. CQTY. . FICSSFE. G. NC. . YLEK. TRH. SQONLPKIQDKSSSRVY. . H. L  
KFRNHDHOFQWKDARIG. TKRCFFGYKRYGHE. V. NYSTWTKGF. I. GTTYCKWNNS. IR  
VVFOTISRSPENY. KNIPYKPKWSC. IEKI. L. FWFN. KSDRWILY. RCN. P. I. INQW  
CKS. SCL. RARRSI. SSBERRY. KR. TAOFSNNSQ. KYKSNLNC. Y. LVTL. . GYCEWKR  
SW. R. . VTFN. RMDNICIT. NRKFIK. KFDYGDG. CK. ESSTSFKS. II. K. AYEGBA  
YTYAKRFSVLNRK. QSSPSN. SHCRY. T. F. CC. RSECSY. KYDDETVSCSWTTR. SC. .  
T. IPISILNSCLINGC. . GNSKW. GNHSIYYRSHQGW. . KQAC. SQNGE. KWRHARNP  
CYYSR. RLD. SNTKINETW. STLCR. TI. VPG. ITT. SF. HLD. G. SGNRSRRESKCYSS  
HVL. PISSRA. HSGC. T. FDF. YCSPYHRCOR. LSKTKIIR. FIT. IC. . NRSL. F. KW  
CRNH. RYDSTTTRIWR. YY. VICC. LILKSS. . DPSYL. KPF. C. SKPND. QRS. SNGCY  
VDEALSCSRNGRSLYINNRRSSKHK. IRNVNKR. SIDLCKNWC. . S. CSD. SS. LRSYS  
. S. RST. S. RST. S. RST. S. RST. S. RST. S. RST. SRST. S. RGT. NPRSTYS. RRL  
OS. . RSSN. YYS. SV. FTKD. DSFRSSYG. NRQ. TDNFSTDC

LNKKVGVGGDGVQIYQYYIKMDNNKPYLSPDKTTVEKLEDRWKKITFKVQDGTGIGLKDVY  
LOSVKYVGGGNNNLLDITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPGKTK

[illegible]

GVQVI QYYII KMDGNPKPYLSPDKDITIVKELEDRWKKITFKVQDITGLKDVYLSQVYVGG  
GNNLLDITPFGPKFKEDKVKPKLDRPGPIDLAPMTRMSRFDYSTTPPGTKPSKPKDLS  
TPPGFPDLNTPPDEAPKDKSKDAIEDKSGAIIKAYKSLVYVDDPILASKVNGLIQVES  
DGKLVIPRNALSNAGQFDDTSLKIIYRNNNRNKNEITITDYFADTKYVNITAVDNGYLSNFE  
QLATGETDYHAI VSSFAANIKDKGKGIYVNDKIQETSRIALKDKSVKIGIELEPNVRHI  
DLSVRRILENVKTVTDLILKNDEQDILNLSKTYQLKYNPNRRLEFILTINNINSSSIIEMTFPK  
DKMPELVBQKQVSLDINDMDMSKFKTIRLGRDKSEFGKGLAKTQTVELMDMFFKQSDQP  
ASIIKKIYLIQNGVPNELKKFDSSTFGLTESQIDGYIYKDAINLKFPLTSGASLKVYVYKG  
QEDPYSHQKEDMTKXGELSHSQNTQANETAKVTIANDWSHYSKVTNVNGKEVGKSELPL  
YKGTWTTFLVHLKTENSLVNKLIMETGSVSKVQVLPISPLRSLKHMRRMDMLITMQKDSAY  
TETSDSLVRILINTADLTKLNFNAVKGASCTANTENMMRQFVAGAVQDOPVSEHKYPSVLL  
TPALLEASEATLNGKEITAGSIIGHIKDQKSKHVEVKVMNENGMDLQTPVIIQGGKLT  
NRTIKPLMSGRRVLVYAGQYVEFRAPKLIPKDFGTNIIRVEVVTIETAGEAKSIVRRMFPDQSPVE  
LNTAVAKRDLTSDALIIHIAKDDSLKLKLYQDDSLLESVDKTKLYSFRNGVMTITKDMTV  
PLEFGDNI I KLSADEVNTSNRYNETLHIYRNRFDVASKQMDTAKGVTVDMILMKHLVPE  
MAGAYTLTIDEAPNTNBSGMLTNAKVISHYVNGGVQKQVDVPIKVVDLEAIRKAEAEHAKD  
EARKAEAEARKAEABAEKVEVRKAEABAEKVEEAP.S. RGT.NPRSTYS.RRLQG..RSSN.  
YYS.SV.FTKD.DSFRSSYG.NRQ.TDNFTSDTC

```

1
50
msa235427.2{195_H36B} ~~~~~G VQIYQYYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVKQ
msa235427.2{195_JM9130013} ~~~~~G VQIYQYYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVKQ
msa235427.2{195_18RS21} LNNKGVGVDG VQIYQYYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVKQ
msa235427.2{195_2603} LNNKGVGVDG VQIYQYYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVKQ
msa235427.2{195_A909} LNNKGVGVDG VQIYQYYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVKQ
msa235427.2{195_COH1} LNNKGVGVDG VQIYQYYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVKQ
msa235427.2{195_M732} LNNKGVGVDG VQIYQYYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVKQ
msa235427.2{195_M781} LNNKGVGVDG VQIYQYYIKM DNNKPYLSPK DKTTVEKLED RWKKITFKVKQ
Consensus *****

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	51	100
msa235427.2{195_H36B}	DTGIGLKDVY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPCLDRPPGI	
msa235427.2{195_JM9130013}	DTGIGLKDVY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPCLDRPPGI	
msa235427.2{195_18RS21}	DTGIGLKDVY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPCLDRPPGI	
msa235427.2{195_2603}	DTGIGLKDVY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPCLDRPPGI	
msa235427.2{195_A909}	DTGIGLKDVY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPCLDRPPGI	
msa235427.2{195_COH1}	DTGIGLKDVY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPCLDRPPGI	
msa235427.2{195_M732}	DTGIGLKDVY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPCLDRPPGI	
msa235427.2{195_M781}	DTGIGLKDVY LQSVKYVGGG NNNLDLITPP GFKKEDKKVE KPCLDRPPGI	
Consensus	*****	*****

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101
msa235427.2{195_H36B} DLpApTSMRS FDYSTPPGTK PSKPKDSLST PPGFPDLNTP PDEAlKdskK
msa235427.2{195_JM9130013} DLpApTSMRS FDYSTPPGTK PSKPKDSLST PPGFPDLNTP PDEApKdskK
msa235427.2{195_18RS21} DLpApTSMRS FDYSTPPGTK PSKPKDSLST PPGFPDLNTP PDEApKdskK
msa235427.2{195_2603} DLpApTSMRS FDYSTPPGTK PSKPKDSLST PPGFPDLNTP PDEApKdskK
msa235427.2{195_A909} DLpPpTSMRS FDYSTPPGTK PSKPKDSLST PPGFPDLNTP PDEAlKdskK
msa235427.2{195_COH1} DLpApTSMRS FDYSTPPGTK PSKPKDSLST PPGFPDLNTP PDEAtKg..K
msa235427.2{195_W732} DLpApTSMRS FDYSTPPGTK PSKPKDSLST PPGFPDLNTP PDEAtKg..K
msa235427.2{195_W781} DLpApTSMRS FDYSTPPGTK PSKPKDSLST PPGFPDLNTP PDEAtKg..K
Consensus *****

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	151			200
msa235427.2{195_H36B}	daiedksgai	kyakslqlsf	vddPilaskv	ngkilqvses
msa235427.2{195_JM9130013}	daiedksgai	kyakslqlsf	vddPilaskv	ngkilqvses
msa235427.2{195_18RS21}	daiedksgai	kyakslqlsf	vddPilaskv	ngkilqvses
msa235427.2{195_2603}	daiedksgai	kyakslqlsf	vddPilaskv	ngkilqvses
msa235427.2{195_A909}	daiedksgai	kyakslqlsf	vddPilaskv	ngkilqvses
msa235427.2{195_COH1}	rry.r.irsn	.ic.vast.l	c..Pyfs.qs	kwgnitstri.
msa235427.2{195_W732}	rry.r.irsn	.ic.vast.l	c..Pyfs.qs	kwgnitstri.
msa235427.2{195_W781}	rry.r.irsn	.ic.vast.l	c..Pyfs.qs	kwgnitstri.
Consensus	-----	-----	*-----	-----

Table 51: Comparative Sequences relating to SAG0677

		201			250
msa235427.2{195_H36B}	sanqfddtsl	kiyrnnnrnk	eitittddyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_JM9130013}	sanqfddtsl	kiyrnnnrnk	eitittddyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_18RS21}	sanqfddtsl	kiyrnnnrnk	eitittddyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_2603}	sanqfddtsl	kiyrnnnrnk	eitittddyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_A909}	sanqfddtsl	kiyrnnnrnk	eitittddyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_COH1}	vs.si..h.s	.nls...sq.	rnyyhnrlFc	ryKicqyhsq	.lfeqyyF.a
msa235427.2{195_M732}	vs.si..h.s	.nls...sq.	rnyyhnrlFc	ryKicqyhsq	.lfeqyyF.a
msa235427.2{195_M781}	vs.si..h.s	.nls...sq.	rnyyhnrlFc	ryKicqyhsq	.lfeqyyF.a
Consensus		-----	-----*	-----*	-----*
		251			300
msa235427.2{195_H36B}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_JM9130013}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_18RS21}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_2603}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_A909}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_COH1}	isyw.nsr1p	chcifklccy	.rqGw.dlc.	r.iarnfsys	a.r.ic.dwy
msa235427.2{195_M732}	isyw.nsr1p	chcifklccy	.rqGw.dlc.	r.iarnfsys	a.r.ic.dwy
msa235427.2{195_M781}	isyw.nsr1p	chcifklccy	.rqGw.dlc.	r.iarnfsys	a.r.ic.dwy
Consensus		-----	-----*	-----*	-----*
		301			350
msa235427.2{195_H36B}	elpndvrhid	slsvrrlnev	ktvndiLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_JM9130013}	elpndvrhid	slsvrrlnev	ktvndiLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_18RS21}	elpndvrhid	slsvrrlnev	ktvndiLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_2603}	elpndvrhid	slsvrrlnev	ktvndiLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_A909}	elpndvrhid	slsvrrlnev	ktvndiLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_COH1}	.itk.cqty.	.ficssfe.g	.nc..yLek.	.trh.sqgnl	piKiqPdkas
msa235427.2{195_M732}	.itk.cqty.	.ficssfe.g	.nc..yLek.	.trh.sqgnl	piKiqPdkas
msa235427.2{195_M781}	.itk.cqty.	.ficssfe.g	.nc..yLek.	.trh.sqgnl	piKiqPdkas
Consensus		-----	-----*	-----*	-----*
		351			400
msa235427.2{195_H36B}	leftinnins	sseimttFkd	gKmpelveqK	dvldindmd	mskfktirlg
msa235427.2{195_JM9130013}	leftinnins	sseimttFkd	gKmpelveqK	dvldindmd	mskfktirlg
msa235427.2{195_18RS21}	leftinnins	sseimttFkd	gKmpelveqK	dvldindmd	mskfktirlg
msa235427.2{195_2603}	leftinnins	sseimttFkd	gKmpelveqK	dvldindmd	mskfktirlg
msa235427.2{195_A909}	leftinnins	sseimttFkd	gKmpelveqK	dvldindmd	mskfktirlg
msa235427.2{195_COH1}	srvyv..h.l	kfrnhdhFqr	wKdarig.tK	rcffgykryg	he.v.nystw
msa235427.2{195_M732}	srvyv..h.l	kfrnhdhFqr	wKdarig.tK	rcffgykryg	he.v.nystw
msa235427.2{195_M781}	srvyv..h.l	kfrnhdhFqr	wKdarig.tK	rcffgykryg	he.v.nystw
Consensus		-----	-----*	-----*	-----*
		401			450
msa235427.2{195_H36B}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq	ngvpnelkKf
msa235427.2{195_JM9130013}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq	ngvpnelkKf
msa235427.2{195_18RS21}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq	ngvpnelkKf
msa235427.2{195_2603}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq	ngvpnelkKf
msa235427.2{195_A909}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq	ngvpnelkKf
msa235427.2{195_COH1}	tKgf.i.Gtt	ycKnwns.ir	yvFqtisrPs	fny.Knipyp	kwcak.ieKi
msa235427.2{195_M732}	tKgf.i.Gtt	ycKnwns.ir	yvFqtisrPs	fny.Knipyp	kwcak.ieKi
msa235427.2{195_M781}	tKgf.i.Gtt	ycKnwns.ir	yvFqtisrPs	fny.Knipyp	kwcak.ieKi
Consensus		-----	-----*	-----*	-----*
		451			500
msa235427.2{195_H36B}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_JM9130013}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_18RS21}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_2603}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_A909}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_COH1}	.l.Fwfn.ks	drwilyl.rc	n.p.i.inqw	cks.scl.ra	rrsi.sserr
msa235427.2{195_M732}	.l.Fwfn.ks	drwilyl.rc	n.p.i.inqw	cks.scl.ra	rrsi.sserr
msa235427.2{195_M781}	.l.Fwfn.ks	drwilyl.rc	n.p.i.inqw	cks.scl.ra	rrsi.sserr
Consensus		-----	-----*	-----*	-----*
		501			550
msa235427.2{195_H36B}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_JM9130013}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_18RS21}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_2603}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_A909}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_COH1}	yd.kr.taqs	fnssq.kysK	snlc.y.lvt	l..gycewKr	sw.r..vtfn
msa235427.2{195_M732}	yd.kr.taqs	fnssq.kysK	snlc.y.lvt	l..gycewKr	sw.r..vtfn
msa235427.2{195_M781}	yd.kr.taqs	fnssq.kysK	snlc.y.lvt	l..gycewKr	sw.r..vtfn
Consensus		-----	-----*	-----*	-----*
		551			600
msa235427.2{195_H36B}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl	sknkhmrdbl
msa235427.2{195_JM9130013}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl	sknkhmrdbl
msa235427.2{195_18RS21}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl	sknkhmrdbl
msa235427.2{195_2603}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl	sknkhmrdbl



Table 51: Comparative Sequences relating to SAG0677

msa235427.2{195_A909}	kgwtffvlhk	tenslnvksl	imetGavskk	vqqlplsprl	sknkhmrndl
msa235427.2{195_COH1}	.rmdnicit.	nrkfiko.kf	dygdG.ck.e	ssttsfks.i	i.k.ayegy.
msa235427.2{195_M732}	.rmdnicit.	nrkfiko.kf	dygdG.ck.e	ssttsfks.i	i.k.ayegy.
msa235427.2{195_M781}	.rmdnicit.	nrkfiko.kf	dygdG.ck.e	ssttsfks.i	i.k.ayegy.
Consensus	-----	-----	-----*	-----	-----
msa235427.2{195_H36B}	601				650
msa235427.2{195_JM9130013}	lTmqkdsayy	etsdsivlri	Nltadtklmf	navkgaSalt	enmmmrqfav
msa235427.2{195_18RS21}	lTmqkdsayy	etsdsivlri	Nltadtklmf	navkgaSalt	enmmmrqfav
msa235427.2{195_2603}	lTmqkdsayy	etsdsivlri	Nltadtklmf	navkgaSalt	enmmmrqfav
msa235427.2{195_A909}	lTmqkdsayy	etsdsivlri	Nltadtklmf	navkgaSalt	enmmmrqfav
msa235427.2{195_COH1}	aTyyakrfsv	lrnk.qsps	N.shcry.t.	f.cc.rSecs	y.kyddetvc
msa235427.2{195_M732}	aTyyakrfsv	lrnk.qsps	N.shcry.t.	f.cc.rSecs	y.kyddetvc
msa235427.2{195_M781}	aTyyakrfsv	lrnk.qsps	N.shcry.t.	f.cc.rSecs	y.kyddetvc
Consensus	-----	-----	-----*	-----*	-----
msa235427.2{195_H36B}	651				700
msa235427.2{195_JM9130013}	agpqddpvse	hkypsvflit	palLetasea	tlngkeitaS	giighikdGd
msa235427.2{195_18RS21}	agpqddpvse	hkypsvflit	palLetasea	tlngkeitaS	giighikdGd
msa235427.2{195_2603}	agpqddpvse	hkypsvflit	palLetasea	tlngkeitaS	giighikdGd
msa235427.2{195_A909}	agpqddpvse	hkypsvflit	palLetasea	tlngkeitaS	giighikdGd
msa235427.2{195_COH1}	scwttr.sc.	.t.ipisisl	nscLignc..	gnskw.gnhS	iwyrrshqGw
msa235427.2{195_M732}	scwttr.sc.	.t.ipisisl	nscLignc..	gnskw.gnhS	iwyrrshqGw
msa235427.2{195_M781}	scwttr.sc.	.t.ipisisl	nscLignc..	gnskw.gnhS	iwyrrshqGw
Consensus	-----	-----	-----*	-----*	-----*
msa235427.2{195_H36B}	701				750
msa235427.2{195_JM9130013}	ksKhvevkmv	nEngdmlgtp	viiggkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_18RS21}	ksKhvevkmv	nEngdmlgtp	viiggkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_2603}	ksKhvevkmv	nEngdmlgtp	viiggkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_A909}	ksKhvevkmv	nEngdmlgtp	viiggkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_COH1}	.Kqac.sqn	gE.kwrharn	pcyyr.rld	.snktinewt	.stlcr.ti.
msa235427.2{195_M732}	.Kqac.sqn	gE.kwrharn	pcyyr.rld	.snktinewt	.stlcr.ti.
msa235427.2{195_M781}	.Kqac.sqn	gE.kwrharn	pcyyr.rld	.snktinewt	.stlcr.ti.
Consensus	-----	-----*	-----	-----	-----
msa235427.2{195_H36B}	751				800
msa235427.2{195_JM9130013}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_18RS21}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_2603}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_A909}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_COH1}	vpg.itt.sf	.hld.g.sgn	rsrreSkycs	shvl.pissr	a.hssc.t.f
msa235427.2{195_M732}	vpg.itt.sf	.hld.g.sgn	rsrreSkycs	shvl.pissr	a.hssc.t.f
msa235427.2{195_M781}	vpg.itt.sf	.hld.g.sgn	rsrreSkycs	shvl.pissr	a.hssc.t.f
Consensus	-----	-----	-----*	-----	-----
msa235427.2{195_H36B}	801				850
msa235427.2{195_JM9130013}	sdtalihiva	kddsLklkly	qddsllesvd	ktglysfrng	veitkdmtp
msa235427.2{195_18RS21}	sdtalihiva	kddsLklkly	qddsllesvd	ktglysfrng	veitkdmtp
msa235427.2{195_2603}	sdtalihiva	kddsLklkly	qddsllesvd	ktglysfrng	veitkdmtp
msa235427.2{195_A909}	sdtalihiva	kddsLklkly	qddsllesvd	ktglysfrng	veitkdmtp
msa235427.2{195_COH1}	df.ycsyphr	cqr.Lsktki	isr.fit.ic	.nrsl.f.k	wcrnh.ryds
msa235427.2{195_M732}	df.ycsyphr	cqr.Lsktki	isr.fit.ic	.nrsl.f.k	wcrnh.ryds
msa235427.2{195_M781}	df.ycsyphr	cqr.Lsktki	isr.fit.ic	.nrsl.f.k	wcrnh.ryds
Consensus	-----	-----*	-----	-----	-----
msa235427.2{195_H36B}	851				900
msa235427.2{195_JM9130013}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_18RS21}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_2603}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_A909}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_COH1}	tttriwr.yy	vicc.likls	s..dpsYl.k	pf.c.Skpnd	s.qrs.snec
msa235427.2{195_M732}	tttriwr.yy	vicc.likls	s..dpsYl.k	pf.c.Skpnd	s.qrs.snec
msa235427.2{195_M781}	tttriwr.yy	vicc.likls	s..dpsYl.k	pf.c.Skpnd	s.qrs.snec
Consensus	-----	-----	-----*	-----*	-----
msa235427.2{195_H36B}	901				950
msa235427.2{195_JM9130013}	lmkhlvpem	aGaytl tide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_18RS21}	lmkhlvpem	aGaytl tide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_2603}	lmkhlvpem	aGaytl tide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_A909}	lmkhlvpem	aGaytl tide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_COH1}	yvdealscsr	nGrsllyinnr	rsskhk.irn	vNkr.SIdsl	ckwwc..s.c
msa235427.2{195_M732}	yvdealscsr	nGrsllyinnr	rsskhk.irn	vNkr.SIdsl	ckwwc..s.c
msa235427.2{195_M781}	yvdealscsr	nGrsllyinnr	rsskhk.irn	vNkr.SIdsl	ckwwc..s.c
Consensus	-----	-----*	-----*	-----*	-----

Table 51: Comparative Sequences relating to SAG0677

		951			1000
msa235427.2{195_H36B}	ikvvdleair	kaeeahkade	arkaeearka	deahkaeevr	kaeeahkvee
msa235427.2{195_JM9130013}	ikvvdleair	kaeeahkade	arkaeearka	eeahkaeevr	kaeeahkvee
msa235427.2{195_18RS21}	ikvvdlea..	...irkaee	arkaeearka	eeghktqeap	iveegykvnn
msa235427.2{195_2603}	ikvvdleair	kaeearkaee	arkaeearka	eeghktqeap	iveegykvnn
msa235427.2{195_A909}	ikvvdleair	kaeeahkade	arkaeearka	eearkaeear	kaeehktqe
msa235427.2{195_COH1}	sd.ss.lrsy	s.s.rst.s.	rst.s.rst.	s.rst.s.rs	t.s.rst.sr
msa235427.2{195_M732}	sd.ss.lrsy	s.s.rst.s.	rst.s.rst.	s.rst.s.rs	t.s.rst.sr
msa235427.2{195_M781}	sd.ss.lrsy	s.s.rst.s.	rst.s.rst.	s.rst.s.rs	t.s.rst.sr
	Consensus	-----	-----	-----	-----
		1001			1050
msa235427.2{195_H36B}	arkaeeghkt	geapiveegy	kvnnvhqtdt	tvkasdlpkt	ktvsavhmar
msa235427.2{195_JM9130013}	ap.s.rgt.n	prstys.rrl	qg..rssn.y	ys.sv.ftkd	.dsfrssyg.
msa235427.2{195_18RS21}	vhqtdttvka	sdlpktktvs	avhmartdnk	qitshqthve	-----
msa235427.2{195_2603}	vhqtdttvka	sdlpktktvs	avhmartdnk	qitshqthve	kqikntlpst
msa235427.2{195_A909}	apiveegykv	nnvhqtdttv	kasdlpktkt	vsavhmartd	nkqitshqth
msa235427.2{195_COH1}	rst.s.rgt.	nprstys.rr	lqs..rssn.	yps.sv.ftk	d.dsfrssyg
msa235427.2{195_M732}	rst.s.rgt.	nprstys.rr	lqs..rssn.	yps.sv.ftk	d.dsfrssyg
msa235427.2{195_M781}	rstvklrddi	kpkkh1.lkk	atklitfikl	ilqlkrliyy	rlrqfpqfiw
	Consensus	-----	-----	-----	-----
		1051		1081	
msa235427.2{195_H36B}	tdnkqitshq	th-----	-----	-----	~
msa235427.2{195_JM9130013}	nrq.tdnfts	dte-----	-----	-----	~
msa235427.2{195_18RS21}	-----	-----	-----	-----	~
msa235427.2{195_2603}	gdskrgyyit	gmaivmlsvl	fslakkfksk	y	
msa235427.2{195_A909}	vekqikn---	-----	-----	-----	~
msa235427.2{195_COH1}	.nrq.tdnft	sdTC-----	-----	-----	~
msa235427.2{195_M732}	.nrq.tdnft	sdTC.k----	-----	-----	~
msa235427.2{195_M781}	leqtinr.lh	irhml-----	-----	-----	~
	Consensus	-----	*****	*****	*

Table 52: Comparative Sequences relating to SAG 1823

## SEQ ID NO. 5201

## STRAIN 090

AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGA  
 CAATGCTATCACTAAACAGATAAAACAACAGAAATTATTTCCAACCAGA  
 CAACAAGCCAAACTGGGCAAATTGCCCTTTTGGAAAACTAACACCAGCA  
 CAAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGT  
 CGGCGATCAAAATGCGCTCCTTGATTTTGGACAATCCGAGTAGAAGGCG  
 TTAATACCACTGTAAATCATATCTTGTCTGAGCAGAAAAAATTCAAATT  
 CCTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATT  
 TATTGCCAAATATAAGATGCTACTCCGGCAGAATTAGAGAAAAACCAA  
 ACTTGATTCAAAATTTATCAAACAAAGCAAGACCTCGCTACAGGAATTT  
 TATTTTGACTCACAACATCGAGCAAAAAATGGATATGATGGCAGCGAA  
 TGTGTCAAACAAGAGATCTTTGGCAAGAAATATCGTCTCTGCTGAAA  
 TGCTCATTGAAGATAACTAAATCTATTGAAAAATTTGGTTGGAGTTATT  
 GCTTCTATTGAATCGAGTCAAGCCGAGGCTGCTAATCGTGCAAGCCACTT  
 ACAACAAGAAATCTAGCATTAGATAGCCAAACGTCCGAGTATCAAATTA  
 AAGTAAACCAATTAGCTCGAATGACTGAAGTTATCAATACCTCGAACAG  
 CAACATACTGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACC  
 ACAGATGCGAAACTTTGGTCAAAGTATCGTCAGATATGCGTCAGAACTTG  
 GCATGTTACGTCGAAATACCATTCCAACAATGAACTCTCAATCGCTCAG  
 TTAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTAT  
 TGTCAACGCTAATAATGACGATTTGCAGATGCTGGCTGAACTAGTAAAG  
 AAGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATT  
 AAATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAATGGTAT  
 TATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCAATTGGAATCTG  
 CTGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAATTCGTGAT  
 AAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAAGAAAA  
 AGTTGATGAGTCT

## SEQ ID NO. 5202

## STRAIN A909

AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGA  
 CAATGCTATCACTAAACAGATAAAACAACAGAAATTATTTCCAACCAGA  
 CAACAAGCCAAACTGGGCAAATTGCCCTTTTGGAAAACTAACACCAGCA  
 CAAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGT  
 CGGTGACCAAAATGCGCTCCTTGATTTTGGACAATCCGAGTAGAAGGCG  
 TTAATACCACTGTAAATCATATCTTGTCTGAGCAGAAAAAATTCAAATT  
 CCTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATT  
 TATTGCCAAATATAAGATGCTACTCCGGCAGAATTAGAGAAAAACCAA  
 ACTTGATTCAAAATTTATCAAACAAAGCAAGACCTCGCTACAGGAATTT  
 TATTTTGACTCACAACATCGAGCAAAAAATGGATATGATGGCAGCGAA  
 TGTGTCAAACAAGAGATCTTTGGCAAGAAATATCGTCTCTGCTGAAA  
 TGCTCATTGAAGATAACTAAATCTATTGAAAAATTTGGTTGGAGTTAWT  
 GCTTTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTT  
 ACAACAAGAAATCTAGCATTAGATAGCCAAACGTCCGAGTATCAAATTA  
 AAGTAAACCAATTAGCTCGAATGACTGAAGTTATCAATACCTCGAACAG  
 CAACATACTGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACC  
 ACAGATGCGAAACTTTGGTCAAAGTATCGTCAGATATGCGTCAGAACTTG  
 GCATGTTACGTCGAAATACCATTCCAACAATGAACTCTCAATCGCTCAG  
 TTAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTAT  
 TGTCAACGCTAATAATGACGATTTGCAGATGCTGGCTGAACTAGTAAAG  
 AAGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATT  
 AAATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAATGGTAT  
 TATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCAATTAGAAATCTG  
 CTGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAATTCGTGAT  
 AAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAAGAAAA  
 AGTGTGATGAGTCT

## SEQ ID NO. 5203

## STRAIN H36B

AGCGaTACCTTTAATTTTGATATTGACCAAATTGCAGAC  
 AATGCTATCACTAAACAGATAAAACAACAGAAATTATTTCCAACCAGAC  
 AACAAAGCCAAACTGGGCAAATTGCCCTTTTGGAAAACTAACACCAGCAC  
 AAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGT  
 GTGACCAAAATGCGCTCCTTGATTTTGGACAATCCGAGTAGAAGGCGT  
 TAATACCACTGTAAATCATATCTTGTCTGAGCAGAAAAAATTCAAATTC  
 CTAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATT  
 ATTGCCAAATATAAGATGCTACTCCGGCAGAATTAGAGAAAAACCAA  
 CTTGATTCAAAATTTATCAAACAAAGCAAGACCTCGCTACAGGAATTTT  
 ATTTTGACTCACAACATCGAGCAAAAAATGGATATGATGGCAGCGAAT  
 GTTGTCAAACAAGAGATACCTTTGGCAAGAAATATCGTCTCTGCTGAAAT  
 GCTCATTGAAGATAACTAAATCTATTGAAAAATTTGGTTGGAGTTATTG  
 CTCTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTA  
 CAACAAGAAATCTAGCATTAGATAGCCAAACGTCCGAGTATCAAATTA  
 AAGTAACCAATTAGCTCGAATGACTGAAGTTATCAATACCTCGAACAGC  
 AACATACTGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACCA  
 CAGATGCGAAACTTTGGTCAAAGTATCGTCAGATATGCGTCAGAACTTG  
 CATGTTACGTCGAAATACCATTCCAACAATGAACTCTCAATCGCTCAGT  
 TAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATT  
 GTCAACGCTAATAATGACGATTTGCAGATGCTGGCTGAACTAGTAAAGA  
 AGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATT  
 AATCTGTCACTGCATTATCTGAAAGCTTAGTGGCTCAAAATAATGGTATT  
 ATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCAATTAGAAATCTGC

Table 52: Comparative Sequences relating to SAG 1823

TGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAAATTCGTGATa  
 AAAAAATAGTTGAAGCCTTACTCAaCGAAGGTaAATCTACCCAAGAAAAA  
 GTTGATGAGTCT

SEQ ID NO. 5204

STRAIN 18RS21

TTTTGATATTGACCAAATTGCAGACAATGCTATCACTAAAAACAGATAAAA  
 CAACAGAAATTATTTCCAACCAGACAACAAGCCAAACTGGGCAAAATGGCC  
 TTTTTTGAAAAAATAACACCAGCACAAAAGTCTGCTATCTCTGAAAAAAC  
 ACCAGCTTTGGTAGATACTTTTGTGGCGATCAAAATGCGCTCCTTGATT  
 TTGGACAATCCGCGTAGAAGGCGTTAATACCACCTGTTAATCATATCTTG  
 TCTGAGCAGAAAAAATTCAAATTCCTCAAGTTGATGATTTTACTAAAAAA  
 TGCTAATCGCGAACTAAATGGATTTATTGCCAAATATAAAGATGCTACTC  
 CGCAGAAATTAGAGAAAAACCAAACTTGATTCAAAAATTATTCAAACAA  
 AGCAAGACCTCGCTACAGGAATTTTATTTTGACTCACAAAACATCGAGCA  
 AAAAATGGATATGATGGCAGCGAATGTTGTCAAACAAGAGATACTTTGG  
 CAAGAAATATCGTCTCTGCTGAAATGCTCATGAAGATAATCTAAATCT  
 ATTGAAAATTGGTTGGAGTTATTGCTTTTATTGAATCGAGTCAAGCCGA  
 GGCTGCTAATCGTGCAAGCCACTTACAACAGAAATTCTAGCATTAGATA  
 GCCAAACGTCGAGTATCAAATTAAGTAACCAATTAGCTCGAATGACT  
 GAAGTTATCAATACCCTCGAACAGCAACATCCTGAATATGTCAGCCGTCT  
 CTACGTTGCATGGGCAACAACCAACAGATGCGAACTTGGTCAAGTAT  
 CGTCAGATATGCGTCAGAACTTGGCATGTTACGTCGAAATACCAATCCA  
 ACAATGAACTCTCAATCGCTCAGTTAGGCATGATGCAACAATCTGTCAA  
 ATCCGGTGTCACTGCTGATGCTATTGTCAACGCTAATAATGCAGCATTGC  
 AGATGCTGGCTGAACTAGTAAAGAAGCGATCCGATGTTAGAGAAGACC  
 GCACAAGCCCACTGTTTCTATTAAATCTGTCACTGCATTAGCTGAAAG  
 CTTAGTGGCTCAAAATAATGGTATTATCGCTGCCATAGACAAGGACGTA  
 AGGAACGTGCCCaATTGGAATCTGCTGTTATTAAATCGGCTGAAACAATC  
 AATGATTCTGTCAAAATTCGTGATAAAAAAATAGTTGAAGCCTTACTCAA  
 CGAAGGTaAATCTACCCAAGAAAAGTTGATGAGTCT

SEQ ID NO. 5205

STRAIN M732

AGCGATACCTTTAAATTTTGATATTGACCAAATTGCAGAC  
 AATGCTATCACTAAAACAGATAAAAACAAGAAATTTATTTCCAACCAGAC  
 AACAGGCCAACTGGGCAAAATGCCITTTTTGAAAACTAACACCAGCAC  
 AAAAGTCTGCTATCTCTGAAAAAACACCAAGCTTTGGTAGATACTTTTGT  
 GGTGACCAAAATGCCCTCCTTGATTTTGGACAATCCGCGTAGAAGGCGT  
 TAATACTACTGTTAATCATATCTTGTCTGAGCAGAAAAAATTCAAATTC  
 CTCAGTTGATGATTTACTAAAAATGCTAATCGCGAACTAAATGGATT  
 ATTGCCAAATATAAAGATGCTACTCCGGCAGAAATTAGAGAAAAAACCAAA  
 CTTGATTCAAAAAATTATTCAAACAAGCAAGACCTCGCTACAGGAATTTT  
 ATTTTGACTCACAAAACATCGAGCAAAAAATGGATATGATGGCAGCAAAAT  
 GTTGTCAAACAAGAGATACTTTGGCAAGAAATATCGTCTCTGCTGAAAT  
 GCTCATTGAAGATAATACTAAATCTATTGAAAATTTGGTTGGAGTTATTG  
 CTTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTA  
 CAACAAGAAATTTAGCATTAGATAGCAAAACGTCGGAATATCAAATTAA  
 AGTAACCAATTAGCCCAATGACTGAAGTTATCAATACCCTCGAACAGC  
 AACATCGGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACCA  
 CAGATGCGAACTTGGTCAAAGTATCGTCAGATATGCGTCAGAACTTGG  
 TAGTGTACGTCGAAATACCAATCCAACAATGAACTCTCAATCGCTCAGT  
 TAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATT  
 GTCACCGCTAATAATGCAGCATTGCAAAATGCTGGCTGAAACTAGTAAAGA  
 AGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCACTGTTTCTATTA  
 AATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAATGGTATT  
 ATCGCTGCCATAGACAAGGACGTAAGGAACGTCGCCAATTAGAATCTGC  
 TGTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAAATTCGTGATA  
 AAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAAGAAAAA  
 G

SEQ ID NO. 5206

STRAIN COH1

CTAAAAACAGATAAAAACAAGAAATTTTCCAACCAGACAACAAGCCAA  
 ACTGGGCAAAATGCCITTTTTGAAAACTAACACCAGCACAAAAGTCTGC  
 TWTCTCTGAAAAAACACCAAGCTTTGGTAGATACTTTTGTGGTGACCAAA  
 ATGCGCTCCTTGATTTTGGACAATCCGCGTAGAAGGCGTTAATACTACT  
 GTTAAATCATATCTTGTCTGAGCAGAAAAAATTCAAATTCCTCAAGTTGA  
 TGATTTACTAAAAATGCTAATCGCGAACTAAATGGATTATTGCCAAAT  
 ATAAAGATGCTACTCCGGCaGAATTAGAGAAAAAACCAAACTTGATTCAA  
 AATATTCTCAAACAAGCAAGACCTCGCTACAGGAATTTATTTTGACTC  
 ACAAAACATCGAGCAAAAAATGGATATGATGGCAGCAAAATGTTGTCAAAC  
 AAGAAGTACTTTTGGCAAGAAATATCGTCTCTGCTGAAATGCTCATTGAA  
 GATAATACTAAATCTATTGAAAATTTGGTTGGAGTTATTGCTTTTATTGA  
 ATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTACAACAAGAAA  
 TTCTAGCaATTAGATAGCCAAACGTCGGAATATCAAATTAAGTAACCAA  
 TTAGCCCGAATGACTGAaGTTATCaTaCCCTCGAACAGCAACATACGGA  
 aTATGTCAGCCGTCTCTACGTTGCATGGGCAACAACCAACAGATGCGAA  
 ACTTGGTCAAAGTATCGTCAGATATGCGTCAGAACTTGGTATGTTACGT  
 CGAAATACCAATCCAACAATGAACTCTCAATCGCTCAGTTAGGCATGAT  
 GCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATTGTCAACGCTA  
 ATAATGCAGCATTGCAAATGCTGGCTGAACTAGTAAAGAAGCGATTCCG  
 ATGTTAGAGAAGACCGCACAAAGCCCACTGTTTCTATTAAATCTGTCAC

Table 52: Comparative Sequences relating to SAG 1823

TGCATTAGCTGAAAGCTTAGTGGCTCAAATAATGGTATTATCGCTGCCA  
TAGACAAAGGACGTAAGGAACGTGCCCAATTAGAATCTGCTGTTATTAA  
TCGGCTGAAACAATCAATGATTCTGTCAAATTCGTGATAAAAAAATAGT  
TGAAGCCCTACTCAaCGAAGGTAAATCTACCCAAGAAAAAGTTGATGAGT  
CT

SEQ ID NO. 5207

STRAIN M781

TTTTGATATTGACCAAATTCAGACAATGCTATCACTAAAACAGATAAAA  
CAACAGAAATTATTTCCAACCAGACAACAAGCCAACTGGGCAAAATGGCC  
TTTTTTGAAAACTAACACCAGCACAAAAGTCTGCTATCTCTGAAAAAC  
ACCAGCTTTGGTAGATACTTTTGTGCGGTGACCAAAATGCGCTCCTTGATT  
TTGGACAATCCGCGAGTAGAAGGCGTTAATACTACTGTATAATCATATCTTG  
TCTGAGCAGAAAAAATTCAAATTCCTCAAGTTGATGATTTACTAAAAAA  
TGCTAATCGCGAACTAAATGGATTATTGCGCAATATAAGATGCTACTC  
CGGCAGAATTAGAGAAAAACCAACTTGATTCAAAAATTATTCAAACAA  
AGCAAGACCTCGCTACAGGAATTTTATTTTGACTCACAAAACATCGAGCA  
AAAAATGGATATGATGGCAGCAAAATGTTGTCAAACAAGAAGATACTTTGG  
CAAGAAATATCGTCTCTGCTGAAATGCTCATGAAGATAAATACTAAATCT  
ATTGAAAAATTGGTTGGAGTTATTGCTTTTATTGAATCGAGTCAAGCCGA  
GGCTGCCAATCGTGCAAGCCACTTACAACAAGAAATCTAGCATTAGATA  
GCCAAACGTCGGAATATCAAATTAAGTAACCAATTAGCCCGAATGACT  
GAAGTTATCAATACCCCTCGAACAGCAACATACGGAATATGTCAGCCGTCT  
CTACGTTGATGGGCAACAACACCACAGATGCGAACTTGGTCAAAGTAT  
CGTCAGATATGCGTCAGAAACTTGGTATGTTACGTCGAAATACCATTTCCA  
ACAATGAACTCTCAATCGCTCAGTTAGGCATGATGCAACAATCTGTCAA  
ATCCGGTGTCACTGCTGATGCTATTGTCAACGCTAATAATGCAGCATTGC  
AAATGCTGGCTGAACTAGTAAAGAAGCGATTCCGATGTTAGAGAAGACC  
GCACAAAGCCCCACTGTTTCTATTAATCTGTCACTGCATTAGCTGAAAG  
CTTAGTGGCTCAAATAATGGTATTATCGCTGCCATAGACAAAGGACGTA  
AGGAACGTGCCCAATTAGAATCTGCTGTTTAAATCGGCTGAAACAATC  
AATGATTCTGTCAAATTCGTGATAAAAAAATAGTTGAAGCCTTACTCAA  
CGAAGGTAAATCTACCCAAGAAAAAGTTGATGAGTCT

SEQ ID NO. 5208

STRAIN CJB110

TTTTGATATTGACCAAATTCAGACAATGCTATCACTAAAACAGATAAAA  
CAACAGAAATTATTTCCAACCAGACAACAAGCCAACTGGGCAAAATGGCC  
TTTTTTGAAAACTAACACCAGCACAAAAGTCTGCTATCTCTGAAAAAC  
ACCAGCTTTGGTAGATACTTTTGTGCGCGATCAAATGCGCTCCTTGATT  
TTGGACAATCCGCGAGTAGAAGGCGTTAATACTACTGTATAATCATATCTTG  
TCTGAGCAGAAAAAATTCAAATTCCTCAAGTTGATGATTTACTAAAAAA  
TGCTAATCGCGAACTAAATGGATTATTGCGCAATATAAGATGCTACTC  
CGGCAGAATTAGAGAAAAACCAACTTGATTCAAAAATTATTCAAACAA  
AGCAAGACCTCGCTACAGGAATTTTATTTTGACTCACAAAACATCGAGCA  
AAAAATGGATATGATGGCAGCAAAATGTTGTCAAACAAGAAGATACTTTGG  
CAAGAAATATCGTCTCTGCTGAAATGCTCATGAAGATAAATACTAAATCT  
ATTGAAAAATTGGTTGGAGTTATTGCTTTTATTGAATCGAGTCAAGCCGA  
GGCTGCTAATCGTGCAAGCCACTTACAACAAGAAATCTAGCATTAGATA  
GCCAAACGTCGAGTATCAAATTAAGTAACCAATTAGCTCGAATGACT  
GAAGTTATCAATACCCCTCGAACAGCAaCATACTGAATATGTCAGCCGTCT  
CTACGTTGATGGGCaCaACACCACAGATGCGAACTTGGTCAAAGTAT  
CGTCAGATATGCGTCAGAAACTTGGCATGTTACGTCGAAATACCATTTCCA  
ACAATGAACTCTCAATCGCTCAGTTAGGCATGATGCAACAATCTGTCAA  
ATCCGGTGTCACTGCTGATGCTATTGTCAACGCTAATAATGCAGCATTGC  
AGATGCTGGCTgAACTAGTAAAGAAGCGATTCCGATGTTAGAGAAGACC  
GCACAAAGCCCCACTGTTTCTATTAATCTGTCACTGCATTAGCTGAAAG  
CTTAGTGGCTCAAATAATGGTATTATCGCTGCCATAGACAAAGGACGTA  
AGGAACGTGCCCAATTGGAATCTGCTGTTTAAATCGGCTGAAACAATC  
AATGATTCTGTCAAATTCGTGATAAAAAAATAGTTGAAGCCTTACTCAA  
CGAAGGTAAATCTACCCAAGAAAAAGTTGATGAGTCT

SEQ ID NO. 5209

STRAIN 1169NT

GCAGACAATGCTATCACTAAAACAGATAAAACAACAGAAATTATTTCCA  
CCAGACAACAAGCCAACTGGGCAAAATGCGCTTTTGTGAAAACTAACAC  
CAGCACAAAAGTCTGCTATCTCTGAAAAACACCAGCTTTGGTAGATACT  
TTTGTGCGGTGACCAAAATGCGCTCCTTGATTTTGGACAATCCGAGTAGA  
AGGCGTTAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAATTC  
AAATTCCTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAAT  
GGATTATTGCGCAATATAAGATGCTACTCCGGCAGAATTAGAGAAAAA  
ACCAAACTTGATCCAAAAATTATTCAAACAAGCAAGACCTCACTACAGG  
AATTTTATTTTGACTCACAAAACATCGAGCAAAAAATGGATATGATGGCA  
GCAAAATGTTGTCAAACAAGAAGATACTTTGGCAAGAAATATCGTCTCTGC  
TGAATGCTCATGAAGATAATACTAAATCTATTGAAATTTGGTTGGAG  
TTATTGCTTTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGC  
CACTTACAACAAGAAATTTAGCATTAGATAGCCAAACGTCGGAGTATCA  
AATTAAGTAACCAATTAGCTCGAATGACTGAAGTTATCAATACCTCTCG  
AaCAGCAACATACTGAATATGTCAGCCGTCTCTACGTTGATGGGCAACA  
aCACCACAGATGCGAACTTGGTCAAAGTATCGTCAGATATGCGTCAAAA  
ACTTGGCATGTTACGTCGAAATACCAATTCACAACATGAACTCTCAATCG  
CTCAGTTAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGAT  
GCTATTGTCAACGCTAATAATGCAGCATTGCAGATGCTGGCTGAAACTAG

Table 52: Comparative Sequences relating to SAG 1823

TAAAGAAGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTT  
CTATTAAATCTGTCACTGCATTAGCTGAAAGCTTAGTGCGCTCAAATAAT  
GGTATTATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCAATTAGA  
ATCTGCTGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAATTC  
GTGATAAAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAA  
GAAAAAGTTGATGAGTCT

SEQ ID NO. 5210

STRAIN JM9130013

AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGAC  
AATGCTATCACTAAACAGATAAAACACAGAAATTATTTCCAACCAGAC  
AACAAGCCAAACTGGGCAAAATTGCCTTTTTTGA AAAA ACTAACACCAGCAC  
AAAAGTCTGCTATCTCTGAAAAAACACCAAGCTTTGGTAGATACCTTTGTC  
GGTGACCAAAATCGCTCCTTGATTTGGACAATCGCAGTAGAAGGCGT  
TAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAATCAAATTC  
CTCAAGTTGATGATTACTAAAAATGCTAATCGCGAACTAAATGGATT  
ATTGCCAAATATAAAGATGCTACTCGGCAGAAATTAGAGAAAAAACCAA  
CTTGATTCAAAAAATTATCAAACAAGCAGACCTCGCTACAGGAATTTT  
ATTTTGACTCACAACATCGAGCAAAAAATGGATATGATGGCAGCGAAT  
GTTGTCAAACAAGAGATACCTTGGCAAGAAATATCGTCTCTGCTGAAAT  
GCTCAITGAAGATAATACTAAATCTATTGAAAAATTGGTTGGAGTTATTG  
CTTTTATTGAATcGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTA  
CAACAAGAAATTCTAGCATTAGATAGCCAAACGTCGGAGTATCAAATtAA  
AAGTaACCAATTAGCTCGAATGACTGAAGTTATCAATACCCCTCGAACGAC  
AACATACCTGAATATGTGAGCGCTCTACGTTGCATGGGCAACAACACCA  
CAGATGCGAAACTTTGGTCAAAGTATCGTCAGATATGCGTCAAAAACTTGG  
CATGTTACGTCGAATACCAATCCAACATGAACTCTCAATCGCTCAGT  
TAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATT  
GTCAACGCTAATAATGACGATGTCAGATGCTGGCTGAAACTAGTAAAGA  
AGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATTA  
AATCTGTCACTGATTAGCTGAAAGCTTAGTGGCTCAAAATAATGTTATT  
ATCGCTGCCATAGACAAAGGACGTAAGGAACGTCGCCAATTAGAACTCTGC  
TGTATTAAATCCGCTGAAACAATCAATGATTCTGTCAAATTCGTGATA  
AAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAAGAAAAA  
GTTGATGAGTCT

SEQ ID NO. 5211

STRAIN 2603

agcgatacctttaattttgatattgaccaaattgcagacaatgctatcac  
taaaacagataaaaaaacagaaattttccaaccagacaacaagccaaa  
ctgggcaaatgtcctttttgaaaaactaacaccagcacaaaagtctgct  
atctctgaaaaaacaccagcttttggtagatacttttgcggcgatcaaaa  
tgcgctccttgatttttgacaatccgcagtagaaggcgcttaataccactg  
ttaatcatatcttgtctgagcagaaaaaaattcaaattcctcaagttgat  
gatttactaaaaaatgctaatcgcgaaactaaattggatttattgccaata  
taaatgctactcggcgagaatttagagaaaaaaccaacttgattcaaaa  
aatttattcaaacaaagcaagacctcgctacaggaattttattttgactca  
caaacatcgagcaaaaaatggatgatggcagcgaatgtgtcaaca  
agaagatactttggcaagaaatcgtctctgctgaaatgctcattgaag  
ataatactaaatctattgaaaatttggttgaggatttattgctttattgaa  
tcgagtcgaagcggaggtgctaatcgtgcaagccacttacaacaagaaat  
tctagcattagatagccaaacgtccgagatcaaataaaagtaaccaat  
tagctcgaatgactgaagttatcaataccctcgaacagcaacatcctgaa  
tatgtcagcgtctctacgttgcatgggcaacaacaccacagatgcgaaa  
cttggtcaaaagtatcgtcagatagcgtcagaaacttggtgctgtacgtc  
gaaataccattccaacaatgaaactctcaatcgctcagttaggcatgatg  
caacaatctgtcaaatccgggtgctcactgctgattgtcaacgctaa  
taatgcagcattgagatgctggtgaaactagtaagaagcgaattccga  
tgtagagaagaccgcacaaagccccactgtttctattaaatctgtcact  
gcattagctgaaagcttagtggtcaaaaataatggattatcgctgccat  
agacaaaggacgtaagggaacgtgcccattggaatctgctgttattaaat  
cggctgaaacaatcaatgattctgtcaaaattcgtgataaaaaaatagtt  
gaagccttactcaacgaaggttaattcaccgaagaaaagttgatgagtc  
t

PRETTY of: /biotmp/msa13607.2{\*} April 22, 2002 03:55 ..

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msa13607.2{201_090}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_CJB110}	-----	TTTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_18RS21}	-----	TTTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_2603}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_A909}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_H36B}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_JM9130013}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_1169NT}	-----	-----	-----	GCAGACA	ATGCTATCAC
msa13607.2{201_M732}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
Consensus	*****	*****	*****	*****	*****

Table 52: Comparative Sequences relating to SAG 1823

	51				100
msa13607.2{201_COH1}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_M781}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_090}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_CJB110}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_18RS21}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_2603}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_A909}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_H36B}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_JM9130013}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_1169NT}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
msa13607.2{201_M732}	TAAACAGAT	AAAACAACAG	AAATTATTTTC	CAACCAGACA	ACAaGCCAAA
Consensus	*****	*****	*****	*****	*****
	101				150
msa13607.2{201_COH1}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_M781}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_090}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_CJB110}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_18RS21}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_2603}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_A909}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_H36B}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_JM9130013}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_1169NT}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
msa13607.2{201_M732}	CTGGGCAAAT	TGCCTTTTTT	GAAAAACTAA	CACCAGCACA	AAAGTCTGCT
Consensus	*****	*****	*****	*****	*****
	151				200
msa13607.2{201_COH1}	wTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCG	GtGAcCAAAA
msa13607.2{201_M781}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCG	GtGAcCAAAA
msa13607.2{201_090}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCG	GcGatCAAAA
msa13607.2{201_CJB110}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCG	GcGatCAAAA
msa13607.2{201_18RS21}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCG	GcGatCAAAA
msa13607.2{201_2603}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCG	GcGatCAAAA
msa13607.2{201_A909}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCG	GtGAcCAAAA
msa13607.2{201_H36B}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCG	GtGAcCAAAA
msa13607.2{201_JM9130013}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCG	GtGAcCAAAA
msa13607.2{201_1169NT}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCG	GtGAcCAAAA
msa13607.2{201_M732}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT	ACTTTTGTCG	GtGAcCAAAA
Consensus	-*****	*****	*****	*****	*-***-*****
	201				250
msa13607.2{201_COH1}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATActACTG
msa13607.2{201_M781}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATActACTG
msa13607.2{201_090}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATAcCACTG
msa13607.2{201_CJB110}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATAcCACTG
msa13607.2{201_18RS21}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATAcCACTG
msa13607.2{201_2603}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATAcCACTG
msa13607.2{201_A909}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATAcCACTG
msa13607.2{201_H36B}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATAcCACTG
msa13607.2{201_JM9130013}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATAcCACTG
msa13607.2{201_1169NT}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATAcCACTG
msa13607.2{201_M732}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT	AGAAGGCGTT	AATActACTG
Consensus	*****	*****	*****	*****	*****-*****
	251				300
msa13607.2{201_COH1}	TTAATCATAT	CTTGCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_M781}	TTAATCATAT	CTTGCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_090}	TTAATCATAT	CTTGCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_CJB110}	TTAATCATAT	CTTGCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_18RS21}	TTAATCATAT	CTTGCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_2603}	TTAATCATAT	CTTGCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_A909}	TTAATCATAT	CTTGCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_H36B}	TTAATCATAT	CTTGCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_JM9130013}	TTAATCATAT	CTTGCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_1169NT}	TTAATCATAT	CTTGCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
msa13607.2{201_M732}	TTAATCATAT	CTTGCTGAG	CAGAAAAAAA	TTCAAATTCC	TCAAGTTGAT
Consensus	*****	*****	*****	*****	*****
	301				350
msa13607.2{201_COH1}	GATTTACTAA	AAAATGCTAA	TCGCGAATA	AATGGATTAA	TTGCCAAATA

Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_M781}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_090}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_CJB110}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_18RS21}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_2603}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_A909}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_H36B}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_JM9130013}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_1169NT}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_M732}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
Consensus	*****	*****	*****	*****	*****
351					
msa13607.2{201_COH1}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_M781}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_090}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_CJB110}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_18RS21}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_2603}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_A909}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_H36B}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_JM9130013}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_1169NT}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_M732}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
Consensus	*****	*****	*****	*****	*****
401					
msa13607.2{201_COH1}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_M781}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_090}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_CJB110}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_18RS21}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_2603}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_A909}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_H36B}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_JM9130013}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_1169NT}	AATTATTCAA	ACAAAGCAAG	ACCTCaCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_M732}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
Consensus	*****	*****	*****	*****	*****
451					
msa13607.2{201_COH1}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_M781}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_090}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_CJB110}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_18RS21}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_2603}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_A909}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_H36B}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_JM9130013}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_1169NT}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_M732}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
Consensus	*****	*****	*****	*****	*****
501					
msa13607.2{201_COH1}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_M781}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_090}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_CJB110}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_18RS21}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_2603}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_A909}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_H36B}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_JM9130013}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_1169NT}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_M732}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
Consensus	*****	*****	*****	*****	*****
551					
msa13607.2{201_COH1}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_M781}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_090}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_CJB110}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_18RS21}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA



Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_2603}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_A909}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAwTGC	TTTTATTGAA
msa13607.2{201_H36B}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_JM9130013}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_1169NT}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_M732}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
Consensus	*****	*****	*****	*****-***	*****
601					
msa13607.2{201_COH1}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_M781}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_090}	TCGAGTCAAG	CCGAGGCTGC	taATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_CJB110}	TCGAGTCAAG	CCGAGGCTGC	taATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_18RS21}	TCGAGTCAAG	CCGAGGCTGC	taATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_2603}	TCGAGTCAAG	CCGAGGCTGC	taATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_A909}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_H36B}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_JM9130013}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_1169NT}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_M732}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
Consensus	*****	*****	-*****	*****	*****
651					
msa13607.2{201_COH1}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaa	AGTAACCAAT
msa13607.2{201_M781}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaa	AGTAACCAAT
msa13607.2{201_090}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaa	AGTAACCAAT
msa13607.2{201_CJB110}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaa	AGTAACCAAT
msa13607.2{201_18RS21}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaa	AGTAACCAAT
msa13607.2{201_2603}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaa	AGTAACCAAT
msa13607.2{201_A909}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaa	AGTAACCAAT
msa13607.2{201_H36B}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaa	AGTAACCAAT
msa13607.2{201_JM9130013}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaa	AGTAACCAAT
msa13607.2{201_1169NT}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaa	AGTAACCAAT
msa13607.2{201_M732}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAaa	AGTAACCAAT
Consensus	*****	*****	*****-*	*****	*****
701					
msa13607.2{201_COH1}	TAGCcCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCgGAA
msa13607.2{201_M781}	TAGCcCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCgGAA
msa13607.2{201_090}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_CJB110}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_18RS21}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATcCtGAA
msa13607.2{201_2603}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATcCtGAA
msa13607.2{201_A909}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_H36B}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_JM9130013}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_1169NT}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_M732}	TAGCcCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCgGAA
Consensus	****-*****	*****	*****	*****	****-***
751					
msa13607.2{201_COH1}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_M781}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_090}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_CJB110}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_18RS21}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_2603}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_A909}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_H36B}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_JM9130013}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_1169NT}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_M732}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
Consensus	*****	*****	*****	*****	*****
801					
msa13607.2{201_COH1}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGt	ATGTTACGTC
msa13607.2{201_M781}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGt	ATGTTACGTC
msa13607.2{201_090}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_CJB110}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_18RS21}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_2603}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_A909}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	aAAACTTGGc	ATGTTACGTC

Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_H36B}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	aaAACTTGGc	ATGTTACGTC
msa13607.2{201_JM9130013}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	aaAACTTGGc	ATGTTACGTC
msa13607.2{201_1169NT}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	aaAACTTGGc	ATGTTACGTC
msa13607.2{201_M732}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGt	ATGTTACGTC
Consensus	*****	*****	*****	-*****-	*****
851					900
msa13607.2{201_COH1}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_M781}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_090}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_CJB110}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_18RS21}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_2603}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_A909}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_H36B}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_JM9130013}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_1169NT}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_M732}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
Consensus	*****	*****	*****	*****	*****
901					950
msa13607.2{201_COH1}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_M781}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_090}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_CJB110}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_18RS21}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_2603}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_A909}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_H36B}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_JM9130013}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_1169NT}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_M732}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
Consensus	*****	*****	*****	*****	*****
951					1000
msa13607.2{201_COH1}	TAATGCAGCA	TTGCAaATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_M781}	TAATGCAGCA	TTGCAaATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_090}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_CJB110}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_18RS21}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_2603}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_A909}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_H36B}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_JM9130013}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_1169NT}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_M732}	TAATGCAGCA	TTGCAaATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
Consensus	*****	*****-*****	*****	*****	*****
1001					1050
msa13607.2{201_COH1}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_M781}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_090}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_CJB110}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_18RS21}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_2603}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_A909}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_H36B}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_JM9130013}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_1169NT}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_M732}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
Consensus	*****	*****	*****	*****	*****
1051					1100
msa13607.2{201_COH1}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_M781}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_090}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_CJB110}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_18RS21}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_2603}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_A909}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_H36B}	GCATTAtCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_JM9130013}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_1169NT}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT

Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_M732}	GCATTAGCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
Consensus	*****-***	*****	*****	*****	*****
	1101				1150
msa13607.2{201_COH1}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_M781}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_090}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_CJB110}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_18RS21}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_2603}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_A909}	AGACAAAGGA	CGTAAaGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_H36B}	AGACAAAGGA	CGTAAaGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_JM9130013}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_1169NT}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_M732}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
Consensus	*****	*****-****	*****	*****	*****
	1151				1200
msa13607.2{201_COH1}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_M781}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_090}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_CJB110}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_18RS21}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_2603}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_A909}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_H36B}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_JM9130013}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_1169NT}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_M732}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
Consensus	*****	*****	*****	*****	*****
	1201				1250
msa13607.2{201_COH1}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_M781}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_090}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_CJB110}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_18RS21}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_2603}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_A909}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_H36B}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_JM9130013}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_1169NT}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_M732}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
Consensus	*****	*****	*****	*****	-----
	1251				
msa13607.2{201_COH1}	t				
msa13607.2{201_M781}	t				
msa13607.2{201_090}	t				
msa13607.2{201_CJB110}	t				
msa13607.2{201_18RS21}	t				
msa13607.2{201_2603}	t				
msa13607.2{201_A909}	t				
msa13607.2{201_H36B}	t				
msa13607.2{201_JM9130013}	t				
msa13607.2{201_1169NT}	t				
msa13607.2{201_M732}	~				
Consensus	-				

## SEQ ID NO. 5212

STRAIN\_090 frame: 1  
SDTFNFDIDQIADNATTKTDKTTETIISNQTTSQTGQIAFFEKLTPAQKSAISEKTPALVD  
TFVGDQNALDLFGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA  
TPAELEKPNLQKLFQSKTSLQEFYFDSQNIIEQKMDMMAANVVKQEDTLARNIVSAEM  
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQQEILALDSQTSYQIKSNQLARMTEV  
INTLEQQHTYVSRLYVAVATTQPMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM  
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAEISLVAQN  
NGIIAAIDKGRKERAQLESAAVSKAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

## SEQ ID NO. 52013

STRAIN\_A909 frame: 1  
SDTFNFDIDQIADNATTKTDKTTETIISNQTTSQTGQIAFFEKLTPAQKSAISEKTPALVD  
TFVGDQNALDLFGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA  
TPAELEKPNLQKLFQSKTSLQEFYFDSQNIIEQKMDMMAANVVKQEDTLARNIVSAEM

Table 52: Comparative Sequences relating to SAG 1823

LIEDNTKSIENLVGVXAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEV  
INTLEQQHTEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM  
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN  
NGIIAAIDKGRKERAQLESASAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

## SEQ ID NO. 5214

STRAIN H36B frame: 1

SDTFNFDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFFEKLTAPAKSAISEKTPALVD  
TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA  
TPAELEKKPNLIQKLFQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM  
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEV  
INTLEQQHTEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM  
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN  
NGIIAAIDKGRKERAQLESASAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

## SEQ ID NO. 5215

STRAIN 18RS21 frame: 2

FDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFFEKLTAPAKSAISEKTPALVDTFVGD  
QNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAEL  
EKKPNLIQKLFQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEMLIEDN  
TKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEVINTLE  
QQHPEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVK  
SGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIA  
AIDKGRKERAQLESASAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

## SEQ ID NO. 5216

STRAIN M732 frame: 1

SDTFNFDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFFEKLTAPAKSAISEKTPALVD  
TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA  
TPAELEKKPNLIQKLFQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM  
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEV  
INTLEQQHTEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM  
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN  
NGIIAAIDKGRKERAQLESASAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEK

## SEQ ID NO. 5217

STRAIN COH1 frame: 3

KTDKTEIISNQTTCTGTGQIAFFFEKLTAPAKSAXSEKTPALVDTFVGDQNALLDGQSAV  
EGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAELEKKPNLIQKLFK  
QSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEMLIEDNTKSIENLVGVIA  
FIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEVINTLEQQHTEYVSRLYV  
AVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTADAIVNAN  
NALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGRKERAQ  
LESASAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

## SEQ ID NO. 5218

STRAIN COH1 frame: 3

KTDKTEIISNQTTCTGTGQIAFFFEKLTAPAKSAXSEKTPALVDTFVGDQNALLDGQSAV  
EGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAELEKKPNLIQKLFK  
QSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEMLIEDNTKSIENLVGVIA  
FIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEVINTLEQQHTEYVSRLYV  
AVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTADAIVNAN  
NALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGRKERAQ  
LESASAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

## SEQ ID NO. 5219

STRAIN M781 frame: 2

FDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFFEKLTAPAKSAISEKTPALVDTFVGD  
QNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAEL  
EKKPNLIQKLFQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEMLIEDN  
TKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEVINTLE  
QQHTEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVK  
SGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIA  
AIDKGRKERAQLESASAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

## SEQ ID NO. 5220

STRAIN CJB110 frame: 2

FDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFFEKLTAPAKSAISEKTPALVDTFVGD  
QNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAEL  
EKKPNLIQKLFQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEMLIEDN  
TKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEVINTLE  
QQHTEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVK  
SGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIA  
AIDKGRKERAQLESASAVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

## SEQ ID NO. 5221

STRAIN 1169NT frame: 1

ADNAITKTDKTEIISNQTTSTGTGQIAFFFEKLTAPAKSAISEKTPALVDTFVGDQNALLD  
FGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAELEKKPNLI  
QKLFQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEMLIEDNTKSIEN  
LVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEVINTLEQQHTEY  
VSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTAD  
AIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGR

Table 52: Comparative Sequences relating to SAG 1823

KERAQLES AVIKSAETINDSVKIRDKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5222

STRAIN JM9130013 frame: 1

SDTFNFDIDQIADNAITKTDKTEIISNQTTSQTGQIAFFEKLTTPAQKSAISEKTPALVD  
 TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIIPQVDDLLKNANRELNGFIAKYKDA  
 TPAALEKKPNLIQKLFQKSKTSQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM  
 LIEDNTKSIENLVGVIAFIESSQAEANRASHLQQEILALDSQTSEYQIKSNQLARMTEV  
 INTLEQQHPEYVSRLYVAWATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM  
 QQSVKSGVTADAI VNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN  
 NGIIAAIDKGRKERAQLES AVIKSAETINDSVKIRDKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5223

STRAIN 2603 frame: 1

SDTFNFDIDQIADNAITKTDKTEIISNQTTSQTGQIAFFEKLTTPAQKSAISEKTPALVD  
 TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIIPQVDDLLKNANRELNGFIAKYKDA  
 TPAALEKKPNLIQKLFQKSKTSQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM  
 LIEDNTKSIENLVGVIAFIESSQAEANRASHLQQEILALDSQTSEYQIKSNQLARMTEV  
 INTLEQQHPEYVSRLYVAWATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM  
 QQSVKSGVTADAI VNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN  
 NGIIAAIDKGRKERAQLES AVIKSAETINDSVKIRDKIVEALLNEGKSTQEKVDES

PRETTY of: /biotmp/msa28369.2{\*} April 22, 2002 04:27 ..

	1				50
msa28369.2{201_090}	sdtfnfdidq	iadnaitKTD	KTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_1169NT}	-----	-adnaitKTD	KTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_A909}	sdtfnfdidq	iadnaitKTD	KTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_JM9130013}	sdtfnfdidq	iadnaitKTD	KTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_COH1}	-----	-----KTD	KTEIISNQT	TcQTGQIAFF	EKLTPAQKSA
msa28369.2{201_CJB110}	-----fdidq	iadnaitKTD	KTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_M781}	-----fdidq	iadnaitKTD	KTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_2603}	sdtfnfdidq	iadnaitKTD	KTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_H36B}	sdtfnfdidq	iadnaitKTD	KTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_18RS21}	-----fdidq	iadnaitKTD	KTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_M732}	sdtfnfdidq	iadnaitKTD	KTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
Consensus	-----	-----***	*****	*-----	*****
	51				100
msa28369.2{201_090}	isektpalvd	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_1169NT}	isektpalvd	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_A909}	isektpalvd	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_JM9130013}	isektpalvd	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_COH1}	xsektpalvd	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_CJB110}	isektpalvd	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_M781}	isektpalvd	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_2603}	isektpalvd	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_H36B}	isektpalvd	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_18RS21}	isektpalvd	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_M732}	isektpalvd	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
Consensus	-*****	*****	*****	*****	*****
	101				150
msa28369.2{201_090}	DLLKNANREL	NGFIAKYKDA	TPAALEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_1169NT}	DLLKNANREL	NGFIAKYKDA	TPAALEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_A909}	DLLKNANREL	NGFIAKYKDA	TPAALEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_JM9130013}	DLLKNANREL	NGFIAKYKDA	TPAALEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_COH1}	DLLKNANREL	NGFIAKYKDA	TPAALEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_CJB110}	DLLKNANREL	NGFIAKYKDA	TPAALEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_M781}	DLLKNANREL	NGFIAKYKDA	TPAALEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_2603}	DLLKNANREL	NGFIAKYKDA	TPAALEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_H36B}	DLLKNANREL	NGFIAKYKDA	TPAALEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_18RS21}	DLLKNANREL	NGFIAKYKDA	TPAALEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_M732}	DLLKNANREL	NGFIAKYKDA	TPAALEKKPN	LIQKLFQKSK	TSLQEFYFDS
Consensus	*****	*****	*****	*****	*****
	151				200
msa28369.2{201_090}	QNI EQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_1169NT}	QNI EQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_A909}	QNI EQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_JM9130013}	QNI EQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_COH1}	QNI EQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_CJB110}	QNI EQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_M781}	QNI EQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_2603}	QNI EQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_H36B}	QNI EQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE

Table 52: Comparative Sequences relating to SAG 1823

msa28369.2{201_18RS21}	QNIEQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_M732}	QNIEQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
Consensus	*****	*****	*****	*****	*****
201					
msa28369.2{201_090}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_1169NT}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_A909}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_JM9130013}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_COH1}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_CJB110}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_M781}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_2603}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_H36B}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_18RS21}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_M732}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
Consensus	*****	*****	*****	*****	*****
251					
msa28369.2{201_090}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_1169NT}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_A909}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_JM9130013}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_COH1}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_CJB110}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_M781}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_2603}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_H36B}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_18RS21}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_M732}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
Consensus	*****	*****	*****	*****	*****
301					
msa28369.2{201_090}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_1169NT}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_A909}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_JM9130013}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_COH1}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_CJB110}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_M781}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_2603}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_H36B}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_18RS21}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_M732}	QQSVKSGVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
Consensus	*****	*****	*****	*****	*****
351					
msa28369.2{201_090}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_1169NT}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_A909}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_JM9130013}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_COH1}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_CJB110}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_M781}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_2603}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_H36B}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_18RS21}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_M732}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
Consensus	*****	*****	*****	*****	*****
401					
msa28369.2{201_090}	EALLNEGKST	QEKvdes			
msa28369.2{201_1169NT}	EALLNEGKST	QEKvdes			
msa28369.2{201_A909}	EALLNEGKST	QEKvdes			
msa28369.2{201_JM9130013}	EALLNEGKST	QEKvdes			
msa28369.2{201_COH1}	EALLNEGKST	QEKvdes			
msa28369.2{201_CJB110}	EALLNEGKST	QEKvdes			
msa28369.2{201_M781}	EALLNEGKST	QEKvdes			
msa28369.2{201_2603}	EALLNEGKST	QEKvdes			
msa28369.2{201_H36B}	EALLNEGKST	QEKvdes			
msa28369.2{201_18RS21}	EALLNEGKST	QEKvdes			
msa28369.2{201_M732}	EALLNEGKST	QEKvdes			
Consensus	*****	*****			
417					
msa28369.2{201_090}	EALLNEGKST	QEKvdes			
msa28369.2{201_1169NT}	EALLNEGKST	QEKvdes			
msa28369.2{201_A909}	EALLNEGKST	QEKvdes			
msa28369.2{201_JM9130013}	EALLNEGKST	QEKvdes			
msa28369.2{201_COH1}	EALLNEGKST	QEKvdes			
msa28369.2{201_CJB110}	EALLNEGKST	QEKvdes			
msa28369.2{201_M781}	EALLNEGKST	QEKvdes			
msa28369.2{201_2603}	EALLNEGKST	QEKvdes			
msa28369.2{201_H36B}	EALLNEGKST	QEKvdes			
msa28369.2{201_18RS21}	EALLNEGKST	QEKvdes			
msa28369.2{201_M732}	EALLNEGKST	QEKvdes			
Consensus	*****	*****			

Table 53: Comparative Sequences relating to SAG 0755

## SEQ ID NO. 5301

## STRAIN 2603

acaaataactttgaaaaaagaatttagttgaagctaaaaagacaattccatc  
cgtaaaagcttcaaaagtaccgcaaaaatcaacatcatcgaaagataaag  
agtttgttcttaaacgattatcgatgtctctggttggcaacttcctaag  
gagattgattacgatacgctttcaaaaaatatttcaggtgtgttatttcg  
tgtctttggtggatcaaagatatctaaagactaataacgctgcttatcaa  
ctggaatcgataaatacggtttaagaccatatacaagaatttcaaaagcga  
aatatcccagtagctgtctacagttatgcacttgggttcaagtggttaaaga  
aatgaaagaagaggctcagatatatttataagaatgcagctccttacaac  
caactttttattggattgacgtagaagaggagacaatgtctaactgaat  
aaaggtgtccaagcattccgaaagaattaaaaagacttgggtgctaaaaa  
tggttggtatctacattgggtacttactttatgactgagcaaggcatctctg  
taaaaggatttgacgctgttttggattccaacttatggtagcgattctgga  
tactatgaagcggtccgcaaaactgaacttaaatacgatttacaccaata  
cacctctcaagggttatctaccaggawtcaatcaaccgcttgatttaaatc  
aaattgcagttaataaagacaagaagaaaacttatgagaaacttttggga  
aaagtaaaagag

## SEQ ID NO. 5302

## STRAIN 090

ACAAATACTTTGAAAAAAGAATTAG  
TTGAAGCTAAAAAGACAATTCCATCCGTAAAAGCTTCAAAGTACCGCAA  
AAATCAACATCATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGA  
TGTCTCTGTTGGCAACTTCTTAAGGAGATTGATTACGATACGCTTTCAA  
AAAATATTTCAAGTGTGTATTTCGTGTCTTTGGTGGATCAAAGATATCT  
AAGACTAATAAACGCTGCTTATACAACTGGAATCGATAAATCGTTAAGAC  
CCATATCAAGAATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTT  
ATGCACCTTGGTTCAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTT  
TATAAGAATGCAGCTCCTTACAAACCAACTTTTATTGGATTGACGTAGA  
AGAGGAGACAATGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAG  
AATTAAAAAGACTTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTAC  
TTTATGACTGAGCAAGGCATCTCTGTAAAAGGATTGACGCTGTTTGGAT  
TCCAACCTTATGGTAGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTG  
AACTTAAATACGATTACACCAATACACCTCTCAAGGTTATCTACCAGGA  
TTCAATCAACCGCTTGATTAAATCAAATTGCAGTTAATAAAGACAAGAA  
GAAAACCTTATGAGAACTTTTGGAAAAGTAAAAGAG

## SEQ ID NO. 5303

## STRAIN A909

ACAAATACTTTGAAAAAAGAATTAGTTGAAGCTAAAA  
AGACAATTCCATCCGTAAAAGCTTCAAAGTACCGCAAAATCAACATCA  
TCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGTTG  
GCAACTTCTTAAGGAGATTGATTACGATACGCTTTCAAATAATATTTAG  
GTGTTGTATTTCGTGTCTTTGGTGGATCAAAGATATCTAAGACTAATAAC  
GCTGCTTATACAACTGGAATCGATAAATCGTTAAGACCCATATCAAAGA  
ATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTTATGCACTTGGTT  
CAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTTTATAAGAAATGCA  
GCTCCTTACAAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAAT  
GTCTAAGATGAATAAAGGTGTCCAAGCATTCCGAAAAGAAATTAAGAAGAC  
TTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTACTTTATGACTGAG  
CAAGGCATCTCTGTAAAAGGATTGACGCTGTTTGGATTCCAACCTTATGG  
TAGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTGAACCTTAATACG  
ATTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCG  
CTTGATTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAACCTATGA  
GAAACTTTTGGAAAAGTAAAAGAG

## SEQ ID NO. 5304

## STRAIN H36B

ACAAATACTTTGAAAAAAGAATTAG  
TTGAAGCTAAAAAGACAATTCCATCCGTAAAAGCTTCAAAGTACCGCAA  
AAATCAACATCATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGA  
TGTCTCTGTTGGCAACTTCTTAAGGAGATTGATTACGATACGCTTTCAA  
AAAATATTTCAAGTGTGTATTTCGTGTCTTTGGTGGATCAAAGATATCT  
AAGACTAATAACGCTGCTTATACAACTGGAATCGATAAATCGTTAAGAC  
CCATATCAAGAATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTT  
ATGCACCTTGGTTCAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTT  
TATAAGAATGCAGCTCCTTACAAACCAACTTTTATTGGATTGACGTAGA  
AGAGGAGACAATGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAG  
AATTAAAAAGACTTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTAC  
TTTATGACTGAGCAAGGCATCTCTGTAAAAGGATTGACGCTGTTTGGAT  
TCCAACCTTATGGTAGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTG  
AACTTAAATACGATTACACCAATACACCTCTCAAGGTTATCTACCAGGA  
TTCAATCAACCGCTTGATTAAATCAAATTGCAGTTAATAAAGACAAGAA  
GAAAACCTTATGAGAACTTTTGGAAAAGTAAAAGAG

## SEQ ID NO. 5305

## STRAIN 18R821

ACAAATACTTTGAAAAAAGAATTAGTTGAAGCTAAAA  
GACAAATCCATCCGTAAAAGCTTCAAAGTACCGCAAAATCAACATCAT  
CGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGTTGG  
CAACTTCTTAAGGAGATTGATTACGATACGCTTTCAAATAATATTTCAAG  
TGTTGTTATTCTGTGTCTTTGGTGGATCAAAGATATCTAAGACTAATAACG

Table 53: Comparative Sequences relating to SAG 0755

CTGCTTATACAACTGGAATCGATAAATCGTTTAAAGACCCATATCAAAGAA  
 TTTCAAAAGCGAAATATCCAGTAGCTGTCTACAGTTATGCACTTGGTTC  
 AAGTGTAAAGAAATGAAGAAGAGGCTCAGATATTTATAAGAAATGCAG  
 CTCTTACAAACCAACTTTTATTTGGATTGACGTAGAAGAGGAGACAATG  
 TCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAAATAAAAAGACT  
 TGGTGTCTAAAAATGTTGGTATCTACATTGGTACTTACTTTATGACTGAGC  
 AAGGCATCTCTGTAAAAGGATTGACGCTGTTGGATTCCAACCTTATGGT  
 AGCGATTCTGGATACTATGAAGCGGCTCCGCAAACTGAACTTAATACGA  
 TTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCGC  
 TTGATTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTATGAG  
 AAACCTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5306  
 STRAIN M732

ACAAATACTTTGAAAAAGAATTAGTTGAAGCTAAA  
 AAGACAATTCCATCCGTAAAAGCTTCAAAGTACCGCAAAAATCAACATC  
 ATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTT  
 GGCAACTTCTTAAGGAGATTGATTACGATACGCTTCAA AAAATATTTCA  
 GGTGTTGTTTATTCGTATCTTGGTGGATCAAAGATATCTAAGACTAATAA  
 CGCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGACCCATATCAAAG  
 AATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTTATGCACTTGGT  
 TCAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTTATAAGAAATGC  
 AGCTCCTTACAAAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAA  
 TGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAGTTAAAAAGA  
 CTGGTGCTAAAAATGTTGGTATCTACATCGGTACTTACTTTATGACTGA  
 GCAAGGTATCTCTGTAAAAGGATTGACGCTGTTGGATTCCAACCTTATG  
 GTAGCGATTCTGGATACTATGAAGCAGCTCCACAACTGAACTTAAATAC  
 GATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACC  
 GCTTGATTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTTATG  
 AGAACTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5307  
 STRAIN COH1

ACAAATACTTTGAAAAAGAATTAGTTGAAGCTAAA  
 AGACAATTCCATCCGTAAAAGCTTCAAAGTACCGCAAAAATCAACATCA  
 TCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTTG  
 GCAACTTCTTAAGGAGATTGATTACGATACGCTTCAA AAAATATTTCA  
 GTGTTGTTTATTCGTATCTTGGTGGATCAAAGATATCTAAGACTAATAAC  
 GCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGACCCATATCAAAGA  
 AITTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTTATGCACTTGGTT  
 CAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTTATAAGAAATGCA  
 GCTCCTTACAAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAAT  
 GTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAGTTAAAAAGAC  
 TTGGTGCTAAAAATGTTGGTATCTACATCGGTACTTACTTTATGACTGAG  
 CAAGGTATCTCTGTAAAAGGATTGACGCTGTTGGATTCCAACCTTATGG  
 TAGCGATTCTGGATACTATGAAGCAGCTCCACAACTGAACTTAAATACG  
 AITTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCG  
 CTTGATTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTTATGA  
 GAACTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5308  
 STRAIN M781

ACAAATACTTTGAAAAAGAATTAGTTGAAGCTAAA  
 AAGACAATTCCATCCGTAAAAGCTTCAAAGTACCGCAAAAATCAACATC  
 ATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTT  
 GGCAACTTCTTAAGGAGATTGATTACGATACGCTTCAA AAAATATTTCA  
 GGTGTTGTTTATTCGTATCTTGGTGGATCAAAGATATCTAAGACTAATAA  
 CGCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGACCCATATCAAAG  
 AATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTTATGCACTTGGT  
 TCAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTTATAAGAAATGC  
 AGCTCCTTACAAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAA  
 TGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAGTTAAAAAGA  
 CTGGTGCTAAAAATGTTGGTATCTACATCGGTACTTACTTTATGACTGA  
 GCAAGGTATCTCTGTAAAAGGATTGACGCTGTTGGATTCCAACCTTATG  
 GTAGCGATTCTGGATACTATGAAGCAGCTCCACAACTGAACTTAAATAC  
 GATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACC  
 GCTTGATTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTTATG  
 AGAACTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5309  
 STRAIN CJB110

AAATACTTTGAAAAAGAATTAGTTGAAGCTAAAAGACAATTCCATCCG  
 TAAAGCTTCAAAGTACCGCAAAAATCAACATCATCGAAAGATAAAGAG  
 TTTGTTCTTAAACCGATTATCGATGTCTCTGGTTGGCAACTTCTTAAGGA  
 GATTGATTACGATACGCTTCAA AAAATATTTCAAGGTGTTGTTATTCGTG  
 TCTTTGGTGGATCAAAGATATCTAAGACTAATAACGCTGCTTATACAACT  
 GGAATCGATAAATCGTTTAAAGACCCATATCAAAGAAATTTCAAAGCGAAA  
 TATCCAGTAGCTGTCTACAGTTATGCACTTGGTTCAAGTGTAAAGAAA  
 TGAAGAAGAGGCTCAGATATTTATAAGAAATGCAGCTTCTTACAAACCA  
 ACTTTTATTGGATTGACGTAGAAGAGGAGACAATGTCTAACATGAATAA  
 AGGTGCTCAAGCATTCCGAAAAGAAATTAAGAAGACTTGGTGCTAAAAATG  
 TTGGTATCTACATTTGGTACTTACTTTATGACTGAGCAAGGCATCTCTGTA  
 AAAGGATTGACGCTGTTTGGATTCCAACCTATGGTAGCGATTCTGGATA



Table 53: Comparative Sequences relating to SAG 0755

CTATGAAGCGGCTCCGCAAACTGAACCTAAATACGATTTACACCAATACA  
CCTCTCAAGGTTATCTACCAGGATTCAATCAACCGCTTGATTTAAATCAA  
ATTACAGTTAATAAGACAAGAAGAAACTTTATGAGAACTTTTGGAAA  
AGTAAAGAG

SEQ ID NO. 5310

STRAIN 1169NT

ACAAATACTTTGAAAAAGAATTAGTTGAAGCTAAAAAGACAATTCC  
ATCCGTAAAGCTTCAAAAGTACCGCAAAATCAACATCATCGAAAGATA  
AAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTTGGCACTTCCT  
AAGGAGATTGATTACGATACGCTTTCAAAAAATATTTCAGGTGTGTTAT  
TCGTGTCTTTGGTGGATCAAGATATCTAAGACTAATAACGCTGCTTATA  
CAACTGGAATCGATAAATCCTTTAAGACCCATATCAAGAATTTCAAAAG  
CGAAATATCCAGTAGCTGTCTACAGTTATGCACTTGGTTCAAGTGTAA  
AGAAATGAAAGAGAGGCTCAGATATTTATAAGATGCAAGCTCCTTACA  
AACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAATGTCTAACATG  
AATAAAGGTGTCCAAGCATTCCGAAAAGAATTAAAAAGACTTGGCGCTAA  
AAATGTTGGTATCTACATCGGTACTTACTTTATGACTGAGCAAGGTATCT  
CTGTAAAGGATTGACGCTGTTTGGATTCCAACCTATGGTAGCGATTCT  
GGATACATGAAAGCAGCTCCGCAAACTGAACCTAAATACGATTTACACCA  
ATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCGCTTGATTTAA  
ATCAAATTGCAGTTAATAAGACAAGAAGAAACTTTATGAGAACTTTT  
GGAAAAGTAAAGAG

SEQ ID NO. 5311

STRAIN JM9130013

ACAAATACTTTGAAAAAGAATTAG  
TTGAAGCTAAAAAGACAATTCCATCCGTAAAGCTTCAAAAGTACCGCAA  
AAATCAACATCATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGA  
TGCTCTGGTTGGCACTTCTAAGGAGATTGATTACGATACGCTTTCAA  
AAAATATTTCAAGGTGTGTTATTCTGTCTTTGGTGGATCAAAGATATCT  
AAGACTAATAACGCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGAC  
CCATATCAAAGAATTTCAAAAGCGAAATATCCAGTAGCTGTCTACAGTT  
ATGCACCTTGGTTCAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTT  
TATAAGAAATGCAGCTCCTTACAAACCACTTTTATTGGATTGACGTAGA  
AGAGGAGACAATGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAG  
AATTAAAAAGACTTGGTGTCTAAAAATGTTGGTATCTACATTGGTACTTAC  
TTTATGACTGAGCAAGGCATCTCTGTAAAGGATTGACGCTGTTTGGAT  
TCCAACCTATGGTAGCGATTCTGGATACATGAAAGCGGCTCCGCAAACTG  
AATCTAAATACGATTACACCAATACACCTCTCAAGGTTATCTACCAGGA  
TTCAATCAACCGCTTGATTTAAATCAAATTGCAGTTAATAAGACAAGAA  
GAAACTTATGAGAACTTTTGGAAAAGTAAAGAG

PRETTY of: /biotmp/msa21441.2{\*} January 20, 2003 03:46 ...

	1				50
msa21441.2{206_090}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_18RS21}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_2603}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_A909}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_H36B}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_JM9130013}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_CJB110}	--AAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_COH1}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_M732}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_M781}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
msa21441.2{206_1169NT}	acAAATACTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCCATC
	Consensus	*****	*****	*****	*****
	51				100
msa21441.2{206_090}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_18RS21}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_2603}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_A909}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_H36B}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_JM9130013}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_CJB110}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_COH1}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_M732}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_M781}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_1169NT}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
	Consensus	*****	*****	*****	*****
	101				150
msa21441.2{206_090}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_18RS21}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_2603}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_A909}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_H36B}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_JM9130013}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_CJB110}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_COH1}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_M732}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG

Table 53: Comparative Sequences relating to SAG 0755

msa21441.2{206_M781}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_1169NT}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	151				200
msa21441.2{206_18RS21}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_2603}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_A909}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_H36B}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_JM9130013}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_CJB110}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_COH1}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_M732}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_M781}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
msa21441.2{206_1169NT}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	201				250
msa21441.2{206_18RS21}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_2603}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_A909}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_H36B}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_JM9130013}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_CJB110}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_COH1}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_M732}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_M781}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
msa21441.2{206_1169NT}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA
Consensus	*_*****	*****	*****	*****	*****
msa21441.2{206_090}	251				300
msa21441.2{206_18RS21}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA
msa21441.2{206_2603}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA
msa21441.2{206_A909}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA
msa21441.2{206_H36B}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA
msa21441.2{206_JM9130013}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA
msa21441.2{206_CJB110}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA
msa21441.2{206_COH1}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA
msa21441.2{206_M732}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA
msa21441.2{206_M781}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA
msa21441.2{206_1169NT}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	301				350
msa21441.2{206_18RS21}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_2603}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_A909}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_H36B}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_JM9130013}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_CJB110}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_COH1}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_M732}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_M781}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
msa21441.2{206_1169NT}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	351				400
msa21441.2{206_18RS21}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_2603}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_A909}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_H36B}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_JM9130013}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_CJB110}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_COH1}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_M732}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_M781}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
msa21441.2{206_1169NT}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	401				450
msa21441.2{206_18RS21}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_2603}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_A909}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_H36B}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_JM9130013}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_CJB110}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_COH1}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT

Table 53: Comparative Sequences relating to SAG 0755

msa21441.2{206_M732}	CAACTTTT	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_M781}	CAACTTTT	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
msa21441.2{206_1169NT}	CAACTTTT	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_18RS21}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_2603}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_A909}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_H36B}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_JM9130013}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_CJB110}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_COH1}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_M732}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_M781}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
msa21441.2{206_1169NT}	AAAGGTGTCC	AAGCATTCCG	AAAAGAAaTTA	AAAAGACTTG	GtGCTAAAAA
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_18RS21}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_2603}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_A909}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_H36B}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_JM9130013}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_CJB110}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_COH1}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_M732}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_M781}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
msa21441.2{206_1169NT}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_18RS21}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_2603}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_A909}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_H36B}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_JM9130013}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_CJB110}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_COH1}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_M732}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_M781}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
msa21441.2{206_1169NT}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA
msa21441.2{206_18RS21}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA
msa21441.2{206_2603}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA
msa21441.2{206_A909}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA
msa21441.2{206_H36B}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA
msa21441.2{206_JM9130013}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA
msa21441.2{206_CJB110}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA
msa21441.2{206_COH1}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA
msa21441.2{206_M732}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA
msa21441.2{206_M781}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA
msa21441.2{206_1169NT}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC
msa21441.2{206_18RS21}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC
msa21441.2{206_2603}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC
msa21441.2{206_A909}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC
msa21441.2{206_H36B}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC
msa21441.2{206_JM9130013}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC
msa21441.2{206_CJB110}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC
msa21441.2{206_COH1}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC
msa21441.2{206_M732}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC
msa21441.2{206_M781}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC
msa21441.2{206_1169NT}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC
Consensus	*****	*****	*****	*****	*****
msa21441.2{206_090}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA
msa21441.2{206_18RS21}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA
msa21441.2{206_2603}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA
msa21441.2{206_A909}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA
msa21441.2{206_H36B}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA
msa21441.2{206_JM9130013}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA
msa21441.2{206_CJB110}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA

Table 53: Comparative Sequences relating to SAG 0755

msa21441.2{206_COH1}	AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTGGGA
msa21441.2{206_M732}	AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTGGGA
msa21441.2{206_M781}	AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTGGGA
msa21441.2{206_1169NT}	AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTGGGA
Consensus	*****-**** ***** ***** ***** ***** *****

  

	751	762
msa21441.2{206_090}	AAAGTAAAAG AG	
msa21441.2{206_18RS21}	AAAGTAAAAG AG	
msa21441.2{206_2603}	AAAGTAAAAG AG	
msa21441.2{206_A909}	AAAGTAAAAG AG	
msa21441.2{206_H36B}	AAAGTAAAAG AG	
msa21441.2{206_JM9130013}	AAAGTAAAAG AG	
msa21441.2{206_CJB110}	AAAGTAAAAG AG	
msa21441.2{206_COH1}	AAAGTAAAAG AG	
msa21441.2{206_M732}	AAAGTAAAAG AG	
msa21441.2{206_M781}	AAAGTAAAAG AG	
msa21441.2{206_1169NT}	AAAGTAAAAG AG	
Consensus	***** **	

**SEQ ID NO. 5312**

STRAIN 2603 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE  
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYLHGYTSQGYLPGFNQPLDLNQIAVNKD  
 KKKTYEKLFGKVKE

**SEQ ID NO. 5313**

STRAIN 090 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE  
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYLHGYTSQGYLPGFNQPLDLNQIAVNKD  
 KKKTYEKLFGKVKE

**SEQ ID NO. 5314**

STRAIN A909 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE  
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYLHGYTSQGYLPGFNQPLDLNQIAVNKD  
 KKKTYEKLFGKVKE

**SEQ ID NO. 5315**

STRAIN H36B frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE  
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYLHGYTSQGYLPGFNQPLDLNQIAVNKD  
 KKKTYEKLFGKVKE

**SEQ ID NO. 5316**

STRAIN 18RS21 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE  
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYLHGYTSQGYLPGFNQPLDLNQIAVNKD  
 KKKTYEKLFGKVKE

**SEQ ID NO. 5317**

STRAIN M732 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE  
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYLHGYTSQGYLPGFNQPLDLNQIAVNKD  
 KKKTYEKLFGKVKE

**SEQ ID NO. 5318**

STRAIN COH1 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE  
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYLHGYTSQGYLPGFNQPLDLNQIAVNKD  
 KKKTYEKLFGKVKE

**SEQ ID NO. 5319**

STRAIN M781 frame: 1

TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN  
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE  
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYYEAPQTELKYLHGYTSQGYLPGFNQPLDLNQIAVNKD  
 KKKTYEKLFGKVKE

Table 53: Comparative Sequences relating to SAG 0755

## SEQ ID NO. 5320

STRAIN CJB110 frame: 2

NTLKKELVEAKKTIIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEDYDTLSKN  
 ISGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIIPVAVYSYALGSSVKEMKEE  
 AQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQG  
 ISVKGFDVAVWIPTYGSDSGYEAAPQTELKYLHQQYTSQGYLPGFNQPLDLNQITVNNKD  
 KKITYEKLFGKVKE

## SEQ ID NO. 5321

STRAIN 1169NT frame: 1

TNTLKKELVEAKKTIIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEDYDTLSKN  
 ISGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIIPVAVYSYALGSSVKEMKEE  
 EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYEAAPQTELKYLHQQYTSQGYLPGFNQPLDLNQIAVNKD  
 KKITYEKLFGKVKE

## SEQ ID NO. 5322

STRAIN JM9130013 frame: 1

TNTLKKELVEAKKTIIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEDYDTLSKN  
 ISGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIIPVAVYSYALGSSVKEMKEE  
 EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ  
 GISVKGFDVAVWIPTYGSDSGYEAAPQTELKYLHQQYTSQGYLPGFNQPLDLNQIAVNKD  
 KKITYEKLFGKVKE

PRETTY of: /biotmp/msa21641.2{\*} January 20, 2003 03:59 ..

	1		50
msa21641.2{206_090}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_1169NT}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_18RS21}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_2603}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_A909}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_H36B}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_JM9130013}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_COH1}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_M732}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_M781}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_CJB110}	-NTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
Consensus	*****	*****	*****
	51		100
msa21641.2{206_090}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_1169NT}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_18RS21}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_2603}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_A909}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_H36B}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_JM9130013}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_COH1}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_M732}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_M781}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_CJB110}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
Consensus	*****	*****	*****
	101		150
msa21641.2{206_090}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_1169NT}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_18RS21}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_2603}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_A909}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_H36B}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_JM9130013}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_COH1}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_M732}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_M781}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_CJB110}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
Consensus	*****	*****	*****
	151		200
msa21641.2{206_090}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_1169NT}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_18RS21}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_2603}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_A909}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_H36B}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_JM9130013}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_COH1}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_M732}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_M781}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_CJB110}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
Consensus	*****	*****	*****

Table 53: Comparative Sequences relating to SAG 0755

	201		250
msa21641.2{206_090}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_1169NT}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_18RS21}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_2603}	YYEAAPQTEL KYDLHQYTSQ GYLPGxNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_A909}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_H36B}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_JM9130013}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_COH1}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_M732}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_M781}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_CJB110}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
Consensus	*****	*****	*****
	251		
msa21641.2{206_090}	KVKE		
msa21641.2{206_1169NT}	KVKE		
msa21641.2{206_18RS21}	KVKE		
msa21641.2{206_2603}	KVKE		
msa21641.2{206_A909}	KVKE		
msa21641.2{206_H36B}	KVKE		
msa21641.2{206_JM9130013}	KVKE		
msa21641.2{206_COH1}	KVKE		
msa21641.2{206_M732}	KVKE		
msa21641.2{206_M781}	KVKE		
msa21641.2{206_CJB110}	KVKE		
Consensus	****		

Table 54: Comparative Sequences relating to SAG0949

## SEQ ID NO. 5401

## STRAIN 2603

TTGACTCACAAAAATATATTATTAACCATTATATTGGATTATTT  
 ATGATTATATTATCAGCATGTGGTATGTCTAATAAGGAAATGGCTGGTATTGATAATTGG  
 GAACATTATCAAAGGAAAGAAAAATTACTATTGGATTGATAATACTTTTGTTCCTATG  
 GGATTGAAAGTCGTTCTGGTGACTATACCGGCTTGATATTGATTTAGCTAATGCTGTT  
 TTTAAAGAATACGGTATTTTCAGTGAATGGCAGCCTATTAAGTGGGATATGAAAGAACT  
 GAACCTTAATAATGGTAATATAGACCTTATTGGAAATGGTTATTCAAAAACGGCAGAACGT  
 GCTAAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTACTAAA  
 ACTTCATCAGATATTAAAGTATTAAGGATATGAAGGGGAAAAAACTAGGAGCCCAGTCG  
 GGTTTCATCTGGTTTGGATGCTTTTAAACGCTAAACCTGATATTTTAAAAAAGTTTGTAAAA  
 GGAAAAGAAGCAGTTCAATACGATACCTTCACTCAGGCTTTGATTGATTTAAAAAATAAC  
 CGTATTGATGGTCTTTTGGATTGATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGA  
 AATATAAAAGCTTATTATTTTGTAAAACTGCTTATCAAGGAGAAAAATTTGTAGTAGGA  
 GCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGCTTTCAAACAGCTTCAT  
 AATAAGGGGAGATTTCAAAAAATCTCTTACAAATGGTTTGGTGAAGATGTTTATAGTAAA  
 GAA

## SEQ ID NO. 5402

## STRAIN 090

## ATTGGGaaCATTATC

AAAAGGAAAAGAAAATTACTATTGGATTGATAATACTTTTGTTCCTATG  
 GGATTGAAAGCCGTTCTGGTGACTATACCGGCTTGATATTGATTTAGC  
 TAATGCTGTTTAAAGAATACGGTATTTTCAGTGAATGGCAGCCTATTA  
 ACTGGGATATGAAAGAACTGAACCTTAATAATGGTAATATAGACCTTATT  
 TGGAAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGTCGCTTTTAC  
 AAACCCATATATGAATAATCATCAAGTAATTGTTACTAAAACCTCATCAC  
 ATATTAAATAGTATTAAAGGATATGAAGGGGAAAAAACTAGGAGCCCAGTCG  
 GGTTTCATCTGGTTTGGATGCTTTTAAATGCTAAACCTGATATTTTAAAAAA  
 GTTTGTAAAGGAAAAGAAGCAGTTCAATACGATACCTTCACTCAGGCTT  
 TGATTGATTTAAAAAATAACCGTATTGATGGTCTTTTGGATTGATGAAGTT  
 TATGCTAACTATTATTAAAGCAAGAAGGAATATAAAAGCTTATTATT  
 TGTAAAACTGCTTATCAAGGAGAAAAATTTGTAGTAGGAGCTCGCAAAG  
 TTGATCGTAGACTAATTGAAAAGATTAAACAAAGCTTTCAAACAGCTTCAT  
 AATAAGGGAATAATTTCAAAAAATCTCTTACAAATGGTTTGGTGAAGATGT  
 TTATAGTAAAGAA

## SEQ ID NO. 5403

## STRAIN A909

## ATTGGG

aACATTATCAAAGGAAAAGAAAATTACTATTGGATTGATAATACTTTT  
 GTTCCTATGGGATTGAAAGTCGTTCTGGTGACTATACCGGCTTGATAT  
 TGATTAGCTAATGCTGTTTAAAGAATACGGTATTTTCAGTGAATGGC  
 AGCCTATTAACTGGGATATgAAAGAACTGAACCTTAATAATGGTAATATA  
 GACCTTATTGGAAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGT  
 CGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTACTAAAA  
 CTTCATCAGATATTAAAGTATTAAAGGATATGAAGGGGAAAAAACTAGGA  
 GCCCAGTCGGGTTTCATCTGGTTTGGATGCTTTTAAACGCTAAACCTGATAT  
 TTTAAAAAAGTTTGTAAAGGAAAAGAGCAGTCAATACGATACCTTCA  
 CTGAGGCTTTGATTGATTTAAAAAATAACCGTATTGATGGTCTTTTGGATT  
 GATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAATATAAAAGC  
 TTATTATTGTTTAAAACTGCTTATCAAGGAGAAAAATTTGTAGTAGGAG  
 CTGCTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGCTTTCAA  
 CAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAATGGTTTGG  
 TGAAGATGTTTATAGTAAAGaa

## SEQ ID NO. 5404

## STRAIN H36B

ATTGGGAACATTATCAAAGGAAAAGAAAATTACTATTGGATT  
 TGATAATACTTTTGTTCCTATGGGATTGAAAGTCGTTCTGGTGACTATA  
 CCGGCTTTGATATTGATTTAGCTAATGCTGTTTAAAGAATACGGTATT  
 TCAGTGAATGGCAGCCTATTAAGTGGGATATGAAAGAACTGAACCTAA  
 TAATGGTAATATAGACCTTATTGGAAATGGTTATTCAAAAACGGCAGAAC  
 GTGCTAAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTA  
 ATTGTTACTAAAACCTCATCAGATATTAAAGTATTAAGGATATGAAGGG  
 GAAAAAAGCTAGGAGCCAGTCGGGTTTCATCTGGTTTGGATGCTTTTAAACG  
 CTAACCTGATATTTTAAAAAAGTTTGTAAAGGAAAAGAGCAGTCAA  
 TACGATACCTTCACTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGA  
 TGGTCTTTTGGATTGATGAAGTCTATGCTAACTATTATTAAAGCAAGAAG  
 GAAATATAAAAGCTTATTATTGTTTAAAACTGCTTATCAAGGAGAAAAT  
 TTTGTAGTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAA  
 CAAAGCTTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTT  
 ACAATATGTTTGGTGAAGATGTTTATAGTAAAGAA

## SEQ ID NO. 5405

## STRAIN 18RS21

## ATTGGGAACATTA

TCAAAGGAAAAGAAAATTACTATTGGATTGATAATACTTTTGTTCCTA  
 TGGGATTGAAAGTCGTTCTGGTGACTATACCGGCTTGATATTGATTTA  
 GCTAATGCTGTTTAAAGAATACGGTATTTTCAGTGAATGGCAGCCTAT  
 TAAGTGGGATATGAAAGAACTGAACCTTAATAATGGTAATATAGACCTTA  
 TTTGGAAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGTCGCTTTT  
 ACAACCCATATATGAATAATCATCAAGTAATTGTTACTAAAACCTTCATC

Table 54: Comparative Sequences relating to SAG0949

ACATATTAAATAGTATTAAAGGATATGAAGGGGAAAAAACTAGGAGCCAGT  
CGGGTTCATCTGGTTTGTGATGCTTTAAAGCTAAACCTGATATTTAAAA  
AAGTTTGTAAAGGAAAAGAAGCAGTTCAATACGATACCTTCACTCAGGC  
TTTGATTGATTTAAAAAATAACCGTATTGATGGTCTTTGATTGATGAAG  
TTTATGCTAACTATTATTTAAAGCAAGAAGGAAATATAAAAGCTTATTAT  
TTTGTTAAACCTGCTTATCAAGGAGAAAAATTTGTAGTAGGAGCTCGTAA  
AGTTGATCGTAGACTAATTGAAAAGATTACAAAGCTTTCAAACAGCTTC  
ATAATAAGGGGAGATTTCAAAAATCTCTTACAAATGGTTTGGTGAAGAT  
GTTTATAGTAAAGAA

## SEQ ID NO. 5406

STRAIN M732

ATTGGGAACATTATCAAAAGGAAAAAGAAATTACTATTGGATTGATAA  
TACTTTTGTTCCTATGGGATTGAAAGTCGTTCTGGTGACTATACCGGCT  
TTGATATTGATTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCACTG  
AAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACCTTAATAATGG  
TAATATAGACCTTATTGGAATGGTTATTCAAAAACGGCAGAACCGTGCTA  
AAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTT  
ACTAAAACCTTCATCACATATTAAATAGTATTAAAGGATATGAAGGGGAAAA  
CTAGGAGCCAGTCGGGTTTCATCTGGTTTGTGATGCTTTTAAAGCTAAAC  
CTGATATTTTAAAAAAGTTTGTAAAGGAAAAAGAGCAGTTCAATACGAT  
ACTTTCACTCAGGCTTTGATTGATTAAAAAATAACCGTATTGATGGTCT  
TTTGATTGATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAAATA  
TAAAGCTTATTATTGTTTAAAGCTGCTTATCAAGGAGAAAAATTTGTGTA  
GTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTACAAAGC  
TTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAATCTCTTACAAAT  
GGTTTGGTGAAGATGTTTATAGTAAAGAA

## SEQ ID NO. 5407

STRAIN COH1

ATTGGGAACATTATCAAAAGGAAAAAGAAATTACTATTGGATTGATAA  
TACTTTTGTTCCTATGGGATTGAAAGTCGTTCTGGTGACTATACCGGCT  
TTGATATTGATTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCACTG  
AAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACCTTAATAATGG  
TAATATAGACCTTATTGGAATGGTTATTCAAAAACGGCAGAACCGTGCTA  
AAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTT  
ACTAAAACCTTCATCACATATTAAATAGTATTAAAGGATATGAAGGGGAAAA  
CTAGGAGCCAGTCGGGTTTCATCTGGTTTGTGATGCTTTTAAAGCTAAAC  
CTGATATTTTAAAAAAGTTTGTAAAGGAAAAAGAGCAGTTCAATACGAT  
ACTTTCACTCAGGCTTTGATTGATTAAAAAATAACCGTATTGATGGTCT  
TTTGATTGATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAAATA  
TAAAGCTTATTATTGTTTAAAGCTGCTTATCAAGGAGAAAAATTTGTGTA  
GTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTACAAAGC  
TTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAATCTCTTACAAAT  
GGTTTGGTGAAGATGTTTATAGTAAAGAA

## SEQ ID NO. 5408

STRAIN M781

ATTGGGAACATTATCAAAAGGAAAAAGAAATTACTATTGGATTGATAA  
ATACTTTTGTTCCTATGGGATTGAAAGTCGTTCTGGTGACTATACCGGC  
TTTGATATTGATTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCACTG  
GAAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACCTTAATAATGG  
GTAATATAGACCTTATTGGAATGGTTATTCAAAAACGGCAGAACCGTGCT  
AAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGT  
TACTAAAACTTCATCACATATTAAATAGTATTAAAGGATATGAAGGGGAAAA  
AACTAGGAGCCAGTCGGGTTTCATCTGGTTTGTGATGCTTTTAAAGCTAAAC  
CTGATATTTTAAAAAAGTTTGTAAAGGAAAAAGAGCAGTTCAATACGA  
TACTTTCACTCAGGCTTTGATTGATTAAAAAATAACCGTATTGATGGTC  
TTTGATTGATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAAAT  
ATAAAGCTTATTATTGTTTAAAGCTGCTTATCAAGGAGAAAAATTTGT  
AGTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTACAAAG  
CTTTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAATCTCTTACAA  
TGGTTTGGTGAAGATGTTTATAGTAAAGAA

## SEQ ID NO. 5409

STRAIN CJB110

ATTGGGAACATTATCAAAAGGAAAAAGAAATTACTATTGGATTGATAA  
ACTTTTGTTCCTATGGGATTGAAAGTCGTTCTGGTGACTATACCGGCTT  
TGATATTGATTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCACTG  
AATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACCTTAATAATGGT  
AATATAGACCTTATTGGAATGGTTATTCAAAAACGGCAGAACCGTGCTAA  
AAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTA  
CTAAAACCTTCATCACATATTAAATAGTATTAAAGGATATGAAGGGGAAAA  
CTAGGAGCCAGTCGGGTTTCATCTGGTTTGTGATGCTTTTAAAGCTAAAC  
TGATATTTTAAAAAAGTTTGTAAAGGAAAAAGAGCAGTTCAATACGATA  
CTTTCACTCAGGCTTTGATTGATTAAAAAATAACCGTATTGATGGTCTT  
TTGATTGATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAAATAT  
AAAAGCTTATTATTGTTTAAAGCTGCTTATCAAGGAGAAAAATTTGTAG  
TAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTACAAAGCT  
TTCAAACAGCTTCATAATAAGGGGAGATTTCAAAAATCTCTTACAAATG  
GTTTGGTGAAGATGTTTATAGTAAAGAA

## SEQ ID NO. 5410



Table 54: Comparative Sequences relating to SAG0949

STRAIN 1169NT  
 ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTGATAA  
 TACTTTTGTTCCTATGGGATTGAAAAGTCGTTCTGGTGACTATACCGGCT  
 TTGATATTGATTTAGCTAATGCTGTTTTTAAAGAAATACGGTATTTCAAGT  
 AAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACTCAATAATGG  
 TAATATAGACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGTCCTA  
 AAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTT  
 ACTAAACTTCATCACATATTAAATAGTATTAAAGGATATGAAGGGAAAAA  
 ACTAGGAGCCAGTCGGTTTCATCTGGTTTTGATGCTTTTAATGCTAAAC  
 CTGACATTTTAAAAAAGTTTGTAAGGAAAAGAGCAGTTCAATACGAT  
 ACTTTCACTCAGGCTTTGATTGATTAAAAAATAACCGTATTGATGGTCT  
 TTTGATTGATGAAGTTTATGCTAATATTATTAAAGCAAGAGGAAATA  
 TAAAAGCTTATTATTGTTAAACTGCTTATCAAGGAGAAAAATTTGTA  
 GTAGGAGCTCGCAAAGTTGATCGTAGACTAATTGAAAAGATTACAAAGC  
 TTTCAAACAGCTTCATAATAAGGGAAATTTCAAAAAATCTCTACAAAT  
 GGTTCGTTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5411  
 STRAIN JM9130013

ATTGGGAACATTATC  
 AAAAGGAAAAGAAAATTACTATGGATTGATAATACTTTGTTCCTATG  
 GGATTGAAAAGTCGTTCTGGTGACTATACCGGCTTTGATATTGATTTAGC  
 TAATGCTGTTTTTAAAGAAATACGGTATTTCAAGTAAATGGCAGCCTATTA  
 ACTGGGATATGAAAGAACTGAACTTAATAATGGTAATATAGACCTTATT  
 TGGAAATGGTTATTCAAAACGGCAGAACGTCGCTAAAAAAGTCGCTTTTAC  
 AAACCCATATATGAATAATCATCAAGTAATTGTTACTAAAACTTCATCAC  
 ATATTAAATAGTATTAAAGGATATGAAGGGGAAAAAACTAGGAGCCAGTCG  
 GGTTTCATCTGGTTTTGATGCTTTTAAACGCTAAACCTGATATTTAAAAA  
 GTTTGTAAAAGGAAAAGAGCAGTTCAATACGATACCTTCACTCAGGCTT  
 TGATTGATTTAAAAAATAACCGTATTGATGCTTTTGTGATGATGAAGTT  
 TATGCTAACTATTATTAAAGCAAGAGGAAATATAAAAGCTTATTATT  
 TGTATAAAGCTGCTTATCAAGGAGAAAAATTTGTAGTAGGAGCTCGTAAAG  
 TTGATCGTAGACTAATTGAAAAGATTAAACAAAGCTTTCAAACAGCTTCAT  
 AATAAGGGAGATTTCAAAAATCTCTTACAAATGGTTTGGTGAAGATGT  
 TTATAGTAAAGAA

PRETTY of: /biotmp/msa39314.2{\*} February 18, 2003 11:01 ..

	1				50
msa39314.2{225_18RS21}	-----	-----	-----	-----	-----
msa39314.2{225_2603}	ttgactcaca	aaaatatatt	attaaccatt	atatttggat	tatttatgat
msa39314.2{225_A909}	-----	-----	-----	-----	-----
msa39314.2{225_CJB110}	-----	-----	-----	-----	-----
msa39314.2{225_COH1}	-----	-----	-----	-----	-----
msa39314.2{225_H36B}	-----	-----	-----	-----	-----
msa39314.2{225_KM9130013}	-----	-----	-----	-----	-----
msa39314.2{225_M732}	-----	-----	-----	-----	-----
msa39314.2{225_M781}	-----	-----	-----	-----	-----
msa39314.2{225_090}	-----	-----	-----	-----	-----
msa39314.2{225_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa39314.2{225_18RS21}	-----	-----	-----	-----	-----
msa39314.2{225_2603}	tatatattatca	gcatgtggta	tgtctaataa	ggaaatggct	ggtattgata
msa39314.2{225_A909}	-----	-----	-----	-----	-----
msa39314.2{225_CJB110}	-----	-----	-----	-----	-----
msa39314.2{225_COH1}	-----	-----	-----	-----	-----
msa39314.2{225_H36B}	-----	-----	-----	-----	-----
msa39314.2{225_KM9130013}	-----	-----	-----	-----	-----
msa39314.2{225_M732}	-----	-----	-----	-----	-----
msa39314.2{225_M781}	-----	-----	-----	-----	-----
msa39314.2{225_090}	-----	-----	-----	-----	-----
msa39314.2{225_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	101				150
msa39314.2{225_18RS21}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_2603}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_A909}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_CJB110}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_COH1}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_H36B}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_KM9130013}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_M732}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_M781}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_090}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_1169NT}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
Consensus	*****	*****	*****	*****	*****
	151				200
msa39314.2{225_18RS21}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCGGCTT
msa39314.2{225_2603}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCGGCTT

Table 54: Comparative Sequences relating to SAG0949

msa39314.2{225_A909}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_CJB110}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_COH1}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_H36B}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_KM9130013}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_M732}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_M781}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_090}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_1169NT}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
Consensus	*****	*****	*****_***	*****	*****
201					
msa39314.2{225_18RS21}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_2603}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_A909}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_CJB110}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_COH1}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_H36B}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_KM9130013}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_M732}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_M781}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_090}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_1169NT}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
Consensus	*****	*****	*****	*****	*****
251					
msa39314.2{225_18RS21}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	TAATAATGGT
msa39314.2{225_2603}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	TAATAATGGT
msa39314.2{225_A909}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	TAATAATGGT
msa39314.2{225_CJB110}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	TAATAATGGT
msa39314.2{225_COH1}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	TAATAATGGT
msa39314.2{225_H36B}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	TAATAATGGT
msa39314.2{225_KM9130013}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	TAATAATGGT
msa39314.2{225_M732}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	TAATAATGGT
msa39314.2{225_M781}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	TAATAATGGT
msa39314.2{225_090}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	TAATAATGGT
msa39314.2{225_1169NT}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	TAATAATGGT
Consensus	*****	*****	*****	*****	*****
301					
msa39314.2{225_18RS21}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_2603}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_A909}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_CJB110}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_COH1}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_H36B}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_KM9130013}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_M732}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_M781}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_090}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_1169NT}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
Consensus	*****	*****	*****	*****	*****
351					
msa39314.2{225_18RS21}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_2603}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_A909}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_CJB110}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_COH1}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_H36B}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_KM9130013}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_M732}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_M781}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_090}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_1169NT}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
Consensus	*****	*****	*****	*****	*****
401					
msa39314.2{225_18RS21}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_2603}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_A909}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_CJB110}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_COH1}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_H36B}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_KM9130013}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_M732}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_M781}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_090}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_1169NT}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
Consensus	*****	*****	*****	*****	*****
451					
msa39314.2{225_18RS21}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTTT	GATGCTTTTA	AcGCTAAACC
500					

Table 54: Comparative Sequences relating to SAG0949

msa39314.2{225_2603}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_A909}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_CJB110}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_COH1}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_H36B}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_KM9130013}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_M732}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_M781}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_090}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_1169NT}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
Consensus	*****	*****	*****	*****	*****
501					550
msa39314.2{225_18RS21}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_2603}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_A909}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_CJB110}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_COH1}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_H36B}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_KM9130013}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_M732}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_M781}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_090}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_1169NT}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
Consensus	***-*****	*****	*****	*****	*****
551					600
msa39314.2{225_18RS21}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_2603}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_A909}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_CJB110}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_COH1}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_H36B}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_KM9130013}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_M732}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_M781}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_090}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_1169NT}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
Consensus	*****	*****	*****	*****	*****
601					650
msa39314.2{225_18RS21}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_2603}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_A909}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_CJB110}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_COH1}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_H36B}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_KM9130013}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_M732}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_M781}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_090}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_1169NT}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
Consensus	*****	*****	*****	*****	*****
651					700
msa39314.2{225_18RS21}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_2603}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_A909}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_CJB110}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_COH1}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_H36B}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_KM9130013}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_M732}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_M781}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_090}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_1169NT}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
Consensus	*****	*****	*****	*****	*****
701					750
msa39314.2{225_18RS21}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_2603}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_A909}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_CJB110}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_COH1}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_H36B}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_KM9130013}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_M732}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_M781}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_090}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_1169NT}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
Consensus	*****	*****	*****	*****	*****
751					800

Table 54: Comparative Sequences relating to SAG0949

msa39314.2{225_18RS21}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_2603}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_A909}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_CJB110}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_COH1}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_H36B}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_KM9130013}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_M732}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_M781}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_090}	TTCAAACAGC	TTCATAATAA	GGGgAaATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_1169NT}	TTCAAACAGC	TTCATAATAA	GGGgAaATTT	CAAAAAATCT	CTTACAAATG
Consensus	*****	*****	***-**-****	*****	*****

	801	828
msa39314.2{225_18RS21}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_2603}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_A909}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_CJB110}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_COH1}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_H36B}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_KM9130013}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_M732}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_M781}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_090}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_1169NT}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
Consensus	*****	*****

## SEQ ID NO. 5412

STRAIN 2603 frame: 1

LTHKNILLTIIFGLFMIILSACGMSNKEMAGIDNWEHYQKEKKITIGFDNTFVPMGFESR  
SGDYTGFDIDLAVFKEYGISVKWQPINWDMKETLNNGNIDLIWNGYSKTAERAKKVA  
FTNPYMNHHQVIVTKTSSHINSIKDMKGKGLGAQSGSSGFDFAFNAPDILKKFVKGKEAV  
QYDTFTQALIDLKNNRIDGLLIDEVYANYLKEGNIKAYYFVKITAYQGENFVVGARKVD  
RRLEIKINKAFKQLHNKGRFQKISYKWFGEDEVYSKE

## SEQ ID NO. 5413

STRAIN 090 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLAVFKEYGISVKWQPINWDMKE  
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHHQVIVTKTSSHINSIKDMKGKGLGAQ  
SGSSGFDFAFNAPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLKEG  
NIKAYYFVKITAYQGENFVVGARKVDRLLEIKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
KE

## SEQ ID NO. 5414

STRAIN A909 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLAVFKEYGISVKWQPINWDMKE  
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHHQVIVTKTSSHINSIKDMKGKGLGAQ  
SGSSGFDFAFNAPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLKEG  
NIKAYYFVKITAYQGENFVVGARKVDRLLEIKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
KE

## SEQ ID NO. 5415

STRAIN H36B frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLAVFKEYGISVKWQPINWDMKE  
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHHQVIVTKTSSHINSIKDMKGKGLGAQ  
SGSSGFDFAFNAPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLKEG  
NIKAYYFVKITAYQGENFVVGARKVDRLLEIKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
KE

## SEQ ID NO. 5416

STRAIN 18RS21 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLAVFKEYGISVKWQPINWDMKE  
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHHQVIVTKTSSHINSIKDMKGKGLGAQ  
SGSSGFDFAFNAPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLKEG  
NIKAYYFVKITAYQGENFVVGARKVDRLLEIKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
KE

## SEQ ID NO. 5417

STRAIN M732 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLAVFKEYGISVKWQPINWDMKE  
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHHQVIVTKTSSHINSIKDMKGKGLGAQ  
SGSSGFDFAFNAPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLKEG  
NIKAYYFVKITAYQGENFVVGARKVDRLLEIKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
KE

## SEQ ID NO. 5418

STRAIN COH1 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLAVFKEYGISVKWQPINWDMKE  
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHHQVIVTKTSSHINSIKDMKGKGLGAQ  
SGSSGFDFAFNAPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLKEG  
NIKAYYFVKITAYQGENFVVGARKVDRLLEIKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
KE

Table 54: Comparative Sequences relating to SAG0949

## SEQ ID NO. 5419

STRAIN M781 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE  
 TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHNQVIVTKTSSHINSIKDMKGKGLGAQ  
 SGSSGDFAFNAKPDILKKFVKGEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLQKE  
 GNIKAYYFVKTAQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
 KE

## SEQ ID NO. 5420

STRAIN CJB110 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE  
 TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHNQVIVTKTSSHINSIKDMKGKGLGAQ  
 SGSSGDFAFNAKPDILKKFVKGEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLQKE  
 GNIKAYYFVKTAQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
 KE

## SEQ ID NO. 5421

STRAIN 1169NT frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE  
 TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHNQVIVTKTSSHINSIKDMKGKGLGAQ  
 SGSSGDFAFNAKPDILKKFVKGEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLQKE  
 GNIKAYYFVKTAQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
 KE

## SEQ ID NO. 5422

STRAIN JM9130013 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE  
 TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHNQVIVTKTSSHINSIKDMKGKGLGAQ  
 SGSSGDFAFNAKPDILKKFVKGEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLQKE  
 GNIKAYYFVKTAQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS  
 KE

PRETTY of: /biotmp/msa45901.2(\*) February 19, 2003 03:09 ..

	1				50
msa45901.2{225_090}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_1169NT}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_18RS21}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_2603}	lthknillti	ifglfmiils	acgmsnkema	gidn	WEHYQK EKKITIGFDN
msa45901.2{225_A909}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_CJB110}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_COH1}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_H36B}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_JM9130013}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_M732}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_M781}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
Consensus	*****	*****	*****	*****	*****
	51				100
msa45901.2{225_090}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_1169NT}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_18RS21}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_2603}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_A909}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_CJB110}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_COH1}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_H36B}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_JM9130013}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_M732}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_M781}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
Consensus	*****	*****	*****	*****	*****
	101				150
msa45901.2{225_090}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_1169NT}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_18RS21}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_2603}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_A909}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_CJB110}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_COH1}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_H36B}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_JM9130013}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_M732}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_M781}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
Consensus	*****	*****	*****	*****	*****
	151				200
msa45901.2{225_090}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_1169NT}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_18RS21}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_2603}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_A909}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_CJB110}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGEAV	QYDTFTQALI	DLKNNRIDGL

Table 54: Comparative Sequences relating to SAG0949

msa45901.2{225_COH1}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_H36B}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_JM9130013}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_M732}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_M781}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
Consensus	*****	*****	*****	*****	*****
201					
msa45901.2{225_090}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_1169NT}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_18RS21}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_2603}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_A909}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_CJB110}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_COH1}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_H36B}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_JM9130013}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_M732}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_M781}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
Consensus	*****	*****	*****	*****	*****
251					
msa45901.2{225_090}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_1169NT}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_18RS21}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_2603}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_A909}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_CJB110}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_COH1}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_H36B}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_JM9130013}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_M732}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_M781}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
Consensus	*****	*****	*****		
276					
msa45901.2{225_090}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_1169NT}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_18RS21}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_2603}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_A909}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_CJB110}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_COH1}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_H36B}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_JM9130013}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_M732}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
msa45901.2{225_M781}	FKQLHNKGKf	QKISYKWFG	DVYSKE		
Consensus	*****	*****	*****		

Table 55: Comparative Sequences relating to SAG1592

SEQ ID NO. 5501  
STRAIN 2603  
ATGCTTAAATCTTTTGTGATTTCCTTAGTTCGCTTTTACCAAAAAATATTTCTCCAGCT  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGAAGCTATTCAA  
AAACATGCTCTAAAAGGTGTGTGATGGGGATTGCACGTAATTTGCGATGTCATCCCTTA  
GCCACGGAGGAAATGATCCTGTCCCTGATCAITTTAGCTTAAGACGTAATAAACGGAT  
ATATCAGAT

SEQ ID NO. 5502  
STRAIN 090  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA  
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA  
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT  
CATTTTAGCTT

SEQ ID NO. 5503  
STRAIN A909  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA  
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA  
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT  
CATTTTAGCTTAAGACGTAATAAACGGATATA

SEQ ID NO. 5504  
STRAIN H36B  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA  
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA  
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT  
CATTTTAGCTTAAGACGTAATAAACGGATATATCAGAT

SEQ ID NO. 5505  
STRAIN 18RS21  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA  
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA  
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT  
CATTTTAGCTTAAGACGTAATAAACGGATATATCAGAT

SEQ ID NO. 5506  
STRAIN M732  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA  
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA  
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT  
CATTTTAGCTTAAGACGTAATAAACGGATATATCAGAT

SEQ ID NO. 5507  
STRAIN COH1  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGAAGCTATTCAA  
AAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTAATTTGCGATGTCATCCCTTA  
GCCACGGAGGAAATGATCCTGTCCCTGATCAITTTAGCT

SEQ ID NO. 5508  
STRAIN M781  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA  
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA  
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT  
CATTTTAGCTTAAGACGTAATAAACGGATATATCAGAT

SEQ ID NO. 5509  
STRAIN CJB110  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA  
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA  
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT  
CATTTTAGCTTAAGACGTAATAAACGGATATATCAGAT

SEQ ID NO. 5510  
STRAIN 1169NT  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA  
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA  
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT  
TAITTTAGCTTAAGACGTAATAAACGGATATATCAGAT

SEQ ID NO. 5511  
STRAIN JM9130013  
TTCCCAGCTAGCTGTCGTTATCGTCCAACCTTGCTCTACGTATATGATAGA  
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA  
TTTTGCGATGTCATCCCTTAGCCCACGGAGGAAATGATCCTGTCCCTGAT  
CATTTTAGCTTAAGACGTAATAAACGGATATATCAGAT

PRETTY of: /biotmp/msa119306.2{\*} April 29, 2003 06:23 ..

	1	50
msa119306.2{233_H36B}	-----	-----
msa119306.2{233_JM9130013}	-----	-----

Table 55: Comparative Sequences relating to SAG1592

msa119306.2{233_090}	-----	-----	-----	-----	-----
msa119306.2{233_18RS21}	-----	-----	-----	-----	-----
msa119306.2{233_2603}	atgcttaaat	cttttttgat	tttcttagtt	cgtttttacc	aaaaaaatat
msa119306.2{233_A909}	-----	-----	-----	-----	-----
msa119306.2{233_CJB110}	-----	-----	-----	-----	-----
msa119306.2{233_COH1}	-----	-----	-----	-----	-----
msa119306.2{233_M732}	-----	-----	-----	-----	-----
msa119306.2{233_M781}	-----	-----	-----	-----	-----
msa119306.2{233_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
51					
msa119306.2{233_H36B}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_JM9130013}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_090}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_18RS21}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_2603}	ttctccagct	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_A909}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_CJB110}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_COH1}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_M732}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_M781}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_1169NT}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
Consensus	*****	*****	*****	*****	*****
101					
msa119306.2{233_H36B}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	tctGATGGGG
msa119306.2{233_JM9130013}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	tctGATGGGG
msa119306.2{233_090}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_18RS21}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_2603}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_A909}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_CJB110}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_COH1}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_M732}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_M781}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_1169NT}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	ggTGATGGGG
Consensus	*****	*****	*****	*****	-----
151					
msa119306.2{233_H36B}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_JM9130013}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_090}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_18RS21}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_2603}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_A909}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_CJB110}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_COH1}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_M732}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_M781}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_1169NT}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
Consensus	*****	*****	*****	*****	*****
201					
msa119306.2{233_H36B}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_JM9130013}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_090}	TGTCCTTGAT	cATTTTAGCT	t-----	-----	-----
msa119306.2{233_18RS21}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_2603}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_A909}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	ata-----
msa119306.2{233_CJB110}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_COH1}	TGTCCTTGAT	cATTTTAGCT	-----	-----	-----
msa119306.2{233_M732}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_M781}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_1169NT}	TGTCCTTGAT	tATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
Consensus	*****	*****	-----	-----	-----
249					
SEQ ID NO. 5512					
STRAIN 2603 frame: 1					
MLKSFLIFLVRFYQKNISPAFPASCRRYPTCSTYMIETAIQKHGLKGVLMIARILRCHPL					
AHGGNDPVPDHFSLRRNKTDISD					
SEQ ID NO. 5513					
STRAIN 090 frame: 1					
FPASCRRYPTCSTYMIETAIQKHGLKGVLMIARILRCHPLAHGGNDPVPDHFSLRRNKTD					
I					
SEQ ID NO. 5514					
STRAIN A909 frame: 1					
FPASCRRYPTCSTYMIETAIQKHGLKGVLMIARILRCHPLAHGGNDPVPDHFSLRRNKTD					
I					
SEQ ID NO. 5515					
STRAIN H36B frame: 1					



Table 55: Comparative Sequences relating to SAG1592

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD  
ISD

SEQ ID NO. 5516

STRAIN 18RS21 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD  
ISD

SEQ ID NO. 5517

STRAIN M732 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD  
ISD

SEQ ID NO. 5518

STRAIN COH1 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD

SEQ ID NO. 5519

STRAIN M781 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD  
ISD

SEQ ID NO. 5520

STRAIN CJB110 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD  
ISD

SEQ ID NO. 5521

STRAIN 1169NT frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVVMGIARILRCHPLAHGGNDPVPDYFSLRRNKTD  
ISD

SEQ ID NO. 5522

STRAIN JM9130013 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD  
ISD

PRETTY of: /biotmp/msa119415.2{\*} April 29, 2003 06:25 ..

	1		50
msa119415.2{233_090}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_18RS21}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_COH1}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_A909}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_2603}	mlksfliflv rfyqknispa	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_CJB110}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_H36B}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_JM9130013}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_M732}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_M781}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_1169NT}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVVMG
Consensus	*****	*****	*****-*
	51		83
msa119415.2{233_090}	IARILRCHPL AHGGNDPVPD	hFS-----	---
msa119415.2{233_18RS21}	IARILRCHPL AHGGNDPVPD	hFSLRNKTD	ISD
msa119415.2{233_COH1}	IARILRCHPL AHGGNDPVPD	hFS-----	---
msa119415.2{233_A909}	IARILRCHPL AHGGNDPVPD	hFSLRNKTD	I--
msa119415.2{233_2603}	IARILRCHPL AHGGNDPVPD	hFSLRNKTD	ISD
msa119415.2{233_CJB110}	IARILRCHPL AHGGNDPVPD	hFSLRNKTD	ISD
msa119415.2{233_H36B}	IARILRCHPL AHGGNDPVPD	hFSLRNKTD	ISD
msa119415.2{233_JM9130013}	IARILRCHPL AHGGNDPVPD	hFSLRNKTD	ISD
msa119415.2{233_M732}	IARILRCHPL AHGGNDPVPD	hFSLRNKTD	ISD
msa119415.2{233_M781}	IARILRCHPL AHGGNDPVPD	hFSLRNKTD	ISD
msa119415.2{233_1169NT}	IARILRCHPL AHGGNDPVPD	yFSLRNKTD	ISD
Consensus	*****	*****	*****

Table 56: Comparative Sequences relating to SAG0806

## SEQ ID NO. 5601

## STRAIN 2603

aagaagcttacttttatttgggatttagatgggacattaatagattcgta  
tgtaccaattatggaagctcttgaagaacctatcgctcatttttggtttaa  
tatttgataaagaattaatccatgaatatattttacaggaatcagtgggg  
aaattatttggttaacctttcagaggaagagcaaatacctcatgaaaaact  
gaaagcatattttacaaaagaacaagaaagtcgagattctaaaaatcatt  
taatgccatattgcaaaagagattttagaatggaccaagaacaagatatc  
cccaattttatgtatacacataaaggagcaagtacgcattcagtggtgga  
aaccttgagatctctcattattttgatgaaattttaactggtgtttcgg  
gattcgagcgaaaaccacatccacaagggattaaatttttagttaaacga  
tattcttttagataaatcaatgacttattacataggagatcgccactaga  
tttggaggttgctcaaaatgctggtataaaatccataaacttaaggttag  
agaattccaaagaaaactataatatttcaagctcctcaagatataatatca  
cttgatttctactcggttggat

## SEQ ID NO. 5602

## STRAIN COH1

AAGAAGCTTACTTTTATTGGGATTAGATGGGACATTAA  
TAGATTCTGATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCAT  
TTTGGCTTAATAATTGATAAAGAATTAATCCATGAATATATTTTACAGGA  
ATCAGTGGGGCAATTATTTGGTAAACCTTTAGAGGAAGAGCAAATACCTC  
ATGAAAAAAGTGAAGCATATTTTACAAAAGAACAAGAAAGTCGAGATTCT  
AAAATACATTAAATGCCATATGCAAAAGAGATTTAGAATGGACCAAGA  
ACAAGATATTCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATT  
CAGTGTGGAAACCTTGCGAGATCTCTCATTATTTTGAATGAAATTTAACT  
GGTGTTCGGGATTCGAGCGAAAACCATCCACAAGGGATTAAATTTATTT  
AGTTAAACGATATTCTTTAGATAAATCAATGACTTATTACATAGGAGATC  
GTCCACTAGATTGGAGGTTGCTCAAAATGCTGGTATAAAATCCATAAAC  
TTAAGGTTAGAGAATTCCAAAGAAAACATAATATTCAAGTCTCAAAGA  
TATAATATCACTTGATTTCACCTCGTTGGAT

## SEQ ID NO. 5603

## STRAIN A909

AAGAAGCTTACTTTTATTGGGATTAGATGGGACATTAAAT  
AGATTCTGATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATT  
TTTGGTTTAAATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAAT  
CAGTGGGGAAATTATTTGGTAAACCTTTAGAGGAAGAGCAAATACCTCAT  
GAAAAAAGTGAAGCATATTTTACAAAAGAACAAGAAAGTCGAGATTCT  
AAAATACATTAAATGCCATATGCAAAAGAGATTTAGAATGGACCAAGA  
ACAAGATATTCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATT  
CAGTGTGGAAACCTTGCGAGATCTCTCATTATTTTGAATGAAATTTAACT  
GGTGTTCGGGATTCGAGCGAAAACCATCCACAAGGGATTAAATTTATTT  
AGTTAAACGATATTCTTTAGATAAATCAATGACTTATTACATAGGAGATC  
GTCCACTAGATTGGAGGTTGCTCAAAATGCTGGTATAAAATCCATAAAC  
TTAAGGTTAGAGAATTCCAAAGAAAACATAATATTCAAGTCTCAAAGA  
TATAATATCACTTGATTTCACCTCGTTGGAT

## SEQ ID NO. 5604

## STRAIN H3B6

AAGAAGCTTACTTTTATTGGGATTAGATGGGACATTAAATAGATTCTG  
TATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGTTTAA  
TATTGATTAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGAA  
ATTATTTGGTAAACCTTTAGAGGAAGAGCAAATACCTCATGAAAAAAGT  
GAAGCATATTTTACAAAAGAACAAGAAAGTCGAGATTCTAAAATACATT  
TAATGCCATATGCAAAAGAGATTTAGAATGGACCAAGAACAAGATATC  
CCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTGAGTGTG  
GAAACCTTGCGAGATCTCTCATTATTTTGAATGAAATTTAACTGGTGTTC  
GGGATTCGAGCGAAAACCATCCACAAGGGATTAAATTTATTTAGTTAAAC  
GATATTCTTTAGATAAATCAATGACTTATTACATAGGAGATCGTCCACTAG  
ATTGGAGGTTGCTCAAAATGCTGGTATAAATCCATAAACTTAAGGTTAGAG  
AATTCCAAAGAAAACATAATATTCAAGTCTCAAAGATATAATATCACTTG  
ATTTCACCTCGTTGGAT

## SEQ ID NO. 5605

## STRAIN 18RS21

AAGAAGCTTACTTTTATTGGGATTAGATGGGACATTAAATAGATTCTG  
TATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGTTTAA  
TATTGATTAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGAA  
ATTATTTGGTAAACCTTTAGAGGAAGAGCAAATACCTCATGAAAAAAGT  
GAAGCATATTTTACAAAAGAACAAGAAAGTCGAGATTCTAAAATACATT  
TAATGCCATATGCAAAAGAGATTTAGAATGGACCAAGAACAAGATATC  
CCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTGAGTGTG  
GAAACCTTGCGAGATCTCTCATTATTTTGAATGAAATTTAACTGGTGTTC  
GGGATTCGAGCGAAAACCATCCACAAGGGATTAAATTTATTTAGTTAAAC  
GATATTCTTTAGATAAATCAATGACTTATTACATAGGAGATCGTCCACTAG  
ATTGGAGGTTGCTCAAAATGCTGGTATAAATCCATAAACTTAAGGTTAGAG  
AATTCCAAAGAAAACATAATATTCAAGTCTCAAAGATATAATATCACTTG  
ATTTCACCTCGTTGGAT

## SEQ ID NO. 5606

## STRAIN M732

AAGAAGCTTACTTTTATTGGGATTAGATGGGACATTAAATAGAT  
TCGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTAA  
TATTGATTAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGGCA  
ATTATTTGGTAAACCTTTAGAGGAAGAGCAAATACCTCATGAAAAAAGT  
GAAGCATATTTTACAAAAGAACAAGAAAGTCGAGATTCTAAAATACATT  
TAATGCCATATGCAAAAGAGATTTAGAATGGACCAAGAACAAGATATC  
CCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTGAGTGTG  
GAAACCTTGCGAGATCTCTCATTATTTTGAATGAAATTTAACTGGTGTTC  
GGGATTCGAGCGAAAACCATCCACAAGGGATTAAATTTATTTAGTTAAAC  
GATATTCTTTAGATAAATCAATGACTTATTACATAGGAGATCGTCCACTAG  
ATTGGAGGTTGCTCAAAATGCTGGTATAAATCCATAAACTTAAGGTTAGAG  
AATTCCAAAGAAAACATAATATTCAAGTCTCAAAGATATAATATCACTTG  
ATTTCACCTCGTTGGAT

Table 56: Comparative Sequences relating to SAG0806

TTGGAAACCTTGCAGATCTCTCATTATTTTGTGATAAAATTTAACTGGTGTTCGGGATTTC  
GAGCGAAAACCCACATCCACAAGGGATTAAATATTTAGTTAAACGATATCTTTAGATAAA  
TCAATGACTTATTACATAGGAGATCGTCCACTAGATTTGGAGGTTGCTCAAATGCTGGT  
ATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATAATATTTCAAGTCTC  
AAGATATAATATCACTTGATTTCACCTCGTTTGGAT

SEQ ID NO. 5607

STRAIN CJB110

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATT  
AATAGATTTCGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTT  
AATATTTGATAAAGAATTAAATCCATGAATATATTTTACAGGAATCAGTGGGGCAATTATT  
GGTAAACCTTTTCAGAGGAAGAGCAAATACCTCATGAAAACTGAAAGCATATTTTACAAA  
AGAACAAGAAAGTCGAGATTCTAAAATACATTTAATGCCATATGCAAAAGAGATTTTAGA  
ATGGACCAAGAACAAGATATCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCA  
TTCAGTGTGGAAACCTTGCAGATCTCTCATTTATTTGATGAAATTTTAACTGGTGTTC  
TGGATTTCGAGCGAAAACCATCCACAAGGGATTAAATATTTAGTTAAACGATATCTTT  
AGATAAATCAATGACTTATTTACATAGGAGATCGTCCCCTAGATTGGAGGTTGCTCAAAA  
TGCTGGTATAAAATCCATAAACCTTAAGGTTAGAGAATTCCAAAGAAAACATAATATTTT  
AAGTCTCAAGGATATAATATCACTTGATTTCACCTCGTT

SEQ ID NO. 5608

STRAIN 1169NT

aAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGATTTCGTATGTACCAATTA  
TAGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTAATATTTGATAAAGAATTAAATCC  
ATGAATATATTTTACAGGAATCAGTGGGGAAATTATTTGGTAAACCTTTTCAGAGGAAGAGC  
AAATACCTCATGAAAACTGAAAGCATATTTTACAAAAGAACAAAGTTCGAGATTCTA  
AAATACATTTTAAATGCCATACGCAAAAGAGATTTTGAATGGACCAAGAACAGATATCC  
CCAAATTTTATGTATACACATAAAGGAGCAAGTACGCATTTCAGTGTGGAAACCTTGCAGA  
TCTCTCATTTTGTGATAAATTTAACTGGTGTTCGGGATTTCGAGCGAAAACCCACATC  
CACAAGGGATTAAATATTTAGTTAAACGATATCTTTAGATAAATCAATGACTTATTACA  
TAGGAGATCGTCCCCTAGATTGGAGGTTGCTCAAATGCTGGTATAAAATCCATAAACT  
TAAGGTTAGAGAATTCCAAAGAAAACATAATATTTCAAGTCTCAAGGATATAATATCAC  
TTGATTTCACTCGTTTGGAT

SEQ ID NO. 5609

STRAIN JM9130013

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGA  
TTTGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGTTTAAATATT  
TGATAAAGAATTAAATCCATGAATATATTTTACAGGAATCAGTGGGGAAATTATTTGGTAAA  
CCTTTTCAGAGGAAGAGCAAATACCTCATGAAAACTGAAAGCATATTTTACAAAAGAACAA  
AGAAAGTCGAGATTCTAAAATACATTTTAAATGCCATATGCAAAAGAGATTTTGAATGGAC  
CAAAGAACAAGATATCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTTCAGT  
GTTGGAACCTTGCAGATCTCTCATTTATTTGATGAAATTTTAACTGGTGTTCGGGATT  
CGAGCGAAAACCATCCACAAGGGATTAAATATTTAGTTAAACGATATCTTTAGATAAA  
ATCAATGACTTATTACATAGGAGATCGTCCACTAGATTGGAGGTTGCTCAAATGCTGG  
TATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATAATATTTCAAGTCT  
CAAAGATATAATATCACTTGATTTCACCTCGT

SEQ ID NO. 5610

STRAIN 090

AAGAAGCTTACTTTTATTTGG  
GATTTAGATGGGACATTAATAGATTTCGTATGTACCAATTATGGAAGCTCT  
TGAAGAAACCTATCGTCATTTTGGCTTAATATTTGATAAAGAATTAAATCC  
ATGAATATATTTTACAGGAATCAGTGGGGCAATTATTTGGTAAACCTTTCA  
GAGGAAGAGCAAATACCTCATGAAAACTGAAAGCATATTTTACAAAAGA  
ACAAAGAAAGTCGAGATTCTAAAATACATTTAATGCCATATGCAAAAGAGA  
TTTTAGAAATGGACCAAGAACAAAGATATCCCAATTTTATGTATACACAT  
AAAGGAGCAAGTACGCATTTCAGTGTGGAAACCTTGCAGATCTCTCATTA  
TTTTGATGAAATTTTAACTGGTGTTCCTGGATTTCGAGCGAAAACCATC  
CACAAGGGATTAAATATTTAGTTAAACGATATCTTTAGATAAATCAATG  
ACTTATTACATAGGAGATCGTCCCCTAGATTGGAGGTTGCTCAAATGCT  
TGGTATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATA  
ATATTTCAAGTCTCAAGGATATAATATCACTTGATTTCACCTCGT

SEQ ID NO. 5611

STRAIN M781

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGATTTCGT  
ATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTA  
ATATTTGATAAAGAATTAAATCCATGAATATATTTTACAGGAATCAGTGGG  
GCAATTTATTTGGTAAACCTTTTCAGAGGAAGAGCAAATACCTCATGAAAAAC  
TGAAAGCATATTTTACAAAAGAACAAAGTTCGAGATTyTAAAATACAT  
TTAATGCCATATGCAAAAGAGATTTTGAATGGACCAAGAACAAAGATAT  
TCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTTCAGTGTGG  
AAACCTTGCAGATCTCTCATTTATTTGATGAAATTTTAACTGGTGTTCG  
GGATTTCGAGCGAAAACCATCCACAAGGGATTAAATATTTAGTTAAACG  
ATATTTCTTAGATAAATCAATGACTTATTACATAGGAGATCGTCCACTAG  
ATTTGGAGGTTGCTCAAATGCTGGTATAAAATCCATAAACTTAAGGTTA  
GAGAATTCCAAAGAAAACATAATATTTCAAGTCTCAAGATATAATATC  
ACTTGATTTCACTCGT

PRETTY of: /biotmp/msa45163.2{\*} January 21, 2003 06:53 ..

Table 56: Comparative Sequences relating to SAG0806

	1				50
msa45163.2{240_18RS21}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_2603}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_A909}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_H36B}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_JM9130013}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_COH1}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_M732}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_M781}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_090}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_CJB110}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_1169NT}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
Consensus	*****	*****	*****	*****	*****
	51				100
msa45163.2{240_18RS21}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_2603}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_A909}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_H36B}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_JM9130013}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_COH1}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_M732}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_M781}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_090}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_CJB110}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
msa45163.2{240_1169NT}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGTTTAA
Consensus	*****	*****	*****	*****	*****
	101				150
msa45163.2{240_18RS21}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_2603}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_A909}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_H36B}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_JM9130013}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_COH1}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_M732}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_M781}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_090}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_CJB110}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_1169NT}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
Consensus	*****	*****	*****	*****	*****
	151				200
msa45163.2{240_18RS21}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_2603}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_A909}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_H36B}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_JM9130013}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_COH1}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_M732}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_M781}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_090}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_CJB110}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_1169NT}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
Consensus	*****	*****	*****	*****	*****
	201				250
msa45163.2{240_18RS21}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_2603}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_A909}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_H36B}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_JM9130013}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_COH1}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_M732}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_M781}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTyT	AAAATACATT
msa45163.2{240_090}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_CJB110}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_1169NT}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
Consensus	*****	*****	*****	*****	*****
	251				300
msa45163.2{240_18RS21}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_2603}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_A909}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_H36B}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_JM9130013}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_COH1}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_M732}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_M781}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_090}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_CJB110}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_1169NT}	TAATGCCATA	cGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
Consensus	*****	*****	*****	*****	*****

Table 56: Comparative Sequences relating to SAG0806

301						350					
msa45163.2{240_18RS21}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_2603}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_A909}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_H36B}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_JM9130013}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_COH1}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_M732}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_M781}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_090}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_CJB110}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
msa45163.2{240_1169NT}	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA						
Consensus	*****	*****	*****	*****	*****						
351						400					
msa45163.2{240_18RS21}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCcGg						
msa45163.2{240_2603}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCcGg						
msa45163.2{240_A909}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCcGg						
msa45163.2{240_H36B}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCcGg						
msa45163.2{240_JM9130013}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCcGg						
msa45163.2{240_COH1}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCcGg						
msa45163.2{240_M732}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCcGg						
msa45163.2{240_M781}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCcGg						
msa45163.2{240_090}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCcGg						
msa45163.2{240_CJB110}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCcGg						
msa45163.2{240_1169NT}	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCcGg						
Consensus	*****	*****	*****	*****	*****						
401						450					
msa45163.2{240_18RS21}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_2603}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_A909}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_H36B}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_JM9130013}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_COH1}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_M732}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_M781}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_090}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_CJB110}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
msa45163.2{240_1169NT}	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA						
Consensus	*****	*****	*****	*****	*****						
451						500					
msa45163.2{240_18RS21}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA						
msa45163.2{240_2603}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA						
msa45163.2{240_A909}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA						
msa45163.2{240_H36B}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA						
msa45163.2{240_JM9130013}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA						
msa45163.2{240_COH1}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA						
msa45163.2{240_M732}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA						
msa45163.2{240_M781}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA						
msa45163.2{240_090}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCcCTAGA						
msa45163.2{240_CJB110}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCcCTAGA						
msa45163.2{240_1169NT}	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCcCTAGA						
Consensus	*****	*****	*****	*****	*****						
501						550					
msa45163.2{240_18RS21}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_2603}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_A909}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_H36B}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_JM9130013}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_COH1}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_M732}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_M781}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_090}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_CJB110}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
msa45163.2{240_1169NT}	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG						
Consensus	*****	*****	*****	*****	*****						
551						600					
msa45163.2{240_18RS21}	AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_2603}	AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_A909}	AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_H36B}	AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_JM9130013}	AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_COH1}	AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_M732}	AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_M781}	AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_090}	AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_CJB110}	AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA						
msa45163.2{240_1169NT}	AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA						

Table 56: Comparative Sequences relating to SAG0806

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Consensus ***** ***** ***** *****_** *****
msa45163.2{240_18RS21} 601          621
msa45163.2{240_2603} CTTGATTTCa CTCGTttgga t
msa45163.2{240_A909} CTTGATTTCa CTCGT----- ~
msa45163.2{240_H36B} CTTGATTTCa CTCGTttgga t
msa45163.2{240_JM9130013} CTTGATTTCa CTCGT----- ~
msa45163.2{240_COH1} CTTGATTTCa CTCGTttgga t
msa45163.2{240_M732} CTTGATTTCa CTCGTttgga t
msa45163.2{240_M781} CTTGATTTCa CTCGT----- ~
msa45163.2{240_090} CTTGATTTCa CTCGT----- ~
msa45163.2{240_CJB110} CTTGATTTCa CTCGTt----- ~
msa45163.2{240_1169NT} CTTGATTTCa CTCGTttgga t
Consensus ***** *****----- -

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## SEQ ID NO. 5612

STRAIN 2603 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGKLLVNLSEEE  
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN  
 LRLENSKENYNISSLKDIISLDFTRLD

## SEQ ID NO. 5613

STRAIN A909 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGKLLVNLSEEE  
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN  
 LRLENSKENYNISSLKDIISLDFTR

## SEQ ID NO. 5614

STRAIN H36B frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGKLLVNLSEEE  
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN  
 LRLENSKENYNISSLKDIISLDFTRLD

## SEQ ID NO. 5615

STRAIN 18RS21 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGKLLVNLSEEE  
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN  
 LRLENSKENYNISSLKDIISLDFTRLD

## SEQ ID NO. 5616

STRAIN M732 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGQLLVNLSEEE  
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN  
 LRLENSKENYNISSLKDIISLDFTRLD

## SEQ ID NO. 5617

STRAIN COH1 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGQLLVNLSEEE  
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN  
 LRLENSKENYNISSLKDIISLDFTRLD

## SEQ ID NO. 5618

STRAIN CJB110 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGQLLVNLSEEE  
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN  
 LRLENSKENYNISSLKDIISLDFTR

## SEQ ID NO. 5619

STRAIN 1169NT frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGKLLVNLSEEE  
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN  
 LRLENSKENYNISSLKDIISLDFTRLD

## SEQ ID NO. 5620

STRAIN JM9130013 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGKLLVNLSEEE  
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
 ISHYFDEILTGVSGFERKPHPGQGINYLVKRYSLDKSMYYIGDRPLDLEVAQNAGIKSIN  
 LRLENSKENYNISSLKDIISLDFTR

## SEQ ID NO. 5621

STRAIN 090 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGQLLVNLSEEE  
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ

Table 56: Comparative Sequences relating to SAG0806

ISHYFDEILTGVSGFERKPHPGQGINYLKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN  
LRLNSKENYNISSLKDIISLDFTR

SEQ ID NO. 5622

STRAIN M781 frame: 1

KKLTFIWDLDGTLIDSYPVIMEALEETRYRHFGFLIFDKELIHEYILQESVQGQLLVNLSEEE  
QIPHEKLKAYFTKEQESRDXXKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ  
ISHYFDEILTGVSGFERKPHPGQGINYLKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN  
LRLNSKENYNISSLKDIISLDFTR

PRETTY of: /biotmp/msa45645.2(\*) January 21, 2003 06:57 ..

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1
msa45645.2{240_18RS21} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_A909} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_JM9130013} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_2603} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_H36B} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_090} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_CJB110} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_M781} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_COH1} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_M732} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_1169NT} KKLTFIWDLD GTLIDSYPVI iEAL EETRYH FGLIFDKELI HEYILQESVG
Consensus ***** -*****
50

51
msa45645.2{240_18RS21} KLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_A909} KLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_JM9130013} KLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_2603} KLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_H36B} KLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_090} qLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_CJB110} qLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_M781} qLLVNLSEEE QIPHEKLKAY FTKEQESRDx KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_COH1} qLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_M732} qLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPLYAKE ILEWTKEQDI
msa45645.2{240_1169NT} KLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMPLYAKE ILEWTKEQDI
Consensus -*****
100

101
msa45645.2{240_18RS21} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_A909} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_JM9130013} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_2603} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_H36B} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_090} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_CJB110} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_M781} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_COH1} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_M732} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_1169NT} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
Consensus *****
150

151
msa45645.2{240_18RS21} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_A909} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_JM9130013} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_2603} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_H36B} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_090} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_CJB110} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_M781} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_COH1} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_M732} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_1169NT} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
Consensus *****
200

201
msa45645.2{240_18RS21} LDFTRld
msa45645.2{240_A909} LDFTR--
msa45645.2{240_JM9130013} LDFTR--
msa45645.2{240_2603} LDFTRld
msa45645.2{240_H36B} LDFTRld
msa45645.2{240_090} LDFTR--
msa45645.2{240_CJB110} LDFTR--
msa45645.2{240_M781} LDFTR--
msa45645.2{240_COH1} LDFTRld
msa45645.2{240_M732} LDFTRld
msa45645.2{240_1169NT} LDFTRld
Consensus *****

```

Table 57: Comparative Sequences relating to SAG 1488

SEQ ID NO: 5701

STRAIN 2603

ATGCTTATGACAAAAATAATAGGACTGACAGGAGGGATAGCTTCT  
 GGAAAGTCAACGGTAACAAAAATAATACGAGAATCAGGTTTAAAGTCATAGATGCGGAT  
 CAAGTGGTTTCATAAAATGCAAGCTAAGGGTGGGAACTTTACCAAGCTTTATTAGAATGG  
 TTGGGTCCCGAGATACCTGATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATG  
 ATTTTTGGCTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTGCT  
 CAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAAACAGAAGAGATATTTTTCATGGAT  
 ATTCCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTTGATGAGATTGGTTGGTATT  
 GTTGATAAAGAAAAACAATTACAAACGATTAAATGGCCCGTAACAACTACAGTCGAGAAGAA  
 GCAGAAATACGACTTTACACCAAAATGCCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTT  
 ATTATTGACAATAATGGTGATTATAAATCTTTAAAGAGCAAATATTGGATGCTCTTCAA  
 CGTTTA

SEQ ID NO: 5702

STRAIN 090

AAGTCAACGGTAACAAAAATAATACGAGAATCAG  
 GTTTTAAAGTCATAGATGCGGATCAAGTGGTTTCATAAATTGCAAGCTAAG  
 GGTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACT  
 TGATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTCG  
 CTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT  
 CGTCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAAACAGAAGAGAT  
 ATTTTTCGTGGATATTCCCTTTATTGATTGAAGAAAAGTATATAAAATGGT  
 TTGATGAGATTGGTTGGTATTGTTGATAAAGAAAAACAATTACAAACGA  
 TTAATGGCCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTC  
 ACACCAAATGCCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTA  
 ATAATAATGGTGATTATAAATCTTTAAAGAGCAAATATTGGATGCTCTT  
 CAACGTTTA

SEQ ID NO: 5703

STRAIN A909

AAGTCAACGGTAACAAAAATAATACGAGAATCAG  
 GTTTTAAAGTCATAGATGCGGATCAAGTGGTTTCATAAATTGCAAGCTAAG  
 GGTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACT  
 TGATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTCG  
 CTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT  
 CGTCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAAACAGAAGAGAT  
 ATTTTTCATGGATATTCCCTTTATTGATTGAAGAAAAGTATATAAAATGGT  
 TTGATGAGATTGGTTGGTATTGTTGATAAAGAAAAACAATTACAAACGA  
 TTAATGGCCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTC  
 ACACCAAATGCCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTA  
 ACAATAATGGTGATTATAAATCTTTAAAGAGCAAATATTGGATGCTCTT  
 CAACGTTTA

SEQ ID NO: 5704

STRAIN H36B

AAGTCAACGGTAACAAAAATAATACGAGAATCAGG  
 TTTTAAAGTCATAGATGCGGATCAAGTGGTTTCATAAATTGCAAGCTAAGG  
 GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTT  
 GATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTCG  
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT  
 GTCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAAACAGAAGAGATA  
 TTTTTCATGGATATTCCCTTTATTGATTGAAGAAAAGTATATAAAATGGT  
 TGATGAGATTGGTTGGTATTGTTGATAAAGAAAAACAATTACAAACGAT  
 TAATGGCCCGTAACAACTACAGTCGAGAAGAAGCGGAATTACGACTTTCA  
 CACCAAATACCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGA  
 TAATAATGGTGATTATAAATCTTTAAAGAGCAAATATTGGATGCTCTTC  
 AACGTTTA

SEQ ID NO: 5705

STRAIN 18RS21

AAGTCAACGGTAACAAAAATAATACGAGAATCAGG  
 TTTTAAAGTCATAGATGCGGATCAAGTGGTTTCATAAATTGCAAGCTAAGG  
 GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTT  
 GATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTCG  
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT  
 GTCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAAACAGAAGAGATA  
 TTTTTCATGGATATTCCCTTTATTGATTGAAGAAAAGTATATAAAATGGT  
 TGATGAGATTGGTTGGTATTGTTGATAAAGAAAAACAATTACAAACGAT  
 TAATGGCCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTCA  
 CACCAAATGCCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGA  
 CAATAATGGTGATTATAAATCTTTAAAGAGCAAATATTGGATGCTCTTC  
 AACGTTTA

SEQ ID NO: 5706

STRAIN M732

AAGTCAACGGTAACAAAAATAATACGAGAATCAGGTT  
 TTTAAAGTCATAGATGCGGATCAAGTGGTTTCATAAATTGCAAGCTAAGGGT  
 GGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTTGA  
 TGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTTCGTA  
 ATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTGCT  
 CAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAAACAGAAGAGATATT



Table 57: Comparative Sequences relating to SAG 1488

TTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTTG  
 ATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAACGATTA  
 ATGGCCCGTAACAACACTACAGTCGAGAAGAAGCAGAATTACGACTTTTCA  
 CCAAATGCCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGACA  
 ATAATGGTGATTTAATAACTTTAAAAAGAGCAAATATTGGATGCTCTTCA  
 CGTTTA

SEQ ID NO: 5707

STRAIN COH1

AAGTCAACGGTAACAAAAATAATACGAGAATCAGGT  
 TTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGGG  
 TGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTTG  
 ATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTGGCT  
 AATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTG  
 TCAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAACAGAAGAGATAT  
 TTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTT  
 GATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAACGATT  
 AATGGCCCGTAAACAACACTACAGTCGAGAAGAAGCAGAATTACGACTTTCA  
 ACCAAATGCCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGAC  
 AATAATGGTGATTTAATAACTTTAAAAAGAGCAAATATTGGATGCTCTTCA  
 ACGTTTA

SEQ ID NO: 5708

STRAIN M781

AAGTCAACGGTAACAAAAATAATACGAGAATCAGG  
 TTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGG  
 GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTT  
 GATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTGGC  
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTG  
 GTCAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAACAGAAGAGATA  
 TTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTT  
 TGATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAACGAT  
 TAATGGCCCGTAACAACACTACAGTCGAGAAGAAGCAGAATTACGACTTTCA  
 CACCAAATGCCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGA  
 CAATAATGGTGATTTAATAACTTTAAAAAGAGCAAATATTGGATGCTCTTCA  
 AACGTTTA

SEQ ID NO: 5709

STRAIN CJB110

AAGTCAACGGTAACAAAAATAATACGAGAA  
 TCAGGTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGC  
 TAAGGGTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGA  
 TACTTGATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATT  
 TTTGCTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTAT  
 CATTGCTCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAACAGAAG  
 AGATATTTTTCGTTGGATATTCCTTTATTGATTGAAGAAAAGTATATAAA  
 TGGTTTGATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACA  
 ACGATTAAATGGCCCGTAAACAACACTACAGTCGAGAAGAAGCAGAATTACGAC  
 TTTTACACCAAATGCCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATT  
 ATTAATAATAATGGTGATTTAATAACTTTAAAAAGAGCAAATATTGGATGCTCTTCA  
 CTCACAGTTTA

SEQ ID NO: 5710

STRAIN 1169NT

AAGTCAACGGTAACAAAAATAATACGAGAATCAGG  
 TTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGG  
 GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTT  
 GATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTGGC  
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTG  
 GTCAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAACAGAAGAGATA  
 TTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTT  
 TGATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAACGAT  
 TAATGGCCCGTAACAACACTACAGTCGAGAAGAAGCAGAATTACGACTTTCA  
 CACCAAATACCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGA  
 TAATAATGGTGATTTAATAACTTTAAAAAGAGCAAATGTTGGATGCTCTTCA  
 AACGTTTA

SEQ ID NO: 5711

STRAIN JM9130013

AAGTCAACGGTAACAAAAATAATACGAGAATCAGGT  
 TTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGGG  
 TGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTTG  
 ATGCTGATGGTGAGTTGGATAGACCAAAGCTTTCTCAAATGATTTTGGCT  
 AATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTG  
 TCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAACAGAAGAGATAT  
 TTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTT  
 GATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAACGATT  
 AATGGCCCGTAACAACACTACAGTCGAGAAGAAGCGGAATTACGACTTTCA  
 ACCAAATACCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGA  
 AATAATGGTGATTTAATAACTTTAAAAAGAGCAAATGTTGGATGCTCTTCA  
 ACGTTTA

Table 57: Comparative Sequences relating to SAG 1488

PRETTY of: /biotmp/msa221059.2{\*} February 10, 2003 07:07 ..

	1				50
msa221059.2{245_H36B}	-----	-----	-----	-----	-----AA
msa221059.2{245_JM9130013}	-----	-----	-----	-----	-----AA
msa221059.2{245_1169NT}	-----	-----	-----	-----	-----AA
msa221059.2{245_090}	-----	-----	-----	-----	-----AA
msa221059.2{245_CJB110}	-----	-----	-----	-----	-----AA
msa221059.2{245_18RS21}	-----	-----	-----	-----	-----AA
msa221059.2{245_2603}	atgctttatga	caaaaataat	aggactgaca	ggaggggatag	cttcttggaAA
msa221059.2{245_A909}	-----	-----	-----	-----	-----AA
msa221059.2{245_COH1}	-----	-----	-----	-----	-----AA
msa221059.2{245_M732}	-----	-----	-----	-----	-----AA
msa221059.2{245_M781}	-----	-----	-----	-----	-----AA
Consensus	*****	*****	*****	*****	*****
	51				100
msa221059.2{245_H36B}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_JM9130013}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_1169NT}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_090}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_CJB110}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_18RS21}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_2603}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_A909}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_COH1}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_M732}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
msa221059.2{245_M781}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTAAAA	GTCATAGATG
Consensus	*****	*****	*****	*****	*****
	101				150
msa221059.2{245_H36B}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_JM9130013}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_1169NT}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_090}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_CJB110}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_18RS21}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_2603}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_A909}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_COH1}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_M732}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_M781}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
Consensus	*****	*****	*****	*****	*****
	151				200
msa221059.2{245_H36B}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_JM9130013}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_1169NT}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_090}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_CJB110}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_18RS21}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_2603}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_A909}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_COH1}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_M732}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_M781}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
Consensus	*****	*****	*****	*****	*****
	201				250
msa221059.2{245_H36B}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_JM9130013}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_1169NT}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_090}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_CJB110}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_18RS21}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_2603}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_A909}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_COH1}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_M732}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_M781}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
Consensus	*****	*****	*****	*****	*****
	251				300
msa221059.2{245_H36B}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_JM9130013}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_1169NT}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_090}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_CJB110}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_18RS21}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_2603}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_A909}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_COH1}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_M732}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT

Table 57: Comparative Sequences relating to SAG 1488

msa221059.2{245_M781}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
Consensus	*****	*****	*****	*****	*****
msa221059.2{245_H36B}	301				350
msa221059.2{245_JM9130013}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_1169NT}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_090}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCg	TGGATATTCC
msa221059.2{245_CJB110}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCg	TGGATATTCC
msa221059.2{245_18RS21}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_2603}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_A909}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_COH1}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_M732}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_M781}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
Consensus	*****	*****	*****	*****	*****
msa221059.2{245_H36B}	351				400
msa221059.2{245_JM9130013}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_1169NT}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_090}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_CJB110}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_18RS21}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_2603}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_A909}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_COH1}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_M732}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_M781}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
Consensus	*****	*****	*****	*****	*****
msa221059.2{245_H36B}	401				450
msa221059.2{245_JM9130013}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_1169NT}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_090}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_CJB110}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_18RS21}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_2603}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_A909}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_COH1}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_M732}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_M781}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
Consensus	*****	*****	*****	*****	*****
msa221059.2{245_H36B}	451				500
msa221059.2{245_JM9130013}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TaCCTTTAAC
msa221059.2{245_1169NT}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TaCCTTTAAC
msa221059.2{245_090}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_CJB110}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_18RS21}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_2603}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_A909}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_COH1}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_M732}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_M781}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
Consensus	*****	*****	*****	*****	*-*****
msa221059.2{245_H36B}	501				550
msa221059.2{245_JM9130013}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAtAATAAT	GGTGATTTAA
msa221059.2{245_1169NT}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAtAATAAT	GGTGATTTAA
msa221059.2{245_090}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TaAtAATAAT	GGTGATTTAA
msa221059.2{245_CJB110}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TaAtAATAAT	GGTGATTTAA
msa221059.2{245_18RS21}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_2603}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_A909}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_COH1}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_M732}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_M781}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
Consensus	*****	*****	*****	*-*****	*****
msa221059.2{245_H36B}	551				591
msa221059.2{245_JM9130013}	TAACTTTAAA	AGAGCAAATg	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_1169NT}	TAACTTTAAA	AGAGCAAATg	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_090}	TAACTTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_CJB110}	TAACTTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_18RS21}	TAACTTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_2603}	TAACTTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_A909}	TAACTTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A
msa221059.2{245_COH1}	TAACTTTAAA	AGAGCAAATa	TTGGATGCTC	TTCAACGTTT	A

Table 57: Comparative Sequences relating to SAG 1488

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msa221059.2{245_M732} TAACTTTAAA AGAGCAAATA TTGGATGCTC TTCAACGTTT A
msa221059.2{245_M781} TAACTTTAAA AGAGCAAATA TTGGATGCTC TTCAACGTTT A
Consensus *****- *****

```

## SEQ ID NO: 5712

STRAIN 2603 frame: 1

MLMTKIIIGLTGGIASGKSTVTTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPET  
LDADGELDRPKLSQMI FANPDNMKTSARLQNSII RQELACQDQLKQTEEFFMDIPLLI  
EEKYIKWFDEIWLWVFDKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNN  
GDLITLKEQILDALQRL

## SEQ ID NO: 5713

STRAIN 090 frame: 1

KSTVTTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI  
FANPDNMKTSARLQNSII RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD  
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI INNNGDLITLKEQILDALQ  
L

## SEQ ID NO: 5714

STRAIN A909 frame: 1

KSTVTTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI  
FANPDNMKTSARLQNSII RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD  
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQ  
L

## SEQ ID NO: 5715

STRAIN H36B frame: 1

KSTVTTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI  
FANPDNMKTSARLQNSII RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD  
DKEKQLQRLMARNNYSREEAELRLSHQIPLTDKKS FASLI IDNNNGDLITLKEQMLDALQ  
L

## SEQ ID NO: 5716

STRAIN 18RS21 frame: 1

KSTVTTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI  
FANPDNMKTSARLQNSII RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD  
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQ  
L

## SEQ ID NO: 5717

STRAIN M732 frame: 1

KSTVTTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI  
FANPDNMKTSARLQNSII RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD  
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQ  
L

## SEQ ID NO: 5718

STRAIN COH1 frame: 1

KSTVTTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI  
FANPDNMKTSARLQNSII RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD  
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQ  
L

## SEQ ID NO: 5719

STRAIN M781 frame: 1

KSTVTTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI  
FANPDNMKTSARLQNSII RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD  
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQ  
L

## SEQ ID NO: 5720

STRAIN CJB110 frame: 1

KSTVTTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI  
FANPDNMKTSARLQNSII RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD  
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI INNNGDLITLKEQILDALQ  
L

## SEQ ID NO: 5721

STRAIN 1169NT frame: 1

KSTVTTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI  
FANPDNMKTSARLQNSII RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD  
DKEKQLQRLMARNNYSREEAELRLSHQIPLTDKKS FASLI IDNNNGDLITLKEQMLDALQ  
L

## SEQ ID NO: 5722

STRAIN JM9130013 frame: 1

KSTVTTKIIRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI  
FANPDNMKTSARLQNSII RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD  
DKEKQLQRLMARNNYSREEAELRLSHQIPLTDKKS FASLI IDNNNGDLITLKEQMLDALQ  
L

Table 57: Comparative Sequences relating to SAG 1488

PRETTY of: /biotmp/msa221398.2(\*) February 10, 2003 07:15 ..

```

1
msa221398.2{245_090} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_CJB110} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_1169NT} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_H36B} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_JM9130013} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_18RS21} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_2603} mlmtkiiglt ggiasgKSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_A909} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_COH1} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_M732} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_M781} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
Consensus *****

51
msa221398.2{245_090} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_CJB110} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_1169NT} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_H36B} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_JM9130013} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_18RS21} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_2603} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_A909} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_COH1} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_M732} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_M781} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
Consensus *****

101
msa221398.2{245_090} QRDQLKQTEE IFFvDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_CJB110} QRDQLKQTEE IFFvDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_1169NT} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_H36B} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_JM9130013} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_18RS21} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_2603} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_A909} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_COH1} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_M732} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_M781} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
Consensus *****

151
msa221398.2{245_090} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_CJB110} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_1169NT} YSREEAELRL SHQiPLTDKK SFASLIIdNN GDLITLKEQm LDALQRL
msa221398.2{245_H36B} YSREEAELRL SHQiPLTDKK SFASLIIdNN GDLITLKEQm LDALQRL
msa221398.2{245_JM9130013} YSREEAELRL SHQiPLTDKK SFASLIIdNN GDLITLKEQm LDALQRL
msa221398.2{245_18RS21} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_2603} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_A909} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_COH1} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_M732} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_M781} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
Consensus *****

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Table 58: Comparative Sequences relating to SAG0182

SEQ ID NO. 5801

STRAIN 2603

ATGTTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTATGATTTTAGCCCTTTTATTG  
 GTAATAATAGTTATTTTAGACAGTTAATTGAAGAGCGGTCTAAACGTGAAACGGTAGTC  
 CTTGTCATCATTTTCGGCTGTTTGTATTATATCTAATATAACAGGAATTGAATAAAAA  
 GGGGATCGAAGTTTGGTCGAGCGCCCTTTCTAACAACGATTCTCATTCTGACTCACTT  
 GCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCTCTGGTTGGA  
 TCAATTGTTGGTTTATTGGAGGAGTTTCATCGCTTTTTCAGGAAGCTTTTCAGGTTCT  
 TTTCTATATTGTTCAGTTTCAGTTCTAGTCGGCATTTGTAGCGGAAAGATTGGTGATAAGCTT  
 AAGGAAAACCATCTCTACCCCTTCAACAAGCCAAGTTATTTAATTAGTATTAATTGCCGAA  
 AGTATCCAGATGCTATTGTTGGCAITTTTACAGGATGGGAACCTGTCAAATGATTGTC  
 ATTTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCCTTGCAGTTTGTAAACT  
 TATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGAGATGTTCTGAATTGACT  
 CGACAGACTCTGCCCTACCTTAGACAAGGTTTGACACCGCAATCTGCTAGGAGCGTTTGC  
 GAAATTATAAAGAGGCATACTAAGTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTA  
 TTAGCTCATATTGGTGTGGCCATGATCACCATTATGTCAGGACAACCGGTCAAACAGAC  
 TTATCTAAAGTGTGTTATTTTGTATGGCGAACCAGAAATGCGCAAGATAAAGCGCGATT  
 TCTTGTCCAGATCACAACCTGTTCAGTTAAATCTGCTATTGTAGTTCCTCTAAAAATAAAT  
 GATAAACTGTGGGTGCCCTTAAATGTACTTTGTCAGGAGATAAGCAATGTCTGAGGTG  
 GAGGAAAACCTAGTCTTGGTTTAGCGCAAATATTTTTCAGGACAACCTGGCAATGGGGATA  
 ACAGAGGAACAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCAAAAATC  
 AACCTCATTTCTTCTTTTAAATGCCATTAAACACAATTAGTGCAATTAATCCGTATTGATTCT  
 GATAAAGCAGGTTATGCTAGTGCAGTTAAGTACTTTTGTAGAACAAGTTTTCAGGGT  
 GGTTCAGGATCGTGAGGTAAAGCTTGAGCAAGAAAATCACATGTGGATGCTTATATGAAT  
 GTTGAAAAATTAAGTTTCCCTGATAAATATCAGTTATCTTATGATATTAGTGACCCAGAA  
 AAAATGAAGTTACCACTTTTGGTTTACAGGTACTGGTAGAGAAATGCAGTTTCGACATGCT  
 TTTCAAGAAACGTAAAGACGACCAACCATATATTGGTTCAAATAAAGCCAGATGGTCATTAT  
 TATTGTTGTTCTGTAGTGACAATGGACAAGGAATCTCAGATACTATCATTGATAAATTA  
 GGTCAAGAAACAGTTGCAGAGAGTAAGGGTACAGGTACTGCTCTAGTTAATCTAAATAAC  
 AGGCTGAATTTATTATATGTTAGTGTAAAGTTGCCCTTCAATTTTCAGCGCAAGAATGGT  
 ACAAAAGTTTGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAAT  
 TCT

SEQ ID NO. 5802

STRAIN 090

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTAT  
 GATTTTAGCCCTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAATTG  
 AAGAGCGGTCTAAACGTGAAACGGTAGTACTTGTCTCATTTTCGGCTTG  
 TTTGTTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAG  
 TTTGGTCGAGCGCCCTTTCTAACAACGATTTCCTATTCTGACTCACTTG  
 CTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCT  
 CTGGTTGGATCAATTGTTGGTTTATTGGAGGAGTTTCATCGCTTTTTC  
 AGGAAGCTTTTCAGGTTCTTTCTATATTGTTCAGTTTCAGTTCTAGTCGGCA  
 TTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCCT  
 TCAACAAGCCAAGTTATTTAATTAGTATTATTGCCGAAAGTATCCAGAT  
 GCTATTGTTGGTATTTTACAGGATGGGAACCTGTCAAATGATTGTCA  
 TTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCCTTGCAGATT  
 TTGAAAACCTTATTGTTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAG  
 AGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTCAGACAAGGTT  
 TGACACCGCAATCTGCTAGGAGCGTTTTCGCAAAATTATAAAGAGGCATACT  
 AACTTTGATGCTGTAGGATTAAACAGATCGGTCAAACGTATTAGCTCATAT  
 TGGTGTGGCCATGATCACCATTATGTCAGGACAACAGTCAAACAGACC  
 TATCTAAAGTGTGTTATTTTGTATGGCGAACCAGAAATTGCGCAAGATAAA  
 GCGGCGATTCTTGTCCAGATCACAACGTTCAGTTAAATCTGCTATTGTT  
 AGTTCCCTCTAAATAAATAAGATAAAACTGTGGGTGCCCTTAAATGTTACT  
 TTGAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGGT  
 TTAGCGCAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACA  
 AATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATCA  
 ACCCTCATTTCTCTTAAATGCCATTAAACCAATTAGTGCAATTAATCCGT  
 ATTGATTCTGATAAAGCAGTTATGCACTGATGCAGTTAAGTACTTTT  
 TAGAACAAGTTTTCAGGTTGGTCAGGATCGTGAGGTAACGCTTGAGCAAG  
 AAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCT  
 GATAAATATCAGTTATCTTATGATATTAGTGACCCAGAAAAATGAAGTT  
 ACCGCTTTTGGTTTACAGGTACTGGTAGAGAAATGCAGTTAGACATGCTT  
 TCAAGAACGTAAGACGGAACAACCATATATTGGTTCAAATAAAGCCAGAT  
 GGTCAATTATTATGTTCTTCTGTTAGTGACAATGGACAAGGAATCTCAGA  
 TACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTA  
 CAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGT  
 AGTGTAAAGTTGCCCTTCAATTTTCAGGCGACAAGAAATGGTACAAAGTTT  
 GTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATT  
 CT

SEQ ID NO. 5803

STRAIN A909

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTAT  
 GATTTTAGCCCTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAATTG  
 AAGAGCGGTCTAAACGTGAAACGGTAGTCTTGTCTCATTTTCGGCTTG  
 TTTGTTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAG  
 TTTGGTCGAGCGCCCTTTCTAACAACGATTTCCTATTCTGACTCACTTG  
 CTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCT  
 CTGGTTGGATCAATTGTTGGTTTATTGGAGGAGTTTCATCGCTTTTTC  
 AGGAAGCTTTTCAGGTTCTTTCTATATTGTTCAGTTTCAGTTCTAGTCGGCA  
 TTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCCT

Table 58: Comparative Sequences relating to SAG0182

TCAACAAGCCAAGTTATTTTAATTAGTATTATGCGGAAAGTATCCAGAT  
GCTATTTGTTGGCAATTTTACAGGATGGGAACCTTGTCAAAATGATTGTCA  
TTCCAAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGGGATT  
TTGAAAACCTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAG  
AGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTT  
TGACACCGCAATCTGTAGGAGCGTTTTCGAAATTATAAAGAGGCATACT  
AACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGCTCATAT  
TGGTGTGGCCATGATCACCATATTGCAGGACAACCGGTCAAACAGACT  
TATCTAAAAGTGTATTTTGTATGGCGAACCAAGAATTGCGCAAGATAAA  
GCGCGCATTTCTGTCCAGATCACAACCTGTCAAGTTAAATTCGTATTGT  
AGTTCTCTAAAAATAAATGATAAACTGTGGGTGCCCTTAAAAATGTACT  
TTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGGT  
TTAGCGCAAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACA  
AAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAATCA  
ACCCTCATTTCTTCTTAAATGCCATTAAACAAATTAGTGCATTAAATCCGT  
ATTGATTCTGATAAAGCACGTTATGCACCTGATGCAGTTAAGTACTTTT  
TAGAACCAAGTTTGCAGGGTGGTCAAGGATCGTGAGGTAACGCTTGAGCAAG  
AAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCT  
GATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAATGAAGTT  
ACCACCTTTTGGTTTACAGGTAAGTGCAGGATGCAGTTGCAGATGCTT  
TCAAAGAGACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGAT  
GGTCATTATTATTTGTGTTCTGTTAGTGACAATGGACAAGGAATCTCAGA  
TACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGGTAAGGGTA  
CAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGT  
AGTGTAAGTTGCCCTTCAATTTTCGAGCGACAAGAAATGGTACAAAAGTTTG  
GTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAAATTTTAATT  
CT

SEQ ID NO. 5804

STRAIN H36B

TTGATGGTGTGTTTATTCCAAAGGCTAGGAATTATTATG  
ATTTTAGCCCTTTTATTTGGTAAATAATAGTTATTTTCAGACAGTTAATTGA  
AGAGCGGTCTAAACGTTGAAACGGTAGTCTTGTCTCATCTTTTCGGCTTGT  
TTGTTATTTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAGT  
TTGGTTCGAGCGCCCTTTTCTAACACGATTTCTCATTTCTGACTCACTTGC  
TAATACAGGACTTTAGTTATTACACCGCAAGTTTGGTTGGTGGACCTC  
TGGTTGGATCAATTTGTTGGTTTATTTGGAGGAGTTTCATCGCTTTTTCAA  
GGAAGCTTTTCAGGTTCTTTCTATATTGTCTAGTTTCTAGTCTCGGCAT  
TGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCTT  
CAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGATG  
CTATTTGTTGGCAATTTTACAGGATGGGAACTTGTCAAAATGATTGTCTAT  
TCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGGCATTT  
TGAAAACCTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGA  
GATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTTT  
GACACCGCAATCTGCTAGGAGCGTTTTCGAAATTATAAAGAGGCATACTA  
ACTTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCATATT  
GGTGTGGCCATGATCACCATTATTCAGGACAACCGGTCAAACAGACTT  
ATCTAAAAGTGTATTTTGTATGGCGAACCAAGAATTGCGCAAGATAAAG  
CGGCGATTTCTTGTCCAGATCACAACCTGTCAAGTTAAATTCGTCTATTGTA  
GTTCTCTAAAAATAAATGATAAACTGTGGGTGCCCTTAAAAATGTACTT  
TGCAAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGGTT  
TAGCGCAAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACA  
AATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAATCAA  
CCCTCATTTCTTCTTAAATGCCATTAAACAAATTAGTGCATTAAATCCGTA  
TTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTT  
AGAACAAGTTTGCAGGGTGGTCAAGGATCGTGAGGTAACGCTTGAGCAAGA  
AAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCTG  
ATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAATGAAGTTA  
CCACCTTTTGGTTTACAGGTAAGTGCAGGATGAGGATGAGGATGCTT  
CAAAGAAGTAAAGACGACAACCATATATTGGTTCAAATAAAGCCAGATG  
GTCATTATTATTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGAT  
ACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTAC  
AGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGTA  
GTGTAAGTTGCCCTTCAATTTTCGAGCGACAAGAAATGGTACAAAAGTTTG  
TATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAAATTTTAATT  
T

SEQ ID NO. 5805

STRAIN 18RS21

TTGATGGTGTGTTTATTCCAAAGGCTAGGAATTATTATG  
ATTTTAGCCCTTTTATTTGGTAAATAATAGTTATTTTAGACAGTTAATTGA  
AGAGCGGTCTAAACGTTGAAACGGTAGTCTTGTCTCATCTTTTCGGCTTGT  
TTGTTATTTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAGT  
TTGGTTCGAGCGCCCTTTTCTAACACGATTTCTCATTTCTGACTCACTTGC  
TAATACAGGACTTTAGTTATTACACCGCAAGTTTGGTTGGTGGACCTC  
TGGTTGGATCAATTTGTTGGTTTATTTGGAGGAGTTTCATCGCTTTTTCAA  
GGAAGCTTTTTCAGGTTCTTTCTATATTGTCTAGTTTCTAGTCTCGGCAT  
TGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCTT  
CAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGATG  
CTATTTGTTGGCAATTTTACAGGATGGGAACTTGTCAAATGATTGTCTAT  
TCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGGCATTT  
TGAAAACCTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGA  
GATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTTT

Table 58: Comparative Sequences relating to SAG0182

GACACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAGAGGCATACTA  
 ACTTTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCATATT  
 GGTGTTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGACTT  
 ATCTAAAAGTGTATTATTTTGTATGGCGAACCAGGATTGCGCAAGATAAAG  
 CGGCGATTCTTGTCCAGATCAACAACGTGTCAGTTAAATTCTGCTATTGTA  
 GTTCCTCTAAAAATAAATGATAAACTGTGGTGCCTTAAAAATGTACTT  
 TGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGGTT  
 TAGCGCAAAATATTTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACAA  
 AATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCAAAATCAA  
 CCTCATTTCTTCTTAATGCCATTAAACAAATTAGTGCATTATCCGTA  
 TTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTTT  
 AGAACCAAGTTTGCAGGGTGGTCAGGATCGTGAGGTAAACGCTTGAGCAAGA  
 AAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCTG  
 ATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAAATGAAGTTA  
 CCACCTTTTGGTTTACAGGTACTGGTAGAGAAATGCAGTTCCGACATGCTTT  
 CAAAGAACGTAAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATG  
 GTCATTATTATTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGAT  
 ACTATCATTTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTAC  
 AGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGTA  
 GTGTAAGTTGCTTCTATTTTTCGAGCGACAAGATGGTACAAAAGTTTGG  
 TATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATTC  
 T

SEQ ID NO. 5806

STRAIN M732

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTATGAT  
 TTTAGCCTTTTATTGGTAAATAATAGTTAATTCAGACAGTTAATTGAAG  
 AGCGGTCTAAACGTGAAACGGTAGTCTTGTCTATCATTTTCGGCTTGT  
 GTTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAGTTT  
 GGTGCGAGCGCCCTTTTCTAACAACGATTCCCATTTCTGACTCAGTTGCTA  
 ATCAAGGACITTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCTCTG  
 GTTGGATCAATTGTTGGTTTATTGGAGGAGTTTATCGCTTTTTTCAAGG  
 AAGCTTTTCAGGTTCTTTCTATATTGTGAGTTCAGTTCTAGTCCGCAATG  
 TTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAAACCATCTCTACCTTCA  
 ACAAGCCAAGTTATTTTAATTAGTATTATTGCGGAAAGTATCCAGATGCT  
 ATTTGTTGGCATTTTTTACAGGATGGGAACCTTGTCAAATGATTGTCAATC  
 CAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTTCGCAATTTG  
 AAAACTTATTGTTCAATGAAAGTCAGTTACGCGCAGTTCAAACGAGAGA  
 TGTTCTTGAATGACTCGACAGACTCTGCCCTACCTTAGACAAGGTTTGA  
 CACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAGAGGCATACTAAC  
 TTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCATATTGG  
 TATTGGCCATGATCACCATTATGCAGGACAACCGGTCAAACAGACTTAT  
 CTAAAAAGTGTATTTTTGTATGGCGAACCAGAAATTGCGCAAGATAAAGCG  
 GCGAATTCTTGTCCAGATCAACAACGTGTCAGTTAAATCTGCTATTGTAGT  
 TCCCTCTAAAAATAAATGATAAACTGTGTGTCCTTAAAAATGTACTTTG  
 CAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGGTTTA  
 GCGCAAAATATTTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACAAA  
 TAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCAAAATCAACC  
 CTCATTTCTTCTTAATGCCATTAAACAAATTAGTGCATTATCCGTATT  
 GATTCTGATAAAGCAGTTATGCACTGATGCAGTTAAGTACTTTTTTTAG  
 AACAGTTTGCAGGTGGTTCAGGATCGTGAGGTAAACGCTTGAGCAAGAAA  
 AATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCTGAT  
 AAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAAATGAAGTTACC  
 GCCTTTTGGTTTACAGGTACTGGTAGAGAAATGCAGTTCCGACATGCTTTCA  
 AAGAACGTAAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATGGT  
 CATATTATTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGATAC  
 TATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGACAG  
 GTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGTAGT  
 GTAAAGTTGCTTCTATTTTTCGAGCGACAAGAAATGGTACAAAAGTTTGGTA  
 TCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATTC

SEQ ID NO. 5807

STRAIN COH1

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTAT  
 TATGATTTTAGCCTTTTATTGGTAAATAATAGTTAATTCAGACAGTTAA  
 TTGAAGAGCGGTCTAAACGTGAAACGGTAGTCTTGTCTATCATTTTCGGC  
 TTGTTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCG  
 AAGTTTGGTTCGAGCGCCCTTTTCTAACAACGATTCCCATTTCTGACTCAC  
 TTGCTAATACAAGGACITTAGTTATTACAACGGCAAGTTTGGTTGGTGGGA  
 CCTCTGGTTGGATCAATTGTTGGTTTATTGGAGGAGTTTATCGCTTTTTT  
 TCAAGGAAGCTTTTTCAGGTTCTTTCTATATTGTGAGTTTCTAGTTCG  
 GCATTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAAACCATCTCTAC  
 CCTTCAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCA  
 GATGCTATTGTTGGCATTTTTACAGGATGGGAACCTTGTCAAATGATTG  
 TCAATTCGAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTTCG  
 ATTTTGAACCTTATTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAAC  
 GAGAGATGTTCTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAG  
 GTTTGACACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAAGAGGCAT  
 ACTAATCTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCA  
 TATTGGTGTGGCCATGATCACCATTATGCAGGACAACCGGTCAAACAG  
 ACTTATCTAAAAGTGTATTTTTGTATGGCGAACCAGAAATTGCGCAAGAT  
 AAAGCGCGGATTCTTGTCCAGATCAACAACGTGTCAGTTAAATCTGCTAT  
 TGTAGTTCTCTAAAAATAAATGATAAACTGTGTGTCCTTAAAAATGT



Table 58: Comparative Sequences relating to SAG0182

ACTTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTT  
 GGTTTAGCGCAAAATATTTTCAGGACCACTGGCAATGGGGATAACAGAGGA  
 ACAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAA  
 TCAACCCCTCATTTCTTCTTTAATGCCATTAAACACAATTAGTGCATTAAATC  
 CGTATTGATTCTGATAAAGCACGTTATGCACGTGATGCAGTTAAGTACTTT  
 TTTTAGAACAAAGTTTGCAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGC  
 AAGAAAATCACATGTGGATGCTTATATGAATGTTGAAAATTACGTTTC  
 CCTGATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAATGAA  
 GTTACCGCCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTTCGACATG  
 CTTTCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCA  
 GATGGTCATTATTATGTGTTTCTGTTAGTGACAATGGACAAGGAATCTC  
 AGATACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGG  
 GGACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATAT  
 GGTAGTGTAAAGTTGCCTTCATTTTCGAGCGACAAGAATGGTACAAAAGT  
 TTGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTA  
 ATTCT

SEQ ID NO. 5808

STRAIN M781

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTA  
 TGATTTAGCCCTTTTATTTGGTAAATAATAGTTATTTTCAGACAGTTAATT  
 GAAGAGCGGTCTAAACGTGAAACGGTAGTCTTGTGTCATCATTTTCGGCTT  
 GTTGTGTTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAA  
 GTTGGTCGAGCGCCCTTTTCTAACAACGATTTCCTATTCTGACTCACTT  
 GCTAATACAGGACTTTAGTTATTACACGGCAAGTTTGGTTGGTGGACC  
 TCTGGTTGGATCAATTGTTGGTTTATTTGGAGGAGTTTCATCGCTTTTTC  
 AAGGAAGCTTTTCAGGTTCTTTCTATATGTCAGTTTCAGTTCTAGTCGGC  
 ATTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCC  
 TTCAACAAGCCAAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGA  
 TGTATTGTTGGCATTTTACAGGATGGGAACCTGTCAAATGATTGTC  
 ATTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGCGAT  
 TTGAAAACCTTATTGTCAAATGAAAGTCAGTTACGCGCAGTCAAAACGA  
 GAGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGT  
 TTGACACCGCAATCTGCTAGGAGCGTTTGGGAAATATAAAGAGGCATAC  
 TAACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTATTAGTCTATA  
 TTGGTGTGGCCATGATCACCATATTGCGAGCAACCGGTCAAACAGAC  
 TTATCTAAAAGTGTATTTTTGATGGCGAACCAGAAATTGCGCAAGATAA  
 AGCGGCGATTCTTGTGTCAGATCACAACTGTCAGTTAAATCTGCTATTG  
 TAGTTCCTCTAAAAATAAATGATAAACTGTGTGTGCTTAAAAATGTAC  
 TTTGCAAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGG  
 TTTAGCGCAAAATATTTTCAGGACAACCTGGCAATGGGATAACAGAGGAAC  
 AAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATC  
 AACCCCTCATTTCTTCTTTAATGCCATTAAACACAATTAGTGCATTAAATCG  
 TATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTT  
 TTAGAACAAGTTTGCAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAA  
 GAAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCC  
 TGATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAATGAAGT  
 TACCGCCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTTCGACATGCT  
 TTCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGA  
 TGGTCATTATTATTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAG  
 ATACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGG  
 ACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGG  
 TAGTGTAAAGTTGCCCTTCATTTTCGAGCGACAAGAATGGTACAAAAGTTT  
 GGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAAT  
 TCT

SEQ ID NO. 5809

STRAIN CJB110

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTAT  
 GATTTTAGCCCTTTTATTTGGTAAATAATAGTTATTTTCAGACAGTTAATTG  
 AAGAGCGGTCTAAACGTGAAACGGTAGTACTTGTGTCATCATTTTCGGCTTG  
 TTTGTTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAG  
 TTTGGTCGAGCGCCCTTTTCTAACAACGATTTCCTATTCTGACTCACTTG  
 CTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCT  
 CTGGTTGGATCAATTGTTGGTTTATTTGGAGGAGTTTCATCGCTTTTTC  
 AGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTTCAGTTCTAGTCGGCA  
 TTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCCT  
 TCAACAAGCCAAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGAT  
 GCTATTGTTGGTATTTTTACAGGATGGGAACCTGTCAAATGATTGTCA  
 TTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGCGATT  
 TTGAAAACCTTATTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAG  
 AGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTCAGACAAGGTT  
 TGACACCGCAATCTGCTAGGAGCGTTTGGGAAATATAAAGAGGCATACCT  
 AACCTTGATGCTGTAGGATTAACAGATCGGTCAAACGTATTAGCTCATAT  
 TGGTGTGGCCATGATCACCATATTGCGAGCAACCAAGTCAAACAGACC  
 TATCTAAAAGTGTATTTTTGGTGGCAACCAAGAATTGCGCAAGATAAA  
 CGGCGGATTTCTGTCAGATCACAACTGTCAGTTAAATCTGCTATTGT  
 AGTTCCTCTAAAAATAAATGATAAACTGTGGGTGCTTAAAAATGTACT  
 TTGCAAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGGT  
 TTAGCGCAAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACA  
 AAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATCA  
 ACCCTCATTTTCTTCTTTAATGCCATTAAACACAATTAGTGCATTAAATCGT  
 ATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTT

Table 58: Comparative Sequences relating to SAG0182

TAGAACAAGTTTTCGAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAG  
 AAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCT  
 GATAAATATCAGTTATCTTATGATATTAGTGACCCAGAAAAAATGAAGTT  
 ACCGCCCTTTGGTTTACAGGTAAGTGGTAGAATGCAGTTAGACATGCTT  
 TCAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGAT  
 GGTCAATTATTATGTTGTTCTGTTAGTGACAATGGACAAGGAATCTCAGA  
 TACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTA  
 CAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGTT  
 AGTGTAAAGTTGCCCTTCATTTTTCGAGCGACAAGAATGTTACAAAAGTTTG  
 GTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAAATTTTAATT  
 CT

SEQ ID NO. 5810

STRAIN 1169NT

TTGATGGTGTGTTATTCCAAGGCTAGGAATTATT  
 ATGATTTTAGCCCTTTTATTGGTAATAATAGTTATTTCAGACAGTTAAT  
 TGAAGAGCGGTCTAAACGTGAAACGGTAGTACTTGTATCATTTTCGGCT  
 TGTTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGA  
 AGTTTGGTCGAGCGCCCTTTCTAACAACGATTTCTCATTTCTGACTCACT  
 TGCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGAC  
 CTCTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTTCATCGCTTTTT  
 CAAGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTTCAAGTTCTAGTCGG  
 CATTGTGAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACC  
 CTTCAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAG  
 ATGCTATTTGTTGGCATTTTTACAGGATGGGAACCTGTCAAATGATTGT  
 CATTCCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTTCGCA  
 TTTTGAAAACTTATTGTTCAAAATGAAAGTCAGTTACGCGCAGTTCAAACG  
 AGAGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGG  
 TTTGACACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAAGAGGCATA  
 CTAATTTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCAT  
 ATTGGTGTGGCCATGATCACCATATTGCAGGACAACCAAGTCAAAACAGA  
 CCTATCTAAAGTGTATTATTGATGGCGAACCAAGAATTGCGCAAGATA  
 AAGCGGCGATTCTTGTCCAGATCACAACGTGTCAGTTAAATTCTGCTATT  
 GTAGTTCTCTAAAAATAAATGATAAACTGTGGGTGCCCTAAAAATGTA  
 CTTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTCTTG  
 GTTTAGCGCAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAA  
 CAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAAT  
 CAACCTCATTTCTCTTTAATGCCATTAAACAATTAGTGCATTATATCC  
 GTATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTT  
 TTTAGAACCAAGTTTGCAGGTGGTCAGGATCGTGAGGTAAACGCTTGAGCA  
 AGAAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCC  
 CTGATAAATATCAGTTATCTTATGATATTAGTGACCCAGAAAAAATGAAG  
 TTACCGCCCTTTGGTTTACAGGTAAGTGGTAGAATGCAGTTCCGACATGC  
 TTTTAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAG  
 ATGGTCATTATTATTTGTTTCTGTTAGTGACAATGGACAAGGAATCTCA  
 GATACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGG  
 TACAGGTAAGTCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATG  
 GTAGTGTAAAGTTGCCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTT  
 TGGTATCGAATACCTAATAGAATAAAGGGAGGATGAGCATGAAAAATTTTAA  
 TTCT

SEQ ID NO. 5810

STRAIN JM9130013

TTGATGGTGTGTTATTCCAAGGCTAGGAATTATT  
 ATGATTTTAGCCCTTTTATTGGTAATAATAGTTATTTCAGACAGTTAAT  
 TGAAGAGCGGTCTAAACGTGAAACGGTAGTCTTGTATCATTTTCGGCT  
 TGTTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGA  
 AGTTTGGTCGAGCGCCCTTTCTAACAACGATTTCTCATTTCTGACTCACT  
 TGCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGAC  
 CTCTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTTCATCGCTTTTT  
 CAAGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTTCAAGTTCTAGTCGG  
 CATTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACC  
 CTTCAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAG  
 ATGCTATTGTTGGCATTTTTACAGGATGGGAACCTGTCAAATGATTGT  
 CATTCCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTTCGCA  
 TTTTGAAAACTTATTGTTCAAAATGAAAGTCAGTTACGCGCAGTTCAAACG  
 AGAGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGG  
 TTTGACACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAAGAGGCATA  
 CTAACCTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCAT  
 ATTGGTGTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGA  
 CTTATCTAAAGTGTATTATTGATGGCGAACCAAGAATTGCGCAAGATA  
 AAGCGGCGATTCTTGTCCAGATCACAACGTGTCAGTTAAATTCTGCTATT  
 GTAGTTCTCTAAAAATAAATGATAAACTGTGGGTGCCCTAAAAATGTA  
 CTTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTCTTG  
 GTTTAGCGCAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAA  
 CAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAAT  
 CAACCTCATTTCTCTTTAATGCCATTAAACAATTAGTGCATTATATCC  
 GTATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTT  
 TTTAGAACCAAGTTTGCAGGTGGTCAGGATCGTGAGGTAAACGCTTGAGCA  
 agAAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCC  
 CTGATAAATATCAGTTATCTTATGATATTAGTGACCCAGAAAAAATGAAG  
 TTACCACTTTTGGTTTACAGGTAAGTGGTAGAATGCAGTTCCGACATGC  
 TTTCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAG

Table 58: Comparative Sequences relating to SAG0182

ATGGTCATTATTATTGTTCTGTTAGTGACAATGGACAAGGAATCTCA  
 GATACATCATTCATTGATAAATTAGGTCAAGAAACAGTTGCGAGAGTAGGAGG  
 TACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTTATTATG  
 GTAGTGTAAAGTTGCTTCTATTTTCGAGCGACAAGAAATGGTACAAAAGTT  
 TGGTATCGAATACCTAATAGAATAAGGAGGATGAGCATGAAAATTTTAA  
 TTCT

## MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa442667.2{\*} January 13, 2003 06:34 ..

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1                                     50
msa442667.2{248_18RS21} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_2603} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_A909} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_H36B} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_JM9130013} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_COH1} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_M781} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_M732} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_090} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_CJB110} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_1169NT} TTGATGGTGT TGTTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
Consensus *****

51                                     100
msa442667.2{248_18RS21} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_2603} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_A909} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_H36B} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_JM9130013} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_COH1} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_M781} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_M732} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_090} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_CJB110} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_1169NT} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
Consensus *****

101                                    150
msa442667.2{248_18RS21} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_2603} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_A909} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_H36B} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_JM9130013} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_COH1} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_M781} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_M732} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_090} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_CJB110} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
msa442667.2{248_1169NT} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTTATTATA
Consensus *****

151                                    200
msa442667.2{248_18RS21} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_2603} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_A909} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_H36B} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_JM9130013} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_COH1} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_M781} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_M732} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_090} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_CJB110} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_1169NT} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
Consensus *****

201                                    250
msa442667.2{248_18RS21} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_2603} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_A909} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_H36B} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_JM9130013} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_COH1} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_M781} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_M732} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_090} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_CJB110} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_1169NT} CCCTTTCTA ACAACGATTT CtCATTCTGA CTCACTTGCT AATACAAGGA
Consensus *****

251                                    300
msa442667.2{248_18RS21} CTTTAGTTAT TACAACGGCA AGTTTGTTG GTGGACCTCT GGTGGATCA
msa442667.2{248_2603} CTTTAGTTAT TACAACGGCA AGTTTGTTG GTGGACCTCT GGTGGATCA

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Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_A909}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_H36B}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_JM9130013}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_COH1}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_M781}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_M732}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_090}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_CJB110}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_1169NT}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_2603}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_A909}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_H36B}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_JM9130013}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_COH1}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_M781}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_M732}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_090}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_CJB110}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_1169NT}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_2603}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_A909}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_H36B}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_JM9130013}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_COH1}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_M781}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_M732}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_090}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_CJB110}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
msa442667.2{248_1169NT}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTAGCGGAA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_2603}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_A909}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_H36B}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_JM9130013}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_COH1}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_M781}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_M732}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_090}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_CJB110}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_1169NT}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_2603}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_A909}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_H36B}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_JM9130013}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_COH1}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_M781}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_M732}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_090}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_CJB110}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_1169NT}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_2603}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_A909}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_H36B}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_JM9130013}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_COH1}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_M781}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_M732}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_090}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_CJB110}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_1169NT}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	TTTTAAATAG	TTTAGTTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACITAT

Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_2603}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_A909}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_H36B}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_JM9130013}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_COH1}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_M781}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_M732}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_090}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_CJB110}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_1169NT}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_2603}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_A909}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_H36B}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_JM9130013}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_COH1}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_M781}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_M732}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_090}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_CJB110}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_1169NT}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_2603}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_A909}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_H36B}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_JM9130013}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_COH1}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_M781}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_M732}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_090}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_CJB110}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_1169NT}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_2603}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_A909}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_H36B}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_JM9130013}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_COH1}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_M781}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_M732}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_090}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_CJB110}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_1169NT}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_2603}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_A909}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_H36B}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_JM9130013}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_COH1}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_M781}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_M732}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_090}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_CJB110}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_1169NT}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_2603}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_A909}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_H36B}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_JM9130013}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_COH1}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_M781}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_M732}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_090}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_CJB110}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_1169NT}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
Consensus	*****	*****	*****	*****	*****

Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_18RS21}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_2603}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_A909}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_H36B}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_JM9130013}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_COH1}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_M781}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_M732}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_090}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_CJB110}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
msa442667.2{248_1169NT}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTTC
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_2603}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_A909}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_H36B}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_JM9130013}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_COH1}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_M781}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_M732}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_090}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_CJB110}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_1169NT}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_2603}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_A909}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_H36B}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_JM9130013}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_COH1}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_M781}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_M732}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_090}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_CJB110}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_1169NT}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_2603}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_A909}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_H36B}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_JM9130013}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_COH1}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_M781}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_M732}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_090}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_CJB110}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_1169NT}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_2603}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_A909}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_H36B}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_JM9130013}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_COH1}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_M781}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_M732}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_090}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_CJB110}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_1169NT}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_2603}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_A909}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_H36B}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_JM9130013}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_COH1}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_M781}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_M732}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_090}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_CJB110}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_1169NT}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
Consensus	*****	*****	*****	*****	*****

Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_18RS21}		1151	1200	
msa442667.2{248_2603}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
msa442667.2{248_A909}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
msa442667.2{248_H36B}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
msa442667.2{248_JM9130013}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
msa442667.2{248_COH1}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
msa442667.2{248_M781}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
msa442667.2{248_M732}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
msa442667.2{248_090}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
msa442667.2{248_CJB110}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
msa442667.2{248_1169NT}		TCTTTAATGC	CATTAACACA	ATTAGTGCAT
Consensus		*****	*****	*****
msa442667.2{248_18RS21}		1201	1250	
msa442667.2{248_2603}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
msa442667.2{248_A909}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
msa442667.2{248_H36B}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
msa442667.2{248_JM9130013}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
msa442667.2{248_COH1}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
msa442667.2{248_M781}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
msa442667.2{248_M732}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
msa442667.2{248_090}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
msa442667.2{248_CJB110}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
msa442667.2{248_1169NT}		AAAGCACGTT	ATGCACGTG	GCAGTTAAGT
Consensus		*****	*****	*****
msa442667.2{248_18RS21}		1251	1300	
msa442667.2{248_2603}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
msa442667.2{248_A909}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
msa442667.2{248_H36B}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
msa442667.2{248_JM9130013}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
msa442667.2{248_COH1}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
msa442667.2{248_M781}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
msa442667.2{248_M732}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
msa442667.2{248_090}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
msa442667.2{248_CJB110}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
msa442667.2{248_1169NT}		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT
Consensus		***-*****	*****	*****
msa442667.2{248_18RS21}		1301	1350	
msa442667.2{248_2603}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
msa442667.2{248_A909}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
msa442667.2{248_H36B}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
msa442667.2{248_JM9130013}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
msa442667.2{248_COH1}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
msa442667.2{248_M781}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
msa442667.2{248_M732}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
msa442667.2{248_090}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
msa442667.2{248_CJB110}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
msa442667.2{248_1169NT}		TGGATGCTTA	TATGAATGTT	GAAAAATTAC
Consensus		*****	*****	*****
msa442667.2{248_18RS21}		1351	1400	
msa442667.2{248_2603}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
msa442667.2{248_A909}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
msa442667.2{248_H36B}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
msa442667.2{248_JM9130013}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
msa442667.2{248_COH1}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
msa442667.2{248_M781}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
msa442667.2{248_M732}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
msa442667.2{248_090}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
msa442667.2{248_CJB110}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
msa442667.2{248_1169NT}		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA
Consensus		*****	*****	*****
msa442667.2{248_18RS21}		1401	1450	
msa442667.2{248_2603}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
msa442667.2{248_A909}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
msa442667.2{248_H36B}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
msa442667.2{248_JM9130013}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
msa442667.2{248_COH1}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
msa442667.2{248_M781}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
msa442667.2{248_M732}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
msa442667.2{248_090}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
msa442667.2{248_CJB110}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
msa442667.2{248_1169NT}		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG
Consensus		*****	*****	*****

	1451		1501
msa442667.2{248_18RS21}	AGACGGGACAA	CCATATATTG	GTTCAAATAA AGCCAGATGG TCATTATTAT
msa442667.2{248_2603}	AGACGGGACAA	CCATATATTG	GTTCAAATAA AGCCAGATGG TCATTATTAT
msa442667.2{248_A909}	AGACGGGACAA	CCATATATTG	GTTCAAATAA AGCCAGATGG TCATTATTAT
msa442667.2{248_H36B}	AGACGGGACAA	CCATATATTG	GTTCAAATAA AGCCAGATGG TCATTATTAT
msa442667.2{248_JM9130013}	AGACGGGACAA	CCATATATTG	GTTCAAATAA AGCCAGATGG TCATTATTAT
msa442667.2{248_COH1}	AGACGGGACAA	CCATATATTG	GTTCAAATAA AGCCAGATGG TCATTATTAT
msa442667.2{248_M781}	AGACGGGACAA	CCATATATTG	GTTCAAATAA AGCCAGATGG TCATTATTAT
msa442667.2{248_M732}	AGACGGGACAA	CCATATATTG	GTTCAAATAA AGCCAGATGG TCATTATTAT
msa442667.2{248_O90}	AGACGGGACAA	CCATATATTG	GTTCAAATAA AGCCAGATGG TCATTATTAT
msa442667.2{248_CJB110}	AGACGGGACAA	CCATATATTG	GTTCAAATAA AGCCAGATGG TCATTATTAT
msa442667.2{248_1169NT}	AGACGGGACAA	CCATATATTG	GTTCAAATAA AGCCAGATGG TCATTATTAT
Consensus	*****	*****	*****
	1501		1550
msa442667.2{248_18RS21}	TGTGTTTTCTG	TTAGTGACAA	TGGACAAGGA ATCTCAGATA CTATCATTTGA
msa442667.2{248_2603}	TGTGTTTTCTG	TTAGTGACAA	TGGACAAGGA ATCTCAGATA CTATCATTTGA
msa442667.2{248_A909}	TGTGTTTTCTG	TTAGTGACAA	TGGACAAGGA ATCTCAGATA CTATCATTTGA
msa442667.2{248_H36B}	TGTGTTTTCTG	TTAGTGACAA	TGGACAAGGA ATCTCAGATA CTATCATTTGA
msa442667.2{248_JM9130013}	TGTGTTTTCTG	TTAGTGACAA	TGGACAAGGA ATCTCAGATA CTATCATTTGA
msa442667.2{248_COH1}	TGTGTTTTCTG	TTAGTGACAA	TGGACAAGGA ATCTCAGATA CTATCATTTGA
msa442667.2{248_M781}	TGTGTTTTCTG	TTAGTGACAA	TGGACAAGGA ATCTCAGATA CTATCATTTGA
msa442667.2{248_M732}	TGTGTTTTCTG	TTAGTGACAA	TGGACAAGGA ATCTCAGATA CTATCATTTGA
msa442667.2{248_O90}	TGTGTTTTCTG	TTAGTGACAA	TGGACAAGGA ATCTCAGATA CTATCATTTGA
msa442667.2{248_CJB110}	TGTGTTTTCTG	TTAGTGACAA	TGGACAAGGA ATCTCAGATA CTATCATTTGA
msa442667.2{248_1169NT}	TGTGTTTTCTG	TTAGTGACAA	TGGACAAGGA ATCTCAGATA CTATCATTTGA
Consensus	*****	*****	*****
	1551		1600
msa442667.2{248_18RS21}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG TAAGGGTACA GGTACTGCTC
msa442667.2{248_2603}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG TAAGGGTACA GGTACTGCTC
msa442667.2{248_A909}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG TAAGGGTACA GGTACTGCTC
msa442667.2{248_H36B}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG TAAGGGTACA GGTACTGCTC
msa442667.2{248_JM9130013}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG TAAGGGTACA GGTACTGCTC
msa442667.2{248_COH1}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG TAAGGGTACA GGTACTGCTC
msa442667.2{248_M781}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG TAAGGGTACA GGTACTGCTC
msa442667.2{248_M732}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG TAAGGGTACA GGTACTGCTC
msa442667.2{248_O90}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG TAAGGGTACA GGTACTGCTC
msa442667.2{248_CJB110}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG TAAGGGTACA GGTACTGCTC
msa442667.2{248_1169NT}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG TAAGGGTACA GGTACTGCTC
Consensus	*****	*****	*****-***
	1601		1650
msa442667.2{248_18RS21}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT TATATGGTAG TGTAAGTTGTC
msa442667.2{248_2603}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT TATATGGTAG TGTAAGTTGTC
msa442667.2{248_A909}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT TATATGGTAG TGTAAGTTGTC
msa442667.2{248_H36B}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT TATATGGTAG TGTAAGTTGTC
msa442667.2{248_JM9130013}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT TATATGGTAG TGTAAGTTGTC
msa442667.2{248_COH1}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT TATATGGTAG TGTAAGTTGTC
msa442667.2{248_M781}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT TATATGGTAG TGTAAGTTGTC
msa442667.2{248_M732}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT TATATGGTAG TGTAAGTTGTC
msa442667.2{248_O90}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT TATATGGTAG TGTAAGTTGTC
msa442667.2{248_CJB110}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT TATATGGTAG TGTAAGTTGTC
msa442667.2{248_1169NT}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT TATATGGTAG TGTAAGTTGTC
Consensus	*****	*****	*****
	1651		1700
msa442667.2{248_18RS21}	CTTCATTTTT	CGAGCGACAA	GAATGGTACA AAAGTTTGGT ATCGAATACC
msa442667.2{248_2603}	CTTCATTTTT	CGAGCGACAA	GAATGGTACA AAAGTTTGGT ATCGAATACC
msa442667.2{248_A909}	CTTCATTTTT	CGAGCGACAA	GAATGGTACA AAAGTTTGGT ATCGAATACC
msa442667.2{248_H36B}	CTTCATTTTT	CGAGCGACAA	GAATGGTACA AAAGTTTGGT ATCGAATACC
msa442667.2{248_JM9130013}	CTTCATTTTT	CGAGCGACAA	GAATGGTACA AAAGTTTGGT ATCGAATACC
msa442667.2{248_COH1}	CTTCATTTTT	CGAGCGACAA	GAATGGTACA AAAGTTTGGT ATCGAATACC
msa442667.2{248_M781}	CTTCATTTTT	CGAGCGACAA	GAATGGTACA AAAGTTTGGT ATCGAATACC
msa442667.2{248_M732}	CTTCATTTTT	CGAGCGACAA	GAATGGTACA AAAGTTTGGT ATCGAATACC
msa442667.2{248_O90}	CTTCATTTTT	CGAGCGACAA	GAATGGTACA AAAGTTTGGT ATCGAATACC
msa442667.2{248_CJB110}	CTTC		



Table 58: Comparative Sequences relating to SAG0182

Consensus \*\*\*\*\*

## SEQ ID NO. 5811

STRAIN 2603 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVVISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE  
 I I KRHTNFDVGLTDRSNVLAHIGVGHDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHNQCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQETVAESKGTGTALVNLNLR  
 LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRIREDEHENFNS

## SEQ ID NO. 5812

STRAIN 090 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVVISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE  
 I I KRHTNFDVGLTDRSNVLAHIGVGHDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHNQCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQETVAESKGTGTALVNLNLR  
 LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRIREDEHENFNS

## SEQ ID NO. 5813

STRAIN A909 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVVISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE  
 I I KRHTNFDVGLTDRSNVLAHIGVGHDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHNQCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQETVAESKGTGTALVNLNLR  
 LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRIREDEHENFNS

## SEQ ID NO. 5814

STRAIN H36B frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVVISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE  
 I I KRHTNFDVGLTDRSNVLAHIGVGHDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHNQCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQETVAESKGTGTALVNLNLR  
 LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRIREDEHENFNS

## SEQ ID NO. 5815

STRAIN 18RS21 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVVISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE  
 I I KRHTNFDVGLTDRSNVLAHIGVGHDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHNQCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQETVAESKGTGTALVNLNLR  
 LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRIREDEHENFNS

## SEQ ID NO. 5816

STRAIN M732 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVVISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE  
 I I KRHTNFDVGLTDRSNVLAHIGVGHDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHNQCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQETVAESKGTGTALVNLNLR  
 LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRIREDEHENFNS

## SEQ ID NO. 5817

Table 58: Comparative Sequences relating to SAG0182

STRAIN COH1 frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVLIIFGLFVIIISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGVISGKIGDKLENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQLTPYLRLQGLTPQSARSVCE  
 IIKRHTNFDVAGLTDNRNLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHCNQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAININTISALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGOETVAESKGTGTALVNLNRR  
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5818

STRAIN M781 frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVLIIFGLFVIIISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGVISGKIGDKLENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQLTPYLRLQGLTPQSARSVCE  
 IIKRHTNFDVAGLTDNRNLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHCNQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAININTISALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGOETVAESKGTGTALVNLNRR  
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5819

STRAIN CJB110 frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVLIIFGLFVIIISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGVISGKIGDKLENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQLTPYLRLQGLTPQSARSVCE  
 IIKRHTNFDVAGLTDNRNLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHCNQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAININTISALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGOETVAESKGTGTALVNLNRR  
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5820

STRAIN 1169NT frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVLIIFGLFVIIISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGVISGKIGDKLENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQLTPYLRLQGLTPQSARSVCE  
 IIKRHTNFDVAGLTDNRNLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHCNQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAININTISALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGOETVAESKGTGTALVNLNRR  
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5821

STRAIN JM9130013 frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVLIIFGLFVIIISNITGIEIKG  
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF  
 YIVSSVLVGVISGKIGDKLENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI  
 PMMILNSLGSTLFLAILKTYLSNESQLRAVQTRDVLELTRQLTPYLRLQGLTPQSARSVCE  
 IIKRHTNFDVAGLTDNRNLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS  
 CPDHCNQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT  
 EEQNKLASMAEIKALQAQINPHFFFNAININTISALIRIDSDKARYALMQLSTFFRTSLQGG  
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF  
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGOETVAESKGTGTALVNLNRR  
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

PRETTY of: /biotmp/msa442834.2{\*} January 13, 2003 06:47 ..

	1		50
msa442834.2{248_090}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_1169NT}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_18921}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_2603}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_A909}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_CJB110}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_H36B}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_JM9130013}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_COH1}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_M781}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_M732}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
Consensus	*****	*****	*****
	51		100
msa442834.2{248_090}	SNITGIEIKG	DRSLVERPFL TTISHSDSLA	NTRTLVITTA SLVGGPLVGS
msa442834.2{248_1169NT}	SNITGIEIKG	DRSLVERPFL TTISHSDSLA	NTRTLVITTA SLVGGPLVGS

Table 58: Comparative Sequences relating to SAG0182

msa442834.2{248_18RS21}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_2603}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_A909}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_CJB110}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_H36B}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_JM9130013}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_COH1}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_M781}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_M732}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_1169NT}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_18RS21}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_2603}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_A909}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_CJB110}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_H36B}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_JM9130013}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_COH1}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_M781}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_M732}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_1169NT}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_18RS21}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_2603}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_A909}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_CJB110}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_H36B}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_JM9130013}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_COH1}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_M781}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_M732}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_1169NT}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_18RS21}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_2603}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_A909}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_CJB110}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_H36B}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_JM9130013}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_COH1}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_M781}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_M732}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_1169NT}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_18RS21}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_2603}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_A909}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_CJB110}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_H36B}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_JM9130013}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_COH1}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_M781}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_M732}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_1169NT}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_18RS21}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_2603}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_A909}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_CJB110}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_H36B}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_JM9130013}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_COH1}	CPDHNCQLNS	AIVVPLKIND	KTVcALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_M781}	CPDHNCQLNS	AIVVPLKIND	KTVcALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_M732}	CPDHNCQLNS	AIVVPLKIND	KTVcALKMYF	AGDKTMSEVE	ENLVLGLAQI
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD

Table 58: Comparative Sequences relating to SAG0182

msa442834.2{248_1169NT}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_18RS21}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_2603}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_A909}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_CJB110}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_H36B}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_JM9130013}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_COH1}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_M781}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_M732}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
Consensus	*****	*****	*****	*****	*****
401					
msa442834.2{248_090}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_1169NT}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_18RS21}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_2603}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_A909}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_CJB110}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_H36B}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_JM9130013}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_COH1}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_M781}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
msa442834.2{248_M732}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYO
Consensus	*****	*****	*****	*****	*****
451					
msa442834.2{248_090}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_1169NT}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_18RS21}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_2603}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_A909}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_CJB110}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_H36B}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_JM9130013}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_COH1}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_M781}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_M732}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
Consensus	*****	*****	*****	*****	*****
501					
msa442834.2{248_090}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_1169NT}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_18RS21}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_2603}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_A909}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_CJB110}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_H36B}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_JM9130013}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_COH1}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_M781}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_M732}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
Consensus	*****	*****	*****	*****	*****
551					
msa442834.2{248_090}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_1169NT}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_18RS21}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_2603}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_A909}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_CJB110}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_H36B}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_JM9130013}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_COH1}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_M781}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_M732}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
Consensus	*****	*****	*****		
580					

Table 59: Comparative Sequences relating to SAG2147

## SEQ ID NO. 5901

## STRAIN 2603

ATGAATAAAGAGAAATTTATCAAAATTTGAATGTAAAAAACATCATTTAGCTTATGGA  
GCTATCACITTTAGTAGCCCTTTTTCATGTATTTTGGCTGTAAATGGTCATCTTTAAAGT  
TCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTCGCGTAGCCAAAAAATCA  
AAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAAACAGGCTCCAAACCT  
TCTCAGGCATCTAATGAAGCCCCAAATCAAGTTCTCAATCTACAGAAGCTAATTCTCAG  
CAACAAGTTTACTGCGAGTGAAGAGGCAGCTGTAGAACAAAGCAGTTGTAAACAGAAACACC  
CCTGCTACCAAGTCAGGCACAAACAGCTTATGCTGTTACTGAGACAACCTTATAGACCTGCT  
CAACACCAGACGAGTGGCCAAATTTAGTAAATGGAATACTGACAGGGCTATTGGCTCA  
GCAGCTGCAGACACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATT  
ATTGCCCGTGAATCAAATGGTAAATCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTT  
TTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAGTTAATTCAGCT  
ATTAAGCTTATCTGCTCAAGGTTTATCAGCTTGGGGTTACTAG

## SEQ ID NO. 5902

## STRAIN JM9130013

AAAAGTTCAAGTTACTACTGAATCTTTGTCAAA  
AGCAGATAAAGTTTCGCGTAGCCAAAAATCAAAATGAATAAGGCAACAT  
CTAAATCAAAAGTAGAAGGTGTAAAAACAGGCTCCAAACCAAGTTCTCAA  
TCTACAGAAGCTAATTCTCAGCAACAAAGTTACTGCGAGTGAAGAGGCGAGC  
TGTAGAACAAAGCAGTTGTAAACAGAAATACCCCTGCTACCAGTCAAGCAC  
AACAAGCTTATGCTGTTACTGAGACAACCTTATAGACCTGCTCAACACCAG  
CCGAGTGGCCCAAGTATTGAGCAATGGAATACTGACAGGGTTATTGGCTC  
AGCAGCAGCAGCACAAATGGCTGCTGCAACGGGAGTTCCTCAGTCTACTT  
GGGAACATATTATTGCCCGTGAATCAAATGGTAAATCCTAACGTTGCTAAT  
GCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAAC  
AGCTACAGTTCAGGATCAAGTTAATCAGCTATTAAAGCTTATCTGCTC  
AAGGTTTATCAGCTTGGGGTTAC

## SEQ ID NO. 5903

## STRAIN 1169NT reverse complement

AAAAGTTCAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTTCGCGTAGCC  
AAAAAATCAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAAACAGGCT  
CCAAACCTTTCTCAGGCATCTAATGAAGTCCCAAAATCAAGTTCTCAATCTACAGAAGCT  
AATTCTCAGCAACAAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAAGCAGTTGTAAAC  
GAAAATACCCCTGCTACCAGTCAGGCACAACTTATGCTGTTACTGAGACAACCTTAC  
AAACCTGCTCAACACCAGACAAAGTGGCCAAAGTATTGAGCAATGGAATACTGACAGGGCG  
GTCGGATCTGCTGCTGACAGCAAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGG  
GAACATATTATTGCCCGTGAATCAAATGGTAAATCCTAATGTTGCTAATGCCTCAGGAGCT  
TCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAGTT  
AATTACAGCTATTAAAGCTTATCTGCTCAAGGTTTATCAGCTTGGGGTTAC

## SEQ ID NO. 5904

## STRAIN 18RS21 reverse complement

AAAAGTTCAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTTC  
GCGTAGCCAAAAATCAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAA  
AACAGGCTCCAAACCTTTCTCAGGCATCTAATGAAGCCCCAAATCAAGTTCTCAATCTA  
CAGAAGCTAATTCTCAGCAACAAAGTTACTGCGAGTGAAGAGGCGAGCTGTAGAACAAAGCAG  
TTGTAAACAGAAACACCCCTGCTACCAGTCAGGCACAAACAGCTTATGCTGTTACTGAGA  
CAACTTATAGACCTGCTCAACACCAGACGAGTGGCCAAAGTATTGAGTAATGGAAATACTG  
CAGGGGCTATTGGCTCAGCAGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGT  
CTACTTGGGAACATATTATTGCCCGTGAATCAAATGGTAAATCCTAATGTTGCTAATGCCT  
CAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGG  
ATCAAGTTAATTACAGCTATTAAAGCTTATCTGCTCAAGGTTTATCAGCTTGGGGTTAC

## SEQ ID NO. 5905

## STRAIN 090 reverse complement

TAGCCAAAAAATCAAAATGATTAAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAAAC  
AGGCTCCAAACCTTTCTCAGGCATCTAATGAAGCCCCAAATCAAGTTCTCAATCTACAG  
AAGCTAATTCTCAGCAACAAAGTTACTGCGAGTGAAGAGGCGAGCTGTAGAACAAAGCAGTTG  
TAACAGAAAAACCCCTGCTACCAGTCAGGCACAAACAGCTTATGCTGTTACTGAGACAA  
CTTATAGACCTGCTCAACACCAGACGAGTGGCCAAAGTATTGAGTAATGGAAATACTGAG  
GGGCTATTGGCTCAGCAGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTA  
CTTGGGAACATATTATTGCCCGTGAATCAAATGGTAAATCCTAATGTTGCTAATGCCTCAG  
GAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGA

## SEQ ID NO. 5906

## STRAIN A909 reverse complement

AAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAAACAGGCTCCAAACCTTTCTCAGGCA  
TCTAATGAAGCCCCAAATCAAGTTCTCAATCTACAGAAGCTAATTCTCAGCAACAAAGTT  
ACTGCGAGTGAAGAGGCGAGCTGTAGAACAAAGCAGTTGTAAACAGAAACACCCCTGCTACC  
AGTCAGGCACAAACAGCTTATGCTGTTACTGAGACAACCTATAGACCTGCTCAACACCAG  
ACAAGTGGCCAAAGTATTGAGTAATGGAATACTGACAGGGCTATTGGCTCAGCAGCTGCA  
GCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGT  
GAATCAAATGGTAAATCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACG  
ATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGAAATCAAGTTAATTCAGCTATTAAAGCT  
TATCTGCTCAAGGTTTATCA

## SEQ ID NO. 5907

## STRAIN CJB110 reverse complement

AATCTTTGTCAAAAGCAGATAAAGTTTCGCGTAGCCAAAAATCAAAATGACTAAGGCGA

Table 59: Comparative Sequences relating to SAG2147

CATCTAAATCAAAGTAGAAGATGTAAACAGGCTCCAAAACCTTCTCAGGCATCTAATG  
 AAGCCCCAAATCAAGTTCTCAATCTACAGAAGCTAATTTCTCAGCAACAAGTTACTGCGA  
 GTGAAGAGGCAGCTGTAGAACAAAGCAGTTGTAAACAGAAAACACCCCTGCTACCAGTCAGG  
 CACAACAAGCTTATGCTGTTACTGAGACAACCTTATAGACCTGCTCAACACCAGACGAGTG  
 GCCAAGTATTGAGTAATGGAAATCTGAGGGGCTATTGGCTCAGCAGCTGCAGCACAAA  
 TGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAA  
 ATGGTAATCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAG  
 GTTGGGGTTCAACAGCTACAGTTCAAGATCAAGTTAATTCAGCTATTAAAGCTTATCGTG  
 CTCAGGTTTATCAGCTTGGGGTTAC

## SEQ ID NO. 5908

STRAIN COH1 reverse complement

AAAAGTTCACAAGTTACTACTGAATCTTTGTCAAAGCAGATAA  
 AGTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAGTAGAAGA  
 TGTAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAATCAAGTTCTCA  
 ATCTACAGAAGCTAATTTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACA  
 AGCAGTTGTAAACAGAAAATACCCCTGCTACCAGTCAGGCACAACAACTTATGCTGTTAC  
 TGAGACAACCTTACAAACCTGCTCAACACCAGACAAGTGGCCAAAGTATTGAGCAATGGAAA  
 TACTGCGAGGGGCGGTCGGATCTGCTGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCC  
 TCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAA  
 TGCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGT  
 TCAGGATCAAGTTAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGG  
 TTAC

## SEQ ID NO. 5909

STRAIN H36B reverse complement

AAAAGTTCACAAGTTACTACTGAATCTTTGTCAAAGC  
 AGATAAAGTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAGT  
 AGAAGATGTAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAATCAAG  
 TTCTCAATCTACAGAAGCTAATTTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGAGTGT  
 AGAACAAGCAGTTGTAAACAGAAAACACCCCTGCTACCAGTCAGGCACAACAAGCTTATGC  
 TGTACTGAGACAACCTTATAGACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGTAA  
 TGGAAATACTGCAGGGGCTATTGGCTCAGCAGCTGCAGCACAAATGGCTGCTGCAACAGG  
 AGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGT  
 TGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGC  
 TACAGTTCAGGATCAAGTTAATTCAGCTATTAAAGCTT

## SEQ ID NO. 5910

STRAIN M732 reverse complement

AAAAGTTCACAAGTTACTACTGAATCTTTGTCAAAGCAGATAAAGTTCGCGTAGC  
 CAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAGTAGAAGATGTAAACAGGC  
 TCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAATCAAGTTCTCAATCTACAGAAGC  
 TAATTTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAAAC  
 AGAAAATACCCCTGCTACCAGTCAGGCACAACAACCTTATGCTGTTACTGAGACAACCTTA  
 CAACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGCAATGGAAATACTGCAGGGGC  
 GGTGGATCTGCTGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTG  
 GGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAGC  
 TTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAAGATCAAGT  
 TAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTA

## SEQ ID NO. 5911

STRAIN M781 reverse complement

TCCTTGTCAAAGCAGATAAAGTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACA  
 TCTAAATCAAAGTAGAAGATGTAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAA  
 GCCCAAAATCAAGTTCTCAATCTACAGAAGCTAATTTCTCAGCAACAAGTTACTGCGAGT  
 GAAGAGGCGGCTGTAGAACAAGCAGTTGTAAACAGAAAATACCCCTGCTACCAGTCAGGCA  
 CAACAACTTATGCTGTTACTGAGACAACCTTACAAACCTGCTCAACACCAGACAAGTGGC  
 CAAGTATTGAGCAATGGAAATACTGCAGGGGCGGTCGGATCTGCTGCTGCAGCACAAATG  
 GCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAAT  
 GGTAAATCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGG  
 TGGGGTTCAACAGCTACAGTTCAAGATCAAGTTAATTCAGCTATTAAAGCTTATCGTGCT  
 CAAGGTTTATCAGCTTGGGGTTAC

PRETTY of: /biotmp/msa519780.2{\*} March 10, 2003 06:25 ..

	1					50
msa519780.2{25_COH1}	-----	-----	-----	-----	-----	-----
msa519780.2{25_M781}	-----	-----	-----	-----	-----	-----
msa519780.2{25_M732}	-----	-----	-----	-----	-----	-----
msa519780.2{25_1169NT}	-----	-----	-----	-----	-----	-----
msa519780.2{25_18RS21}	-----	-----	-----	-----	-----	-----
msa519780.2{25_A909}	-----	-----	-----	-----	-----	-----
msa519780.2{25_090}	-----	-----	-----	-----	-----	-----
msa519780.2{25_CJB110}	-----	-----	-----	-----	-----	-----
msa519780.2{2603}	atgaataaaa	gaagaaaatt	atcaaaattg	aatgtaaaaa	aacatcattt	
msa519780.2{25_H36B}	-----	-----	-----	-----	-----	-----
msa519780.2{25_JM9130013}	-----	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****	*****
	51					100
msa519780.2{25_COH1}	-----	-----	-----	-----	-----	-----
msa519780.2{25_M781}	-----	-----	-----	-----	-----	-----
msa519780.2{25_M732}	-----	-----	-----	-----	-----	-----

	msa519780.2{25_1169NT}	-----	-----	-----	-----	-----
	msa519780.2{25_18RS21}	-----	-----	-----	-----	-----
	msa519780.2{25_A909}	-----	-----	-----	-----	-----
	msa519780.2{25_O90}	-----	-----	-----	-----	-----
	msa519780.2{25_CJB110}	-----	-----	-----	-----	-----
	msa519780.2{2603}	agcttatgga	gctatcactt	tagtagccct	tttttcatgt	attttggctg
	msa519780.2{25_H36B}	-----	-----	-----	-----	-----
	msa519780.2{25_JM9130013}	-----	-----	-----	-----	-----
	Consensus	*****	*****	*****	*****	*****
		101				150
	msa519780.2{25_COH1}	-----	----aaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
	msa519780.2{25_M781}	-----	-----	-----	-----tc	tttgtcaaaa
	msa519780.2{25_M732}	-----	----aaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
	msa519780.2{25_1169NT}	-----	----aaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
	msa519780.2{25_18RS21}	-----	----aaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
	msa519780.2{25_A909}	-----	-----	-----	-----	-----
	msa519780.2{25_O90}	-----	-----	-----	-----aatc	tttgtcaaaa
	msa519780.2{25_CJB110}	-----	-----	-----	-----	tttgtcaaaa
	msa519780.2{2603}	taatgggtcat	c t t t a a a a g t	tcacaagtta	ctactgaatc	tttgtcaaaa
	msa519780.2{25_H36B}	-----	----aaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
	msa519780.2{25_JM9130013}	-----	----aaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
	Consensus	*****	***-----	-----	-----	*****
		151				200
	msa519780.2{25_COH1}	gcagataaaag	t t c g c g t a g c	caaaaaatca	aaaatgactA	AGGCgACATC
	msa519780.2{25_M781}	gcagataaaag	t t c g c g t a g c	caaaaaatca	aaaatgactA	AGGCgACATC
	msa519780.2{25_M732}	gcagataaaag	t t c g c g t a g c	caaaaaatca	aaaatgactA	AGGCgACATC
	msa519780.2{25_1169NT}	gcagataaaag	t t c g c g t a g c	caaaaaatca	aaaatgactA	AGGCgACATC
	msa519780.2{25_18RS21}	gcagataaaag	t t c g c g t a g c	caaaaaatca	aaaatgactA	AGGCgACATC
	msa519780.2{25_A909}	-----	-----tagc	caaaaaatca	aaaatgattA	AGGCgACATC
	msa519780.2{25_O90}	gcagataaaag	t t c g c g t a g c	caaaaaatca	aaaatgactA	AGGCgACATC
	msa519780.2{25_CJB110}	gcagataaaag	t t c g c g t a g c	caaaaaatca	aaaatgactA	AGGCgACATC
	msa519780.2{2603}	gcagataaaag	t t c g c g t a g c	caaaaaatca	aaaatgactA	AGGCgACATC
	msa519780.2{25_H36B}	gcagataaaag	t t c g c g t a g c	caaaaaatca	aaaatgactA	AGGCgACATC
	msa519780.2{25_JM9130013}	gcagataaaag	t t c g c g t a g c	caaaaaatca	aaaatgactA	AGGCgACATC
	Consensus	-----	-----	-----	-----*	****-*****
		201.				250
	msa519780.2{25_COH1}	TAAATCAAAA	GTAGAAGaTG	TAAAAACAGGc	TCCAAAAAcT	tctcaggcat
	msa519780.2{25_M781}	TAAATCAAAA	GTAGAAGaTG	TAAAAACAGGc	TCCAAAAAcT	tctcaggcat
	msa519780.2{25_M732}	TAAATCAAAA	GTAGAAGaTG	TAAAAACAGGc	TCCAAAAAcT	tctcaggcat
	msa519780.2{25_1169NT}	TAAATCAAAA	GTAGAAGaTG	TAAAAACAGGc	TCCAAAAAcT	tctcaggcat
	msa519780.2{25_18RS21}	TAAATCAAAA	GTAGAAGaTG	TAAAAACAGGc	TCCAAAAAcT	tctcaggcat
	msa519780.2{25_A909}	TAAATCAAAA	GTAGAAGaTG	TAAAAACAGGc	TCCAAAAAcT	tctcaggcat
	msa519780.2{25_O90}	TAAATCAAAA	GTAGAAGaTG	TAAAAACAGGc	TCCAAAAAcT	tctcaggcat
	msa519780.2{25_CJB110}	TAAATCAAAA	GTAGAAGaTG	TAAAAACAGGc	TCCAAAAAcT	tctcaggcat
	msa519780.2{2603}	TAAATCAAAA	GTAGAAGaTG	TAAAAACAGGc	TCCAAAAAcT	tctcaggcat
	msa519780.2{25_H36B}	TAAATCAAAA	GTAGAAGaTG	TAAAAACAGGc	TCCAAAAAcT	tctcaggcat
	msa519780.2{25_JM9130013}	TAAATCAAAA	GTAGAAGgTG	TAAAAACAGGc	TCCAAAAAC..	.....
	Consensus	*****	*****.*	*****	*****-	-----
		251				300
	msa519780.2{25_COH1}	ctaataagaac	ccccaaaatCA	AGTTCTCAAT	CTACAGAAGc	TAATTCTCAG
	msa519780.2{25_M781}	ctaataagaac	ccccaaaatCA	AGTTCTCAAT	CTACAGAAGc	TAATTCTCAG
	msa519780.2{25_M732}	ctaataagaac	ccccaaaatCA	AGTTCTCAAT	CTACAGAAGc	TAATTCTCAG
	msa519780.2{25_1169NT}	ctaataagaac	ccccaaaatCA	AGTTCTCAAT	CTACAGAAGc	TAATTCTCAG
	msa519780.2{25_18RS21}	ctaataagaac	ccccaaaatCA	AGTTCTCAAT	CTACAGAAGc	TAATTCTCAG
	msa519780.2{25_A909}	ctaataagaac	ccccaaaatCA	AGTTCTCAAT	CTACAGAAGc	TAATTCTCAG
	msa519780.2{25_O90}	ctaataagaac	ccccaaaatCA	AGTTCTCAAT	CTACAGAAGc	TAATTCTCAG
	msa519780.2{25_CJB110}	ctaataagaac	ccccaaaatCA	AGTTCTCAAT	CTACAGAAGc	TAATTCTCAG
	msa519780.2{2603}	ctaataagaac	ccccaaaatCA	AGTTCTCAAT	CTACAGAAGc	TAATTCTCAG

Table 59: Comparative Sequences relating to SAG2147

msa519780.2{25_M732}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAaCTTAT	GCTGTTACTG
msa519780.2{25_1169NT}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAaCTTAT	GCTGTTACTG
msa519780.2{25_18RS21}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAgCTTAT	GCTGTTACTG
msa519780.2{25_A909}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAgCTTAT	GCTGTTACTG
msa519780.2{25_090}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAgCTTAT	GCTGTTACTG
msa519780.2{25_CJB110}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAgCTTAT	GCTGTTACTG
msa519780.2{2603}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAgCTTAT	GCTGTTACTG
msa519780.2{25_H36B}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAgCTTAT	GCTGTTACTG
msa519780.2{25_JM9130013}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAgCTTAT	GCTGTTACTG
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa519780.2{25_COH1}	AGACAACTTA	cAaACCTGCT	CAACACCAGA	CaAGTGGCCA	AGTATTGAGc
msa519780.2{25_M781}	AGACAACTTA	cAaACCTGCT	CAACACCAGA	CaAGTGGCCA	AGTATTGAGc
msa519780.2{25_M732}	AGACAACTTA	cAaACCTGCT	CAACACCAGA	CaAGTGGCCA	AGTATTGAGc
msa519780.2{25_1169NT}	AGACAACTTA	cAaACCTGCT	CAACACCAGA	CaAGTGGCCA	AGTATTGAGc
msa519780.2{25_18RS21}	AGACAACTTA	tAgACCTGCT	CAACACCAGA	CgAGTGGCCA	AGTATTGAGt
msa519780.2{25_A909}	AGACAACTTA	tAgACCTGCT	CAACACCAGA	CgAGTGGCCA	AGTATTGAGt
msa519780.2{25_090}	AGACAACTTA	tAgACCTGCT	CAACACCAGA	CgAGTGGCCA	AGTATTGAGt
msa519780.2{25_CJB110}	AGACAACTTA	tAgACCTGCT	CAACACCAGA	CgAGTGGCCA	AGTATTGAGt
msa519780.2{2603}	AGACAACTTA	tAgACCTGCT	CAACACCAGA	CgAGTGGCCA	AGTATTGAGt
msa519780.2{25_H36B}	AGACAACTTA	tAgACCTGCT	CAACACCAGA	CgAGTGGCCA	AGTATTGAGt
msa519780.2{25_JM9130013}	AGACAACTTA	tAgACCTGCT	CAACACCAGc	CgAGTGGCCA	AGTATTGAGc
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa519780.2{25_COH1}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTcT	GcTgCtGCAG	CACAAATGGC
msa519780.2{25_M781}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTcT	GcTgCtGCAG	CACAAATGGC
msa519780.2{25_M732}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTcT	GcTgCtGCAG	CACAAATGGC
msa519780.2{25_1169NT}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTcT	GcTgCtGCAG	CACAAATGGC
msa519780.2{25_18RS21}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcCa	GcAgCtGCAG	CACAAATGGC
msa519780.2{25_A909}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcCa	GcAgCtGCAG	CACAAATGGC
msa519780.2{25_090}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcCa	GcAgCtGCAG	CACAAATGGC
msa519780.2{25_CJB110}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcCa	GcAgCtGCAG	CACAAATGGC
msa519780.2{2603}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcCa	GcAgCtGCAG	CACAAATGGC
msa519780.2{25_H36B}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcCa	GcAgCtGCAG	CACAAATGGC
msa519780.2{25_JM9130013}	AATGGAAATA	CTGCAGGGGt	taTtGGcTcCa	GcAgCaGCAG	CACAAATGGC
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa519780.2{25_COH1}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_M781}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_M732}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_1169NT}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_18RS21}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_A909}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_090}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_CJB110}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{2603}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_H36B}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_JM9130013}	TGCTGCAACg	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa519780.2{25_COH1}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_M781}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_M732}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_1169NT}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_18RS21}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_A909}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_090}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_CJB110}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{2603}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_H36B}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_JM9130013}	AATCAAATGG	TAATCCTAAC	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa519780.2{25_COH1}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_M781}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_M732}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_1169NT}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_18RS21}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_A909}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_090}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgA-----
msa519780.2{25_CJB110}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{2603}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_H36B}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_JM9130013}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa519780.2{25_COH1}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***



Table 59: Comparative Sequences relating to SAG2147

msa519780.2{25_M781}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_M732}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_1169NT}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_18RS21}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_A909}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_090}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_CJB110}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{2603}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_H36B}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
msa519780.2{25_JM9130013}	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt
Consensus	taattcagct	attaaagctt	atcgtgctca	aggtttatca	gcttgggggtt

	701
msa519780.2{25_COH1}	ac---
msa519780.2{25_M781}	ac---
msa519780.2{25_M732}	a----
msa519780.2{25_1169NT}	ac---
msa519780.2{25_18RS21}	ac---
msa519780.2{25_A909}	-----
msa519780.2{25_090}	-----
msa519780.2{25_CJB110}	ac---
msa519780.2{2603}	actag
msa519780.2{25_H36B}	-----
msa519780.2{25_JM9130013}	ac---
Consensus	---***

## SEQ ID NO. 5912

STRAIN 2603 frame: 1

MNKRRLSKLNVKKHLLAYGAITLVALFSCILAVMVIKSSQVTTESLSKADKVRVAKKS  
KMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTASEEAAVEQAVVTENT  
PATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQMAAATGVPQSTWEHI  
IARESNGNPNVANASGASGLFQTMFGWGSTATVQDQVNSAIKAYRAQGLSAWGY

## SEQ ID NO. 5913

STRAIN 1169NT frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEVPKSSSQSTEAN  
SQQQVTASEEAAVEQAVVTENTPATSSQAQQTYAVTETTYKPAQHQTSGQVLSNGNTAGAV  
GSAAAAQMAAATGVPQSTWEHI IARESNGNPNVANASGASGLFQTMFGWGSTATVQDQVN  
SAIKAYRAQGLSAWGY

## SEQ ID NO. 5914

STRAIN 18RS21 frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN  
SQQQVTASEEAAVEQAVVTENTPATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI  
GSAAAAQMAAATGVPQSTWEHI IARESNGNPNVANASGASGLFQTMFGWGSTATVQDQVN  
SAIKAYRAQGLSAWGY

## SEQ ID NO. 5915

STRAIN 2603 frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN  
SQQQVTASEEAAVEQAVVTENTPATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI  
GSAAAAQMAAATGVPQSTWEHI IARESNGNPNVANASGASGLFQTMFGWGSTATVQDQVN  
SAIKAYRAQGLSAWGY

## SEQ ID NO. 5916

STRAIN 090 frame: 3

AKKSKMIKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTASEEAAVEQAVV  
TENTPATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQMAAATGVPQST  
WEHI IARESNGNPNVANASGASGLFQTMFGWGSTATVQ

## SEQ ID NO. 5917

STRAIN A909 frame: 1

KATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTASEEAAVEQAVVTENTPAT  
SQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQMAAATGVPQSTWEHI IAR  
ESNGNPNVANASGASGLFQTMFGWGSTATVQDQVNSAIKAYRAQGLS

## SEQ ID NO. 5918

STRAIN CJB110 frame: 3

SLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAS  
EEAAVEQAVVTENTPATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQ  
MAAATGVPQSTWEHI IARESNGNPNVANASGASGLFQTMFGWGSTATVQDQVNSAIKAYRA  
QGLSAWGY

## SEQ ID NO. 5919

STRAIN COH1 frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN  
SQQQVTASEEAAVEQAVVTENTPATSSQAQQTYAVTETTYKPAQHQTSGQVLSNGNTAGAV  
GSAAAAQMAAATGVPQSTWEHI IARESNGNPNVANASGASGLFQTMFGWGSTATVQDQVN  
SAIKAYRAQGLSAWGY

## SEQ ID NO. 5920

STRAIN H36B frame: 1

Table 59: Comparative Sequences relating to SAG2147

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN  
 SQQVVTASEEAAVEQAVVTENTPATSOAQQYAVTETTYRPAQHQTSGQVLSNGNTAGAV  
 GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN  
 SAIKA

SEQ ID NO. 5921

STRAIN M732 frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN  
 SQQVVTASEEAAVEQAVVTENTPATSOAQQYAVTETTYRPAQHQTSGQVLSNGNTAGAV  
 GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN  
 SAIKAYRAQGLSAWG

SEQ ID NO. 5922

STRAIN M781 frame: 4

SLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAS  
 EEAAVEQAVVTENTPATSOAQQYAVTETTYRPAQHQTSGQVLSNGNTAGAVGSAAAAQMA  
 AATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRA  
 QGLSAWG

SEQ ID NO. 5923

STRAIN JM9130013 frame: 1

KSSQVTTESLSKADKVRVAKKSKMNKATSKSKVEGVKQAPKPSQSTEANSQQQVTASEE  
 AAVEQAVVTENTPATSOAQQYAVTETTYRPAQHQTSGQVLSNGNTAGVIGSAAAAQMAA  
 ATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRAQ  
 LSAWG

#### MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa519418.2{\*} March 10, 2003 06:15 ..

	1					50
msa519418.2{25_090}	-----	-----	-----	-----	-----	-----
msa519418.2{25_H36B}	-----	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_COH1}	-----	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_M781}	-----	-----	-----	-----	-----	-----SLSK
msa519418.2{25_1169NT}	-----	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_M732}	-----	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_18RS21}	-----	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_CJB110}	-----	-----	-----	-----	-----	-----SLSK
msa519418.2{25_2603}	-----	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{2603}	mnkrrklsl	nvkhhlayg	aitlvalfsc	ilavmvifks		SQVTTESLSK
msa519418.2{25_A909}	-----	-----	-----	-----	-----	-----
msa519418.2{25_JM9130013}	-----	-----	-----	-----	-----KS	SQVTTESLSK
Consensus	*****	*****	*****	*****	*****	*****
	51					100
msa519418.2{25_090}	-----akks	kmiKATSKSK	VBdVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_H36B}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_COH1}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_M781}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_1169NT}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_M732}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_18RS21}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_CJB110}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_2603}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_A909}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
msa519418.2{25_JM9130013}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ	
Consensus	*****	*****	*****	*****	*****	*****
	101					150
msa519418.2{25_090}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS	
msa519418.2{25_H36B}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS	
msa519418.2{25_COH1}	QQVTASEEAA	VEQAVVTENT	PATSOAQQtY	AVTETTYkPA	QHQtSGQVLS	
msa519418.2{25_M781}	QQVTASEEAA	VEQAVVTENT	PATSOAQQtY	AVTETTYkPA	QHQtSGQVLS	
msa519418.2{25_1169NT}	QQVTASEEAA	VEQAVVTENT	PATSOAQQtY	AVTETTYkPA	QHQtSGQVLS	
msa519418.2{25_M732}	QQVTASEEAA	VEQAVVTENT	PATSOAQQtY	AVTETTYkPA	QHQtSGQVLS	
msa519418.2{25_18RS21}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS	
msa519418.2{25_CJB110}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS	
msa519418.2{25_2603}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS	
msa519418.2{25_A909}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS	
msa519418.2{25_JM9130013}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS	
Consensus	*****	*****	*****	*****	*****	*****
	151					200
msa519418.2{25_090}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL	
msa519418.2{25_H36B}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL	
msa519418.2{25_COH1}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL	
msa519418.2{25_M781}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL	
msa519418.2{25_1169NT}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL	
msa519418.2{25_M732}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL	
msa519418.2{25_18RS21}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL	
msa519418.2{25_CJB110}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNNGNPN	VANASGASGL	

Table 59: Comparative Sequences relating to SAG2147

msa519418.2{25_2603}	NGNTAGaiGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{2603}	NGNTAGaiGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{25_A909}	NGNTAGaiGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{25_JM9130013}	NGNTAGviGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
Consensus	*****--**	*****--**	*****--**	*****--**	*****--**
		201		234	
msa519418.2{25_090}	FQTMPGWGST	ATVQ-----	-----	-----	-----
msa519418.2{25_H36B}	FQTMPGWGST	ATVQDQVNSA	IKA-----	-----	-----
msa519418.2{25_COH1}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_M781}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_1169NT}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_M732}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWG-	
msa519418.2{25_18RS21}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_CJB110}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_2603}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{2603}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_A909}	FQTMPGWGST	ATVQnQVNSA	IKAYRAQGLS	-----	
msa519418.2{25_JM9130013}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
Consensus	*****--**	*****--**	*****--**	*****--**	*****--**

Table 60: Comparative Sequences relating to SAG1945

## SEQ ID NO. 6001

## STRAIN 2603

ATGAAAGAAAAACAGTCGAAAAGGCTTATTTATATACTACTGGTTGTTTCCATTATTTT  
 ATAAGTGTTTTACATACAGTATAGCCAGCCTTCTAAACTACTTCCACCAAAAGAATTA  
 GTTATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTGAGGAA  
 AAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAGATTA  
 AGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTCTTTGGAGGAAATTATACGCAATTT  
 GAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCAAAGAATGTTCACTACTGTTATCCA  
 GACTATATCCATCCAGTGATACGGCGACACCTTATACTATAAATGGGAGTGCTTGATT  
 GTAAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTATTATACGCCT  
 TCCTTAAAAGGTAAAATTGCTTTGCGAGATCCGAATACCTTCTAGTGCTTTCTCACA  
 CTCCTAATATATCTTGGCCAAAGGGTGGTTACCCAATCCAAAGCGTGGAACTATGTT  
 AAAAAGCTACAACATAATATTAATGCTATCAAATCTTCTAGCTCTCAGAAGTTTATCAA  
 TCAGTTGCAGAAAGGAAAAATGATGTGGGGCTGACTTACGAAGACCCCTAGTGCTAATTG  
 CAAAAAGTGGTGCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGCCA  
 TCTTCGGTTGCAATATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTATTAAT  
 TTTATGCTTTCTTAGATGTTCAAAATGCCTTTGGGCAGTCAACGAGTAACCGACCTATT  
 CGTAAAGATGCCCAACGAGTAATGGCATGAAAGCTTTAAAGGATATTGCTACTCTTAAA  
 GAAGATTATCGCTATGCTACTAAGCATAAAGGCCAAATCCTTAAACCTATAATCGTATT  
 CGTAGAATGCTGAT

## SEQ ID NO. 6002

## STRAIN 090

CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGTTATTCTAAGT  
 CCAAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGGAGAAAA  
 ATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAG  
 ATAGATTAAAGTAAAGGAGGGTAAGCAGTTGAAGCGGATATTTCTTTGGA  
 GGAATTTATACGCAATTTGAAAGTCATAGGCATTGTTTGAGTCTTACGT  
 ATCAAAGAATGTTCACTACTGTTATTTCCAGACTATATCCATCCAAGTGATA  
 CGCGACACCTTATACTATAAATGGGAGTGCTTGATTGTAAATAACGAA  
 TTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTATTACAGCCTTC  
 CTTAAAAGGTAAAATTGCTTTGCGAGATCCGAATACCTTCTAGTGCTT  
 TCTCACAACCTCACTAATATACTCTTGGCCAAAGGGTGGTTACCCAATCCA  
 AAGCGTGGAACTATGTTAAAAAGCTACAACATAATATTAATGCTATCAA  
 ATCTTCTAGCTCTTCAAGATTTATCAATCAGTTGCAGAAAGGAAAAATGA  
 TTGTTGGGCTGACTTACGAAGACCCCTAGTGCTCAATTGCAAAAAAGTGGT  
 GCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGCCATC  
 TTGGTTGCAATTTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTAT  
 TTATTAATTTTATGCTTTCTTATAGATGTTCAAATGCCTTTGGGCAGTCA  
 ACGAGTAACCGACCTATTGCTAAAGATGCCCAACGAGTAATGGCATGAA  
 AGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGCTACTA  
 AGCATAAGGGCCAAATCCTTAAACCTATAATCGTATTTCGTAGAAATGCT  
 GAT

## SEQ ID NO. 6003

## STRAIN A909

CAGCCTTCTAAACTACTTCCACCAAAAGAATTAG  
 TTATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCT  
 TTTGAGGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGG  
 TCAACTAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATA  
 TTTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTT  
 GAGTCTTACGTATCAAAGAATATTCACTGTTATTCCAGATTATATCCA  
 TCCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGCTTGATTG  
 TAAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTA  
 TTACAGCCTTCTTAAAAGGTAAAATTGCTTTGCGAGATCCGAATACCTC  
 CTCTAGTGCTTTCTCACAACCTCACTAATATACTCTTGGCCAAAGGGTGGTT  
 ACACCAATCCAAAGCGTGGAACTATGTTAAAAGCTACAACATAATATT  
 AATGCTATCAAATCTTCTAGCTCTTCAAGAGTTTATCAATCAGTTGCAGA  
 AGGAAAAATGATGTGGGGTTGACTTACGAAGACCCCTAGTGCTAATTGTC  
 AAAAAAGTGGTGCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTT  
 TTTGTCCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGA  
 AGCAAAGTTATTATTAAATTTTATGCTTTCTTTAGATGTTCAAAATGCT  
 TTGGGCAGTCAACGAGTAACCGACCTATTGCTAAAGATGCCCAACGAGT  
 AATGGCATGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCG  
 CTATGCTACTAAGCATAAGGGCCAAATCCTTAAACCTATAATCGTATTTC  
 GTAGAAATGCTGAT

## SEQ ID NO. 6004

## STRAIN H36B

TAAACTACTTCCACCAAAAGAATTAGTTATTCTAAGTCCAAATAGTCAAG  
 CCAATTTAAACAGGAACGATTCCAGCTTTTGGAGAAAAATACGGTATAAAA  
 GTTAAAGCTTATTCAAGGTGGGACAGGTCAACTAATAGATAGATTAAAGTAA  
 GGAGGGTAAGCAGTTGAAGGCGGATATTTCTTTGGAGGAAATTATACGC  
 AATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCAAAGAATATT  
 CATACTGTTATTCCAGATTATATCCATCCGAGTGATACGGCGACACCTTA  
 TACTATAAATGGGAGTGCTTGATTGTAAATAACGAATTAGTTAAGGGAC  
 TTACCATCAAGAGTTATGAAGATTTATTACAGCCTTCTTAAAAGGTAAA  
 ATTGCTTTGCGAGATCCGAATACCTTCTCTAGTGCTTTCTCACAACCTCAC  
 TAATATACTCTTGGCCAAAGGGTGGTTACCCAATCCAAAGCGTGGAACT  
 ATGTTAAAAGCTACAACATAATATTAATGCTATCAAATCTTCTAGCTCT  
 TCAGAAGTTTATCAATCAGTTGCAGAAAGGAAAAATGATGTGGGGTTGAC  
 TTACGAAGACCCCTAGTGCTAATTTGCAAAAAAGTGGTGCCAATGTTTCTA  
 TTGTATATCCGACAGAAGGGACAGTTTGTGCCATCTTCGGTTGCAATT

Table 60: Comparative Sequences relating to SAG1945

ATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTTATTAATTTTAT  
GCTTTCTTTAGATGTTCAAATGCTTTTGGGCAGTCAACGAGTAACCGAC  
CTATTGCTAAAGATGCCCAAACGAGTAATGGCATGAAAGCTTTAAAGGAT  
ATTGCTACTCTTAAAGAAGATTATCGCTATGCTACTAAGCATAAGGGCCA  
AATCCTTAAACCTATAATCGTATTCTGTAGAAATGCTGAT

SEQ ID NO. 6005

STRAIN 18RS21

CAGCCTTCTAAACTACTTCCACCAAAGAATTAGTTATTCTAAGTCCAAA  
TAGTCAAGCCATTTTAACAGGAACGATTCCAGCTTTTGGAGAAAAATACG  
GTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCACTAATAGATAGA  
TTAAGTAAGGAGGGTAAGCAGTTGAAGGCCGATATTTCTTTGGAGGAAA  
TTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCAA  
AGAATGTTTATCTGTTATTCCAGACTATATCCATCCAGTGATACGGCG  
ACACCTTATCTATAAATGGGAGTGTCTTGATTGTAAATAACGAATTAGC  
TAAGGGACTTACCATCAAGAGTTATGAAGATTATACAGCCTTCCCTTAA  
AAGGTAAATTTGCTTTGCGAGATCCGAATACTTCTCTAGTGCTTTCTCA  
CAACTCATAATATACTCTTGGCCAAAGGGTGGTTACACCAATCCAAAAGC  
GTGGAACCTATGTTAAAGAGCTACAACATAATATTAAATGCTATCAAATCTT  
CTAGCTCTTCAGAAAGTTTATCAATCAGTTGCGAAGGAAAAATGATTGTG  
GGGCTGACTTACGAAGACCTTAGTGTCAATTTGCAAAAAGTGGTGCCAA  
TGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGCCATCTTCGG  
TTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTATT  
AATTTATGCTTTCTTTAGATGTTCAAATGCTTTGGGCAGTCAACGAG  
TAACCGACCTATTGCTAAAGATGCCCAAACGAGTAATGGCATGAAAGCTT  
TAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGCTACTAAGCAT  
AAGGCCAAATCCTTAAACCTATAATCGTATTCTGTAGAAATGCTGAT

SEQ ID NO. 6006

STRAIN M732

CAGCCTTCTAAACTACTTCCACCAAAGAATTAGT  
TATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTT  
TTGAGGAAAAATACGGTATAAAGTTAAGCTTATTCAAGGTGGGACAGGG  
CAACTAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGCGGATAT  
TTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTG  
AGTCTTACGTATCAAAGAATGTTCACTACTGTTATTCCAGACTATATCCAT  
CCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGT  
AATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTAT  
TACAGCCTTCCCTTAAAGGTAAAATTGCTTTTGCAGATCCGAATACTTCC  
TCTAGTGCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTA  
CACCATCCAAAAGCGTGAAGTATGTTAAAGCTACAACATAATATTA  
ATGCTATCAAATCTTCTAGCTCTTCAAGAGTTTATCAATCAGTTGCGAGAA  
GGAAAAATGATTGTGGGGTTGACTTACGAAGACCTTAGTGTCAATTTGCA  
AAAAAGTGGTGCCAAATGTTTCTATTGTATACCGACAGAAGGGACAGTTT  
TTGTCCCATCTTGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAA  
GCAAAGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAATGCTT  
TGGGCAGTCAACGAGTAACCGACCTATTGCTAAAGATGCCCAAACAGTA  
ATGGCATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGC  
TATGCTACTAAGCATAAGAGCCAAATCCTTAAACCTATAATCGCATTCC  
TAGAAATGCTGAT

SEQ ID NO. 6007

STRAIN COH1

CAGCCTTCTAAACTACTTCCACCAAAGAATTAGT  
ATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTT  
TGAGGAAAAATACGGTATAAAGTTAAGCTTATTCAAGGTGGGACAGGGC  
AACTAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGCGGATATT  
TTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTGA  
GTCCTTACGTATCAAAGAATGTTCACTACTGTTATTCCAGACTATATCCATC  
CGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTA  
AATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTATT  
ACAGCCTTCCCTTAAAGGTAAAATTGCTTTTGCAGATCCGAATACTTCCCT  
CTAGTGCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTAC  
ACCAATCCAAAAGCGTGAAGTATGTTAAAGAGCTACAACATAATATTAA  
TGCTATCAAATCTTCTAGCTCTTCAAGAGTTTATCAATCAGTTGCGAGAAG  
GAAAAATGATTGTGGGGTTGACTTACGAAGACCTTAGTGTCAATTTGCAA  
AAAAGTGGTGCCAAATGTTTCTATTGTATACCGACAGAAGGGACAGTTT  
TGTCCCATCTTGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAG  
CAAAGTTATTATTAATTTTATGCTTTCTTTAGATGTTCAAATGCTTTT  
GGGCAGTCAACGAGTAACCGACCTATTGCTAAAGATGCCCAAACAGTAA  
TGGCATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGCT  
ATGCTACTAAGCATAAGAGCCAAATCCTTAAACCTATAATCGCATTCTG  
AGAAATGCTGAT

SEQ ID NO. 6008

STRAIN M781

CAGCCTTCTAAACTACTTCCACCAAAGAATTAGTTATT  
CTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTGA  
GAAAAATACGGTATAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAAC  
TAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGCGGATATTTC  
TTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTGAGTC  
TTACGTATCAAAGAATGTTCACTACTGTTATTCCAGACTATATCCATCCGA  
GTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAAT

Table 60: Comparative Sequences relating to SAG1945

AACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACA  
 GCCTTCCTTAAAGGTAAGGTTGCTTTGCGAGATCCGAATCTTCTCTA  
 GTGCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTACACC  
 AATCCAAAGCGTGGAACTATGTTAAAGGCTACAACATAATATTATGC  
 TATCAAATCTTCTAGCTCTTCAAGAGTTTATCAATCAGTTGCAGAAAGGAA  
 AAATGATGTGGGGTTGACTTACGAAGACCCCTAGTGTCAATTTGCAAAAA  
 AGTGGTGCCAATGTTTCTATTGTATACCCGACAGAAGGGACAGTTTGT  
 CCCATCTTCGGTTGCAATTATAAAGAAATGCTCCTTCTATGAAAGAAGCAA  
 AGTTATTATTAAATTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGG  
 CAGTCAACGAGTAACCGACCTATTGTAAGATGCCCAACAAAGTAATGG  
 CATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGCTATG  
 TCACTAAGCATAAGAGCCAAATCCTTAAACCTATAATCGCATTGCTAGA  
 AATGCTGAT

SEQ ID NO. 6009

STRAIN CJB110

CAGCCTTTTAAACTACTTCCACCAAAAGAATTAGTTATTCT  
 AAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGAGG  
 AAAAAATACCGGTATAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTA  
 ATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTCTT  
 TGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTGAGTCTT  
 ACGTATCAAAGAATGTTTCACTACTGTTATTCCAGACTATATCCATCCAAGT  
 GATACGGCGACACCTTATCTATAAATGGGAGTGTCTTGATTGTAATAA  
 CGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTATTACAGC  
 CTTCTTAAAGGTAAGGTTGCTTTGCGAGATCCGAATACTTCTCTAGT  
 GCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTACACCAA  
 TCCAAAAGCGTGGAACTATGTTAAAGGCTACAACATAATATTAAATGCTA  
 TCAATCTTCTAGCTCTTCAAGGTTTATCAATCAGTTGCAGAAAGGAAAA  
 ATGATTTGTGGGGCTGACTTACGAAGACCCCTAGTGTCAATTTGCAAAAAAG  
 TGGTGCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGCTC  
 CATCTTCGGTTGCAATTATAAAGAAATGCTCCTTCTATGAAAGAAGCAAAG  
 TTAATTATTAAATTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGGCA  
 GTCACAGGTAACCGACCTATTTCGTAAAGATGCCCAACGAGTAATGGCA  
 TGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTC  
 ACTAAGCATAAGGGCCAAATCCTTAAACCTATAATCGTATTGCTAGAAA  
 TGCTGAT

SEQ ID NO. 6010

STRAIN 1169NT

ATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGAGGAAAAATAC  
 GGTATAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAG  
 ATTAAGTAAGGAGGGTAAGCATTGAAAGGCGGATATTTCTTGGAGGAA  
 ATTATACGCAATTTGAAAGTCATAAGGCATTGTTGAGTCTTACGTATCA  
 AAGAAATGTTCACTACTGTTATTCCAGACTATATCCATCCAAGTGATACGGC  
 GACACCTTATCTATAAATGGGAGTGTCTTGATTGTAATAACGAATTAG  
 CTAAGGGACTTACCATCAAGAGTTATGAAGATTATTACAGCCTTCTTA  
 AAAGGTAATGCTTTGCGAGATCCGAATACTTCTCTAGTGTCTTCTC  
 ACAACTCACCAATATACTCTTGGCAAAGGGTGGTTACACCAATCCAAAG  
 CGTGGAACTATGTTAAAGGCTACAACATAATATTAAATGCTATCAAATCT  
 TCTAGCTCTTCAAGGTTTATCAATCAGTTGCAGAAAGGAAAAATGATTGT  
 GGGGTTGACTTACGAAGACCCCTAGTGTCAATTGCAAAAAAGTGGTGCCA  
 ATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGCTCCATCTTCG  
 GTTGCAATTATAAAGAAATGCTCCTTCTATGAAAGAAGCAAAGTTATTAT  
 TAAATTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGGCAGTCAACGA  
 GTAACCGACCTATTTCGTAAAGATGCCCAACGAGTAATGGCATGAAAGCT  
 TTAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTCATAAGCA  
 TAAGGGCCAAATCCTTAAACCTATAATCGTATTGCTAGAAATGCTGAT

SEQ ID NO. 6011

STRAIN JM91130013

CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGT  
 TATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTT  
 TTGAGGAAAAATACGGTATAAAGTTAAGCTTATTCAAGGTGGGACAGGG  
 CAACTAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATGT  
 TTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTG  
 AGTCTTACGTATCAAAGAATGTTCACTACTGTTATTCCAGACTATATCCAT  
 CCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGT  
 AAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTAT  
 TACAGCCTTCTTAAAGGTAAGGTTGCTTTGCGAGATCCGAATACTTCC  
 TCTAGTGTCTTCTCACAACCTCACCATAATATACTCTTGGCAAAGGGTGGTTA  
 CACCAATCCAAAGCGTGGAACTATGTTAAAGGCTACAACATAATATTA  
 ATGCTATCAAATCTTCTAGCTCTTCAAGGTTTATCAATCAGTTGCAGAA  
 GGCAAAATGATTGTTGGGCTGACTTACGAAGACCCCTAGTGTCAATTTGCA  
 AAAAAAGTGGTGCCAATGTTTCTATTGTGTATCCGACAGAAGGGACAGTTT  
 TGTCCCATCTTCGGTTGCAATTATAAAGAAATGCTCCTTCTATGAAAGAA  
 GCAAGCTATTATTAAATTTATGCTTTCTTTAGATGTTCAAAATGCCTT  
 TGGGAGTCAACGAGTAACCGACCTATTTCGTAAAGATGCCCAACGAGTA  
 ATGGCATGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGC  
 TATGTCATAAGCATAAGGGCCAAATCCTTAAACCTATAATCGTATTGCT  
 TAGAAATGCTGAT

PRETTY of: /biotmp/msa523010.2{\*} April 28, 2003 08:55 ..

Table 60: Comparative Sequences relating to SAG1945

	1				50
msa523010.2{263_COH1}	-----	-----	-----	-----	-----
msa523010.2{263_M732}	-----	-----	-----	-----	-----
msa523010.2{263_M781}	-----	-----	-----	-----	-----
msa523010.2{263_A909}	-----	-----	-----	-----	-----
msa523010.2{263_H36B}	-----	-----	-----	-----	-----
msa523010.2{263_090}	-----	-----	-----	-----	-----
msa523010.2{263_18RS21}	-----	-----	-----	-----	-----
msa523010.2{263_2603}	atgaaagaaa	aacagtcgaa	aaggcttatt	tataactac	tggttggttc
msa523010.2{263_CJB110}	-----	-----	-----	-----	-----
msa523010.2{263_1169NT}	-----	-----	-----	-----	-----
msa523010.2{263_JM91130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa523010.2{263_COH1}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_M732}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_M781}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_A909}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_H36B}	-----	-----	-----	-----taaac	-----
msa523010.2{263_090}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_18RS21}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_2603}	cattattttt	ataagtgtt	ttacatacag	tattagccag	ccttctaaac
msa523010.2{263_CJB110}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_1169NT}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_JM91130013}	-----	-----	-----	-----cag	ccttctaaac
Consensus	*****	*****	*****	*****	-----
	101				150
msa523010.2{263_COH1}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_M732}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_M781}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_A909}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_H36B}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_090}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_18RS21}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_2603}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_CJB110}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_1169NT}	-----	-----	-----	-----ATAG	TCAAGCCATT
msa523010.2{263_JM91130013}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
Consensus	-----	-----	-----	-----****	*****
	151				200
msa523010.2{263_COH1}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_M732}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_M781}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_A909}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_H36B}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_090}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_18RS21}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_2603}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_CJB110}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_1169NT}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_JM91130013}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
Consensus	*****	*****	*****	*****	*****
	201				250
msa523010.2{263_COH1}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_M732}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_M781}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_A909}	GCTTATTCAA	GGTGGGACAG	GtCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_H36B}	GCTTATTCAA	GGTGGGACAG	GtCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_090}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_18RS21}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_2603}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_CJB110}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_1169NT}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_JM91130013}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
Consensus	*****	*****	*****	*****	*****
	251				300
msa523010.2{263_COH1}	GTAAGCagTT	GAAGGCGGAT	aTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_M732}	GTAAGCagTT	GAAGGCGGAT	aTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_M781}	GTAAGCagTT	GAAGGCGGAT	aTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_A909}	GTAAGCagTT	GAAGGCGGAT	aTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_H36B}	GTAAGCagTT	GAAGGCGGAT	aTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_090}	GTAAGCagTT	GAAGGCGGAT	aTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_18RS21}	GTAAGCagTT	GAAGGCGGAT	aTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_2603}	GTAAGCagTT	GAAGGCGGAT	aTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_CJB110}	GTAAGCagTT	GAAGGCGGAT	aTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_1169NT}	GTAAGCagTT	GAAGGCGGAT	aTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_JM91130013}	GTAAGCagTT	GAAGGCGGAT	aTTTCTTTG	GAGGAAATTA	TACGCAATTT
Consensus	*****	*****	*****	*****	*****

Table 60: Comparative Sequences relating to SAG1945

		301			350
msa523010.2{263_COH1}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_M732}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_M781}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_A909}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATaTTCATAC
msa523010.2{263_H36B}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATaTTCATAC
msa523010.2{263_090}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_18RS21}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_2603}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_CJB110}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_1169NT}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_JM91130013}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
Consensus	*****	*****	*****	*****	*_*_*_*_*_*_*_*
		351			400
msa523010.2{263_COH1}	TGTTATTCCA	GACtATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_M732}	TGTTATTCCA	GACtATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_M781}	TGTTATTCCA	GACtATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_A909}	TGTTATTCCA	GACtATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_H36B}	TGTTATTCCA	GACtATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_090}	TGTTATTCCA	GACtATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_18RS21}	TGTTATTCCA	GACtATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_2603}	TGTTATTCCA	GACtATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_CJB110}	TGTTATTCCA	GACtATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_1169NT}	TGTTATTCCA	GACtATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_JM91130013}	TGTTATTCCA	GACtATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
Consensus	*****	**_*_*_*_*_*_*	*****	*****	*****
		401			450
msa523010.2{263_COH1}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_M732}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_M781}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_A909}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_H36B}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_090}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_18RS21}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_2603}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_CJB110}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_1169NT}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_JM91130013}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
Consensus	*****	*****	*****	*****_***	*****
		451			500
msa523010.2{263_COH1}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_M732}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_M781}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_A909}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_H36B}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_090}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_18RS21}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_2603}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_CJB110}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_1169NT}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
msa523010.2{263_JM91130013}	ATCAAGAGTT	ATGAAGATT	ATTACAGCCT	TCCTTAAAAG	GTAATAATTGC
Consensus	*****	*****	*****	*****	*****
		501			550
msa523010.2{263_COH1}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_M732}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_M781}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_A909}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_H36B}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_090}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_18RS21}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_2603}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_CJB110}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_1169NT}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_JM91130013}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
Consensus	*****	*****	*****	*****	*****_****
		551			600
msa523010.2{263_COH1}	TACTCTTGCC	aAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_M732}	TACTCTTGCC	aAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_M781}	TACTCTTGCC	aAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_A909}	TACTCTTGCC	aAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_H36B}	TACTCTTGCC	aAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_090}	TACTCTTGCC	aAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_18RS21}	TACTCTTGCC	aAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_2603}	TACTCTTGCC	aAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_CJB110}	TACTCTTGCC	aAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_1169NT}	TACTCTTGCC	aAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_JM91130013}	TACTCTTGCC	aAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT



Table 60: Comparative Sequences relating to SAG1945

Consensus	*****	*****	*****	*****	*****
	601				650
msa523010.2{263_COH1}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_M732}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_M781}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_A909}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_H36B}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_090}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_18RS21}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_2603}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_CJB110}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_1169NT}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_JM91130013}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
Consensus	*****	*****	*****	*****	*****
	651				700
msa523010.2{263_COH1}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_M732}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_M781}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_A909}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_H36B}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_090}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_18RS21}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_2603}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_CJB110}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_1169NT}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_JM91130013}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
Consensus	*****	*****	*****	*****	*****
	701				750
msa523010.2{263_COH1}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_M732}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_M781}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_A909}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_H36B}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_090}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_18RS21}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_2603}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_CJB110}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_1169NT}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_JM91130013}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTg
Consensus	*****	*****	*****	*****	*****
	751				800
msa523010.2{263_COH1}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_M732}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_M781}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_A909}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_H36B}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_090}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_18RS21}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_2603}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_CJB110}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_1169NT}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_JM91130013}	TAcCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
Consensus	**	*****	*****	*****	*****
	801				850
msa523010.2{263_COH1}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_M732}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_M781}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_A909}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_H36B}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_090}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_18RS21}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_2603}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_CJB110}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_1169NT}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_JM91130013}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
Consensus	*****	*****	*****	*****	*****
	851				900
msa523010.2{263_COH1}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_M732}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_M781}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_A909}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_H36B}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_090}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_18RS21}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_2603}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_CJB110}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_1169NT}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT

Table 60: Comparative Sequences relating to SAG1945

msa523010.2{263_JM91130013}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
Consensus	*****	*****	*****	*****	*****
	901				950
msa523010.2{263_COH1}	CGTAAAGATG	CCCAAACaAG	TAATGGCATG	AAAGCTTTAA	AGGATATcGC
msa523010.2{263_M732}	CGTAAAGATG	CCCAAACaAG	TAATGGCATG	AAAGCTTTAA	AGGATATcGC
msa523010.2{263_M781}	CGTAAAGATG	CCCAAACaAG	TAATGGCATG	AAAGCTTTAA	AGGATATcGC
msa523010.2{263_A909}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_H36B}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_090}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_18RS21}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_2603}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_CJB110}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_1169NT}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_JM91130013}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
Consensus	*****	*****	*****	*****	*****
	951				1000
msa523010.2{263_COH1}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	agCCAAATCC
msa523010.2{263_M732}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	agCCAAATCC
msa523010.2{263_M781}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	agCCAAATCC
msa523010.2{263_A909}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_H36B}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_090}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_18RS21}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_2603}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_CJB110}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_1169NT}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
msa523010.2{263_JM91130013}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCAAATCC
Consensus	*****	*****	*****	*****	*****
	1001				1035
msa523010.2{263_COH1}	TTAAAACCTA	TAATCGcATT	CGTAGAAATG	CTGAT	
msa523010.2{263_M732}	TTAAAACCTA	TAATCGcATT	CGTAGAAATG	CTGAT	
msa523010.2{263_M781}	TTAAAACCTA	TAATCGcATT	CGTAGAAATG	CTGAT	
msa523010.2{263_A909}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_H36B}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_090}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_18RS21}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_2603}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_CJB110}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_1169NT}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_JM91130013}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
Consensus	*****	*****	*****	*****	

## SEQ ID NO. 6012

STRAIN 2603 frame: 1

MKEKQSKRLIYILLVSIIFISVFTYSISQPSKLLPPKELVILSPNSQAILTGTIPAFEE  
 KYGIKVKLIQGGTGQLIDRLSKEGKQLKADIFFGGNYTQFESHKALFESYVSKNVHTVIP  
 DYIHPSTATPYTINGSVLIVNNELAKGLTIKSYEDLLQPSLKGKIAFADPNTSSSAFSQ  
 LTNILLAKGGYTNPKAWNYVKKLQHNINAIKSSSSSEVYQSVAEKGMIVGLTYEDPSVNL  
 QKSGANVSIVYPTEGTVPFSSVAIIKNAPSMKEAKLFINFMLSLDVQNAFGQSTSNRPI  
 RKDAQTSNGMKALKDIATLKEDYRYVTKHKGQILKTYNRIIRNAD

## SEQ ID NO. 6013

STRAIN 090 frame: 1

QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA  
 DIFFGNYTQFESHKALFESYVSKNVHTVIPDYIHPSTATPYTINGSVLIVNNELAKGL  
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA  
 IKSSSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVPFSSVAIIKNA  
 PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH  
 KGQILKTYNRIIRNAD

## SEQ ID NO. 6014

STRAIN A909 frame: 1

QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA  
 DIFFGNYTQFESHKALFESYVSKNIHTVIPDYIHPSTATPYTINGSVLIVNNELAKGL  
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA  
 IKSSSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVPFSSVAIIKNA  
 PSMKEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH  
 KGQILKTYNRIIRNAD

## SEQ ID NO. 6015

STRAIN H36B frame: 2

KLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKADIF  
 FGGNYTQFESHKALFESYVSKNIHTVIPDYIHPSTATPYTINGSVLIVNNELVKGLTIK  
 SYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA  
 SSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSIVYPTEGTVPFSSVAIIKNAPSM  
 KEAKLFINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKHKGQ  
 ILKTYNRIIRNAD

## SEQ ID NO. 6016

**Table 60: Comparative Sequences relating to SAG1945**

STRAIN 18RS21 frame: 1  
QPSKLLPKPELVSLSPNSQAILTGTIPAFEEKYGIVKVL IQGGTGQLIDRLSKEGKQLKA  
DIFFGNNYQFESHKALFESYVSKNVHTVTPDYIHPSDTATPYTTNGSVLIVNNEALKGL  
TKSYEDVLQPSLKGKIAFADPNSSSAPSQLNTLLAKGGYTNPKAWNYVVKLQHNINA  
IKSSSSSEVYQSAEKGMI VGLTVEBPPSNLQKSGANV IYPTETGVFPSSVAI I KNA  
PSMKEAFLIFNMLSLLDVQNAFGQSTSNRI RKDAQTSNGMKALKD IATLKEDYRYVTKH  
KGKILKTYNRI RRND

SEQ ID NO. 6017

STRAIN M732 frame: 1

QPSKLLPPKELVILSNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKREGKOLKA  
 IDFFGGNYIQFESHKALFESYVSKNVHTVIPDYIHPSDATTPTYNGSVILVNNELAKGL  
 TIKSYEDLLQPSKLGKIAFADPNSTSSAFQSLTNLILAKGGTNPKAWNYVKKLQHNIA  
 IKSSSSSEVYQSAEKGKIVGLTYEDPSVNLQKSGANVSI VPTEGTVFVPSSVAI I KNA  
 PSMKEAKLFINFMLSLDVQNAFGQSTSNRP IRKDAQTSNGMKALKDIATLKEDYRYVTKH  
 KSOILITKYNIRLAD

SEQ ID NO. 6018

STRAIN COH1 frame: 1

QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKRGGKQLKA  
 DIFFGNYTQFQSHKALFESVYSKNVHTIPDYIHPSDTATPTYINGSVLVLNNELAKGL  
 TIKFSEYDLLOQPSKLGKIAFADNPSTSSAFSLNTILLAKGGYVPPKAWNVLKQHNINA  
 IKSSSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSIYVTEGTVFVPESSVAIKNA  
 PSMKEAKLPINFLMSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIALTKLEDRYVYTKH  
 KSOILKTYKNRIRRAD

SEQ ID NO. 6019

STRAIN M781 frame: 1

QPSKLLPPPELVLISPNSSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKGKOLKA  
LDFFGNGYLPQFESHKALPESVYSHNVHTVPIDYIHPSDTATPYTNGSLIVNNEKLAGL  
TTKSYEDLLQPSKLGKIAFADNPENTSSAFQSLNTLLAKGGTYNPKAWNYVKKLQHNINA  
IKSSSSSEVYQSVAECKMIVGLTYEDPSVNLQKSGANVSI VPTYEGTVFPVSSVAIIKNA  
PSMKEAKLFINFMLSLDVQNAFGQSTSNRP IRKDAQTSNGMKALKDIALTKEDYRYVTKH  
KSOILATYINRIRNAD

SEO ID NO. 6020

STRAIN CJB110 frame: 1

QPFKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQKLA  
DIFPGGNYQFESHLAKFESVSKNVNIPDYIHPSDTPATPYTNGSVLIVNNEALGL  
TISKSYEDLLQPSLKGKIAFADNPSTSSAFQNTLILAKGGYTNPKAWYVKKLQHNIA  
IKSSSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSIYVPTBGTVPVPSSVAIIKNA  
PMKEAKLFINFMLSLDVQNAFGQSTSNRPTRKDAQTSNGMKALKDIATLKDEYRYVTKH  
KGOILKTYNRIRRND

SEQ ID NO. 6021

STRAIN 1169NT frame: 3

STRAIN 116911 NAME: 5  
 SLALTGTGTPAPEEKYGIKVKLIQGGTGQLIDRLSKEGKHLKADIFFGGNYTQFESHKAL  
 FESYVSKNVHTVPIPDYIHPSDTATPYTINGSVLIVNNELAKGLTISKYEDLLQPSLKGKI  
 AFADPNTSSSAFSQLNTILLAKGGYTPKAWNYVKKLQHNIAIKSSSSSEVYQSVABEG  
 MIVGLTYEDPSVLNQLKSGANVISVYPTEGTVFVPSVDYAIKNAPMSKEAKLFNFMLSLD  
 VONAFGOSTSNRPRIKDAOTSGNMKALKDIATLKEDYRYVTKHKGQILKTYNRI RNAD

SEQ ID NO. 6022

STRAIN JM91130013 frame: 1

STRAIN 361/1506/1991 name: P  
QPSKLLPPEKLVLLSPNSQAALLTGTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA  
DVFFGGNYTQFESHKALFESYVSKNVHTVDPDYIHSSDTPATPYTNGSVLVNNEALAGL  
TIKSYEDLLQPSLKGKIAFADNPNTSSAFSOLQNTNILLKAGGTYTNPKAWYVKVLQHNINA  
IKSSSSSEVYQGSVAEGKMI VGLTYEDPSVNLQKSGANVSI VYPTBGTVFVPSVAIIKNA  
PSMKEAKFLINFMFLSDLVQNAFGQSTSNRP IRKDAQTSNGMKALDIA TLKEDYRYVTKH  
KGOILKTYNRIKSLAD

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PRETTY of: /biotmp/msa523117.2{*} April 28, 2003 08:56 ..
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msa523117.2 {263_COH1} -----q psklppkel vilspnSQAI
msa523117.2 {263_M732} -----q psklppkel vilspnSQAI
msa523117.2 {263_M781} -----q psklppkel vilspnSQAI
msa523117.2 {263_1169NT} -----SQAI
msa523117.2 {263_CJB110} -----q pfklppkel vilspnSQAI
msa523117.2 {263_O90} -----q psklppkel vilspnSQAI
msa523117.2 {263_18RS21} -----q psklppkel vilspnSQAI
msa523117.2 {263_2603} mkekqskrli yillvvsii f iavftyssiq psklppkel vilspnSQAI
msa523117.2 {263_A909} -----q psklppkel vilspnSQAI
msa523117.2 {263_JM91130013} -----q psklppkel vilspnSQAI
msa523117.2 {263_H36B} -----kllppkel vilspnSQAI
Consensus *****

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	51	100
msa523117.2{263_COH1}	LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD iFFGGNYTQF	
msa523117.2{263_M732}	LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD iFFGGNYTQF	
msa523117.2{263_M781}	LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD iFFGGNYTQF	
msa523117.2{263_1169NT}	LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKhLKAD iFFGGNYTQF	

Table 60: Comparative Sequences relating to SAG1945

msa523117.2{263_CJB110}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_090}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_18RS21}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_2603}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_A909}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_JM91130013}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	vFFGGNYTQF
msa523117.2{263_H36B}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_M732}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_M781}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_1169NT}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_CJB110}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_090}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_18RS21}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_2603}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_A909}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_JM91130013}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_H36B}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELvKGLT
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_M732}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_M781}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_1169NT}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_CJB110}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_090}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_18RS21}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_2603}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_A909}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_JM91130013}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_H36B}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_M732}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_M781}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_1169NT}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_CJB110}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_090}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_18RS21}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_2603}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_A909}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_JM91130013}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_H36B}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_M732}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_M781}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_1169NT}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_CJB110}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_090}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_18RS21}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_2603}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_A909}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_JM91130013}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_H36B}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_M732}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_M781}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_1169NT}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_CJB110}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_090}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_18RS21}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_2603}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_A909}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_JM91130013}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_H36B}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
Consensus	*****	*****	*****	*****	*****

Table 61: Comparative Sequences relating to SAG1030

## SEQ ID NO. 6101

## STRAIN 2603

ATGGTAAAAGTTAGTGTAAGTTCTGTAGGAACCTCAAGCATCAACAGTAGCTATTTCTATG  
 TTTAGTCGTGTATCGGCTTTAAATGATGCAATAACAAAACCTATCATCTTTTGCAGAGGCT  
 GCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTGGAACGTTAACT  
 CCGATGCTTCAAGGAATGATTCCTTTCTCTGAAACATTGAGTGAGAAATGTACAGAATTA  
 CAAACCTTATATGTCTCAATTTGTGGTGATGAGGATTTAGACTCTGTCTGTTTAGAATCA  
 AAATTAGCAAGTGATAGGGCATCATTAAGATTGCTGAAGCACITTTAGAGCATCTTAAC  
 GATGATCCAGAACCTTCCAAATCTGCCATAAGTTCTACAAAAGTAATATTAAAAAATTA  
 AAAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAATTTAACGCCCAT  
 TCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAACTGTTAACCAAGCACTAGCG  
 GCTGTTTCAACAGGATTTTCTGGATATAATAGTAAACCCGAGCTTTTGGAAAACCAACA  
 TCCGGACAGATGGAATGGACAAAGACAGTTAAGAAGAATTGGAAGAGCGAGAAGACGCC  
 AAAGCTGAAGAACTGAAAAGTAAAAAGGCTGAAGAAAAGTAAGAAGCTTCAAAAATTGAA  
 AATACTACTAAAAAAGTAATGTTTCAAGTTGATAAAAAGAAATTAATAAAGCGGCTAAT  
 GAAGCGTATAAATTAGGAGAAATTAAAAAGATACCTATGAATCAATTATCAGTGGTTTA  
 AGTAATGCATCGGCTGCCTTACTTAAAGAGGTAGCTAAATCAAAATTGACTGACACAGCT  
 CGGCTATTGATG

## SEQ ID NO. 6102

## STRAIN 090

TTAAATGATGCAATAACAAAACCTATCATCTTTTGCAGAGGCT  
 GCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTGG  
 AACGTTAACTCCGATGCTTCAAGGAATGATTCTTTCTCTGAAACATTGA  
 GTGAGAAATGTACAGAATTACAAACCTTATATGTCTCAATTTGTGGTGAT  
 GAGGATTTAGACTCTGTCTGTTTAGAATCAAAATTAGCAAGTGATAGGGC  
 ATCATTAAAGATTGCTGAAGCACITTTAGAGCATCTTAACGATGATCCAG  
 AACCTTCCAAATCTGCCATAAGTTCTACAAAAGTAATATTAAAAAATTA  
 AAAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAAT  
 TAAGCCCATTCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAA  
 CTGTTAACCAAGCACTAGCGGCTGTTTCAACAGGATTTTCTGGATATAAT  
 AGTAAACCCGAGCTTTTGGAAAACCAACATCCGACAGATGGAATGGAC  
 AAAGACAGTTAAGAAGAATTGGAAGAGCGAGAAGACGCCAAAGCTGAAG  
 AACTGAAAAGTAAAAAGGCTGAAGAAAAGTAAGAAGCTTCAAAAATTGAA  
 AATACTACTAAAAAAGTAATGTTTCAAGTTGATAAAAAGAAATTAATAAA  
 AGCGGCTAATGAAGCGTATAAATTAGGAGAAATTAAAAAGATACCTATG  
 AATCAATTATCAGTGGTTAAGTAATGCATCGGCTGCCTTACTTAAAGAG  
 GTAGCTAAATCAAAATTGACTGACACAGCTCGGCTATTGATG

## SEQ ID NO. 6103

## STRAIN 18RS21

TTAAATGATGCAATAACAAAACCTATCATCTTTTGCAGAGGCT  
 TGCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTG  
 GAACGTTAACTCCGATGCTTCAAGGAATGATTCTTTCTCTGAAACATTG  
 AGTGAGAAATGTACAGAATTACAAACCTTATATGTCTCAATTTGTGGTGAT  
 TGAGGATTTAGACTCTGTCTGTTTAGAATCAAAATTAGCAAGTGATAGGG  
 CATCATTAAAGATTGCTGAAGCACITTTAGAGCATCTTAACGATGATCCA  
 GAACCTTCCAAATCTGCCATAAGTTCTACAAAAGTAATATTAAAAAATTA  
 AAAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAAT  
 TTAACGCCCATTCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAA  
 ACTGTTAACCAAGCACTAGCGGCTGTTTCAACAGGATTTTCTGGATATAA  
 TAGTAAACCCGAGCTTTTGGAAAACCAACATCCGACAGATGGAATGGGA  
 CAAAGACAGTTAAGAAGAATTGGAAGAGCGAGAAGACGCCAAAGCTGAAG  
 GAACGAAAAGTAAAAAGGCTGAAGAAAAGTAAGAAGCTTCAAAAATTGA  
 AATACTACTAAAAAAGTAATGTTTCAAGTTGATAAAAAGAAATTAATAAA  
 AAGCGGCTAATGAAGCGTATAAATTAGGAGAAATTAAAAAGATACCTAT  
 GAATCAATTATCAGTGGTTAAGTAATGCATCGGCTGCCTTACTTAAAGA  
 GGTAGCTAAATCAAAATTGACTGACACAGCTCGGCTATTGATG

PRETTY of: /biotmp/msa185066.2{\*} May 13, 2003 07:01 ..

	1				50
msa185066.2{270_090}	-----	-----	-----	-----	-----
msa185066.2{270_18RS21}	-----	-----	-----	-----	-----
msa185066.2{270_2603}	atggtaaaag	ttagtgtgaag	ttctgttagga	actcaagcat	caacagtagc
Consensus	*****	*****	*****	*****	*****
	51				100
msa185066.2{270_090}	-----	-----	-----TT	AAATGATGCA	ATAACAAAAC
msa185066.2{270_18RS21}	-----	-----	-----TT	AAATGATGCA	ATAACAAAAC
msa185066.2{270_2603}	tattttctatg	tttagtcgtg	tatcggcttt	AAATGATGCA	ATAACAAAAC
Consensus	*****	*****	*****	*****	*****
	101				150
msa185066.2{270_090}	TATCATCTTT	TGCAGAGGCT	GCAACTCTTC	AAGGGACTGC	TTATTCAAAT
msa185066.2{270_18RS21}	TATCATCTTT	TGCAGAGGCT	GCAACTCTTC	AAGGGACTGC	TTATTCAAAT
msa185066.2{270_2603}	TATCATCTTT	TGCAGAGGCT	GCAACTCTTC	AAGGGACTGC	TTATTCAAAT
Consensus	*****	*****	*****	*****	*****
	151				200
msa185066.2{270_090}	GCAAAAAGCT	ATGCTACTGG	AACGTTAACT	CCGATGCTTC	AAGGAATGAT
msa185066.2{270_18RS21}	GCAAAAAGCT	ATGCTACTGG	AACGTTAACT	CCGATGCTTC	AAGGAATGAT
msa185066.2{270_2603}	GCAAAAAGCT	ATGCTACTGG	AACGTTAACT	CCGATGCTTC	AAGGAATGAT

Table 61: Comparative Sequences relating to SAG1030

Consensus	*****	*****	*****	*****	*****
	201				250
msa185066.2{270_090}	TCTTTTCTCT	GAACATTGA	GTGAGAAATG	TACAGAATTA	CAAACCTTAT
msa185066.2{270_18RS21}	TCTTTTCTCT	GAACATTGA	GTGAGAAATG	TACAGAATTA	CAAACCTTAT
msa185066.2{270_2603}	TCTTTTCTCT	GAACATTGA	GTGAGAAATG	TACAGAATTA	CAAACCTTAT
Consensus	*****	*****	*****	*****	*****
	251				300
msa185066.2{270_090}	ATGTCCTCAAT	TTGTGGTGAT	GAGGATTTAG	ACTCTGTCGT	TTTAGAATCA
msa185066.2{270_18RS21}	ATGTCCTCAAT	TTGTGGTGAT	GAGGATTTAG	ACTCTGTCGT	TTTAGAATCA
msa185066.2{270_2603}	ATGTCCTCAAT	TTGTGGTGAT	GAGGATTTAG	ACTCTGTCGT	TTTAGAATCA
Consensus	*****	*****	*****	*****	*****
	301				350
msa185066.2{270_090}	AAATTAGCAA	GTGATAGGGC	ATCATTAAAG	ATTGCTGAAG	CACCTTTAGA
msa185066.2{270_18RS21}	AAATTAGCAA	GTGATAGGGC	ATCATTAAAG	ATTGCTGAAG	CACCTTTAGA
msa185066.2{270_2603}	AAATTAGCAA	GTGATAGGGC	ATCATTAAAG	ATTGCTGAAG	CACCTTTAGA
Consensus	*****	*****	*****	*****	*****
	351				400
msa185066.2{270_090}	GCATCTTAAC	GATGATCCAG	AACCTTCCAA	ATCTGCCATA	AGTTCTACAA
msa185066.2{270_18RS21}	GCATCTTAAC	GATGATCCAG	AACCTTCCAA	ATCTGCCATA	AGTTCTACAA
msa185066.2{270_2603}	GCATCTTAAC	GATGATCCAG	AACCTTCCAA	ATCTGCCATA	AGTTCTACAA
Consensus	*****	*****	*****	*****	*****
	401				450
msa185066.2{270_090}	AAAGTAATAT	TAAAAAATTA	AAAAAACGTA	TAAATCTAA	TCAAAAGAAA
msa185066.2{270_18RS21}	AAAGTAATAT	TAAAAAATTA	AAAAAACGTA	TAAATCTAA	TCAAAAGAAA
msa185066.2{270_2603}	AAAGTAATAT	TAAAAAATTA	AAAAAACGTA	TAAATCTAA	TCAAAAGAAA
Consensus	*****	*****	*****	*****	*****
	451				500
msa185066.2{270_090}	TTAGACAACC	TTAATGAATT	TAACGCCCAT	TCAGCAACAG	TATTTGCGGA
msa185066.2{270_18RS21}	TTAGACAACC	TTAATGAATT	TAACGCCCAT	TCAGCAACAG	TATTTGCGGA
msa185066.2{270_2603}	TTAGACAACC	TTAATGAATT	TAACGCCCAT	TCAGCAACAG	TATTTGCGGA
Consensus	*****	*****	*****	*****	*****
	501				550
msa185066.2{270_090}	CATTTCTAAT	GCACAGTCAA	CTGTTAACCA	AGCACTAGCG	GCTGTTTCAA
msa185066.2{270_18RS21}	CATTTCTAAT	GCACAGTCAA	CTGTTAACCA	AGCACTAGCG	GCTGTTTCAA
msa185066.2{270_2603}	CATTTCTAAT	GCACAGTCAA	CTGTTAACCA	AGCACTAGCG	GCTGTTTCAA
Consensus	*****	*****	*****	*****	*****
	551				600
msa185066.2{270_090}	CAGGATTTC	TGGATATAAT	AGTAAACCG	GAGCTTTTGG	AAAACCAACA
msa185066.2{270_18RS21}	CAGGATTTC	TGGATATAAT	AGTAAACCG	GAGCTTTTGG	AAAACCAACA
msa185066.2{270_2603}	CAGGATTTC	TGGATATAAT	AGTAAACCG	GAGCTTTTGG	AAAACCAACA
Consensus	*****	*****	*****	*****	*****
	601				650
msa185066.2{270_090}	TCCGGACAGA	TGGAATGGAC	AAAGACAGTT	AAGAAGAATT	GGAAAGAGCG
msa185066.2{270_18RS21}	TCCGGACAGA	TGGAATGGAC	AAAGACAGTT	AAGAAGAATT	GGAAAGAGCG
msa185066.2{270_2603}	TCCGGACAGA	TGGAATGGAC	AAAGACAGTT	AAGAAGAATT	GGAAAGAGCG
Consensus	*****	*****	*****	*****	*****
	651				700
msa185066.2{270_090}	AGAAGACGCC	AAAGCTGAAG	AACTGAAAAG	TAAAAAGGCT	GAAGAAAGTA
msa185066.2{270_18RS21}	AGAAGACGCC	AAAGCTGAAG	AACTGAAAAG	TAAAAAGGCT	GAAGAAAGTA
msa185066.2{270_2603}	AGAAGACGCC	AAAGCTGAAG	AACTGAAAAG	TAAAAAGGCT	GAAGAAAGTA
Consensus	*****	*****	*****	*****	*****
	701				750
msa185066.2{270_090}	AGAAAGCTTC	AAAAATTGAA	AATACTACTA	AAAAAAGTAA	TGTTTCAGTT
msa185066.2{270_18RS21}	AGAAAGCTTC	AAAAATTGAA	AATACTACTA	AAAAAAGTAA	TGTTTCAGTT
msa185066.2{270_2603}	AGAAAGCTTC	AAAAATTGAA	AATACTACTA	AAAAAAGTAA	TGTTTCAGTT
Consensus	*****	*****	*****	*****	*****
	751				800
msa185066.2{270_090}	GATAAAAAGA	AATTAATAAA	AGCGGCTAAT	GAAGCGTATA	AATTAGGAGA
msa185066.2{270_18RS21}	GATAAAAAGA	AATTAATAAA	AGCGGCTAAT	GAAGCGTATA	AATTAGGAGA
msa185066.2{270_2603}	GATAAAAAGA	AATTAATAAA	AGCGGCTAAT	GAAGCGTATA	AATTAGGAGA
Consensus	*****	*****	*****	*****	*****
	801				850
msa185066.2{270_090}	AATTAAAAAA	GATACCTATG	AATCAATTAT	CAGTGGTTTA	AGTAATGCAT
msa185066.2{270_18RS21}	AATTAAAAAA	GATACCTATG	AATCAATTAT	CAGTGGTTTA	AGTAATGCAT
msa185066.2{270_2603}	AATTAAAAAA	GATACCTATG	AATCAATTAT	CAGTGGTTTA	AGTAATGCAT
Consensus	*****	*****	*****	*****	*****
	851				900
msa185066.2{270_090}	CGGCTGCCTT	ACTTAAAGAG	GTAGCTAAAT	CAAAATTGAC	TGACACAGCT
msa185066.2{270_18RS21}	CGGCTGCCTT	ACTTAAAGAG	GTAGCTAAAT	CAAAATTGAC	TGACACAGCT

Table 61: Comparative Sequences relating to SAG1030

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msa185066.2{270_2603} CGGCTGCCTT ACTTAAAGAG GTAGCTAAAT CAAAATTGAC TGACACAGCT
Consensus *****
          901          912
msa185066.2{270_090} CGGCTATTGA TG
msa185066.2{270_18RS21} CGGCTATTGA TG
msa185066.2{270_2603} CGGCTATTGA TG
Consensus ***** **

SEQ ID NO. 6104
STRAIN 2603 frame: 1
MVKVSVSSVGTQASTVAISMFSRVSA LNDAITKLSSFAEAATLQGTAYSNKSYATGTLT
PMLQGMILFSETLSEKCTELQTLTVSICGDEDLDSDVLESKLASDRASLKIAEALLEHLN
DDPEPSKSAISSTKSNIKKLKKRIKSNQKKLDNLNEFNAHSATVFADISNAQSTVNQALA
AVSTGFSGYNSKTGAFGKPTSGQMEWTKTVKKNWKEREDAKAEELKSKKAEESKKASKIE
NTTKKSNVSVDDKKLIKAANEAYKLGEIKKDTYESIISGLSNASAALLKEVAKSKLTDTA
RLLM

SEQ ID NO. 6105
STRAIN 090 frame: 1
LNDAITKLSSFAEAATLQGTAYSNKSYATGTLTPMLQGMILFSETLSEKCTELQTLTVS
ICGDEDLDSDVLESKLASDRASLKIAEALLEHLNDDPEPSKSAISSTKSNIKKLKKRIKS
NQKKLDNLNEFNAHSATVFADISNAQSTVNQALAAVSTGFSGYNSKTGAFGKPTSGQMEW
TKTVKKNWKEREDAKAEELKSKKAEESKKASKIENTTKKSNVSVDDKKLIKAANEAYKLGE
EIKKDTYESIISGLSNASAALLKEVAKSKLTDARLLM

SEQ ID NO. 6106
STRAIN 18RS21 frame: 1
LNDAITKLSSFAEAATLQGTAYSNKSYATGTLTPMLQGMILFSETLSEKCTELQTLTVS
ICGDEDLDSDVLESKLASDRASLKIAEALLEHLNDDPEPSKSAISSTKSNIKKLKKRIKS
NQKKLDNLNEFNAHSATVFADISNAQSTVNQALAAVSTGFSGYNSKTGAFGKPTSGQMEW
TKTVKKNWKEREDAKAEELKSKKAEESKKASKIENTTKKSNVSVDDKKLIKAANEAYKLGE
EIKKDTYESIISGLSNASAALLKEVAKSKLTDARLLM
PRETTY of: /biotmp/msa185181.2{*} May 13, 2003 07:03 ..

          1          50
msa185181.2{270_090} ~~~~~~LND AITKLSSFAEAATLQGTAYSN
msa185181.2{270_18RS21} ~~~~~~LND AITKLSSFAEAATLQGTAYSN
msa185181.2{270_2603} mvkvsvssvg tqastvaism fersvaLNDAITKLSSFAEAATLQGTAYSN
Consensus *****

          51          100
msa185181.2{270_090} AKSYATGTLT PMLQGMILFS ETLSEKCTEL QTLVVSICGD EDLDSVVLES
msa185181.2{270_18RS21} AKSYATGTLT PMLQGMILFS ETLSEKCTEL QTLVVSICGD EDLDSVVLES
msa185181.2{270_2603} AKSYATGTLT PMLQGMILFS ETLSEKCTEL QTLVVSICGD EDLDSVVLES
Consensus *****

          101          150
msa185181.2{270_090} KLASDRASLK IAEALLEHLN DDPEPSKSAI SSTKSNIKKL KKRIKSNQKK
msa185181.2{270_18RS21} KLASDRASLK IAEALLEHLN DDPEPSKSAI SSTKSNIKKL KKRIKSNQKK
msa185181.2{270_2603} KLASDRASLK IAEALLEHLN DDPEPSKSAI SSTKSNIKKL KKRIKSNQKK
Consensus *****

          151          200
msa185181.2{270_090} LDNLNEFNAH SATVFADISN AQSTVNQALA AVSTGFSGYN SKTGAFGKPT
msa185181.2{270_18RS21} LDNLNEFNAH SATVFADISN AQSTVNQALA AVSTGFSGYN SKTGAFGKPT
msa185181.2{270_2603} LDNLNEFNAH SATVFADISN AQSTVNQALA AVSTGFSGYN SKTGAFGKPT
Consensus *****

          201          250
msa185181.2{270_090} SGQMEWTKTV KKNWKEREDA KAEELKSKKA EESKKASKIE NTTKKNVSV
msa185181.2{270_18RS21} SGQMEWTKTV KKNWKEREDA KAEELKSKKA EESKKASKIE NTTKKNVSV
msa185181.2{270_2603} SGQMEWTKTV KKNWKEREDA KAEELKSKKA EESKKASKIE NTTKKNVSV
Consensus *****

          251          300
msa185181.2{270_090} DKKKLIKAAN EAYKLGEIKK DYESIISGL SNASAALLKE VAKSKLTDTA
msa185181.2{270_18RS21} DKKKLIKAAN EAYKLGEIKK DYESIISGL SNASAALLKE VAKSKLTDTA
msa185181.2{270_2603} DKKKLIKAAN EAYKLGEIKK DYESIISGL SNASAALLKE VAKSKLTDTA
Consensus *****

          301
msa185181.2{270_090} RLLM
msa185181.2{270_18RS21} RLLM
msa185181.2{270_2603} RLLM
Consensus ****

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Table 62: Comparative Sequences relating to SAG0690

SEQ ID NO. 6201

STRAIN 2603

ATGATTTTAAAAATTTGTCGTGCAGCATATAGTTTACAATGGGGAGGTGTTACCAATTA  
 GCTTTGCTGGATTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATA  
 GCTTACGAGAAACAATATAAAAGAAAACTGAGATACAATGTGACGATAAACATCTCCTC  
 GCAAAATTTGTTCAATTTTAAAAATACAATAGTTTACTTTTCCCTATATTTCCCAATAT  
 AGAGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTTTAACTTCTGATTTTAAAGC  
 CATACATGTACGATTGAAACTGCAAACTAATTTTAAAGAAGGTAAAACTTATCAGCA  
 GTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAAGATAAGAGGAATGCTGCTGGA  
 GACCTTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATCTCGTTTAT  
 CGTTTAGTAATGGAAAGATTGTTAGGCAAGCACCATCTGAACAGGAGTTAACAGTAGGT  
 TTTAAGCCAGGGGTCAGTTTTCATTTTACTTATCAAGATATCATCAATCATCCTGATTCT  
 ATTTTGTATGGTTATCATCCTGCTGCTAAAAATAAAAATCAGCTTCTTTAGCAGAACATTTA  
 GTTGCATGTGTTATCCCAAAACATTATCAAGAAGATTATCAAGCCTTGTGCCCAATGAC  
 TTGAAACACAGGGTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAA  
 AAAGTTTATGATTTTCTTTGTCAATTGGAAAAATAA

SEQ ID NO. 6202

STRAIN 090

TGGATTATCCTCTAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTC  
 ATAGCTTACGAGAAACAATATAAAAGAAAAATTGAGATACAATGTGACGA  
 TAAACATCTCCTCACAAAATTTGTTCAATTTTAAAAATACAATAGTTTAA  
 CTTTTCCCTATATTTCCCAATATAGAGAAGCGGCAGCTACTTTAATGAG  
 GATGGTATTAGTTTAACTTCTGATTTTAAAGCCATACATGTACGATTGA  
 AACTGCAAACTAATTTTAAAGAAGGTAAAACTTATCAGCAGTTAAAG  
 CCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAGAGGAATGCTGCT  
 GGAGACCTTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATAC  
 CAATCTCGTTTATCGTTTAGTAATGGAAAGATTGTTAGGCAAGCACCAT  
 CTGAACAGGAGTTAACAGTAGCTTTTAAAGCCAGGGGTCAGCTTTCATTTT  
 AATTATCAAGATATCATCAATCATCCTGATTCTATTTTGTATGGTTATCA  
 TCCTGCTAAAATTAATAAATCAACTTTCTTTAGCAGAACATTTAGTTGCAT  
 GTGTTATCCCAAAACATTATCAAGAAGATTATCAAGCCTTGTGCCCTAAT  
 GACTTGAAACACAGAGTTTATTATTTAGATTACTGTAACGAAACACTTTA  
 TGAGTGGAATCAAAAAGTTTATGATTTCTTTGTCAATTGGAAAAATAA

SEQ ID NO. 6203

STRAIN A909

TTGCTGGATTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATA  
 GGAGCTTTCTATAGCTTACGAGAAACAATATAAAAGAAAAATTGAGATACA  
 ATGTGACGATAAACATCTCCTCACAAAATTTGTTCAATTTTAAAAATACA  
 ATAGTTTACTTTTCCCTATATTTCCCAATATAGAGAAGCGGCAGCTACT  
 TTTAATGAGGATGGTATAGTTTAACTTCTGATTTTAAAGCCATACATG  
 TACGATTGAACTGCAAACTAATTTTAAAGAAGGTAAAACTTATCAG  
 CAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAGAGG  
 AATGCTGCTGGAGACCTTAAAGATTACTTTGACTATGTGATGTTGAACTG  
 GTCAAATACCAATCTCGTTTATCGTTTAGTAATGGAAAGATTGTTAGGCA  
 AAGCACCATCTGAACAGGAGTTAACAGTAGCTTTTAAAGCCAGGGGTCAGC  
 TTTCAATTTAATTATCAAGATATCATCAATCATCCTGATTCTATTTTGA  
 TGGTTATCATCTGCTAAAATTAATAAATCAACTTTCTTTAGCAGAACATT  
 TAGTTGCATGTGTTATCCCAAAACATTATCAAGAAGATTATCAAGCCTT  
 GTGCCCTAATGACTTGAAACACAGAGTTTATTATTTAGATTACTGTAACGA  
 AACACTTTATGAGTGGAATCAAAAAGTTTATGATTTCTTTGTCAATTGG  
 AAAATAAA

SEQ ID NO. 6204

STRAIN H36B

TTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAA  
 CAATATAAAAGAAAAATTGAGATACAATGTGACGATAAACATCTCCTCAC  
 AAAAATTTGTTCAATTTTAAAAATACAATAGTTTACTTTTCCCTATATTC  
 CCAATATAGAGAAGCGGCAGCTACTTTAATGAGGATGGTATTAGTTTA  
 ACTTCTGATTTTAAAGCCATACATGTACGATTGAAACTGCAAACTAAT  
 TTTTAAAGAAGGTAAAACTTATCAGCAGTTAAAGCCTTTAATAAGCCTG  
 CTGAAGTACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCTTAAAGAT  
 TACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATCTGGTTATCG  
 TTTAGTAATGGAAAGATTGTTAGGCAAGCACCATCTGAACAGGAGTTAA  
 CAGTAGCTTTTAAAGCCAGGGGTCAGCTTTCAATTTAATTATCAAGATATC  
 ATCAATCATCCTGATTCTATTTTGTATGGTTATCATCCTGCTAAAATTA  
 AATCAACTTTCTTTAGCAGAACATTAGTTGCATGTGTTATCCCAAAAC  
 ATTATCAAGAAGATTATCAAGCCTTGTGCCCTAATGACTTGAACACAGA  
 GTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAA  
 AGTTTATGATTTTCTTTGTCAATTGGAAAAATAA

SEQ ID NO. 6205

STRAIN 18RS21

TTGCTGGATTATCCTCGAATTAAGGCGTT  
 TGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATAAA  
 GAAAAACTGAGATACAATGTGACGATAAACATCTCCTCGCAAAATTTGTT  
 CATTTTAAAAATACAATAGTTTACTTTTCCCTATATTTCCCAATATAG  
 AGAAGCGGCAGCTACTTTAATGAGGATGGTATTAGTTTAACTTCTGATT  
 TTTTAAAGCCATACATGTACGATTGAACTGCAAACTAATTTTAAAGAA  
 GGTAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACT  
 GGTAAAGATAAGAGGAATGCTGCTGGAGACCTTAAAGATTACTTTGACT  
 ATGTGATGTTGAACTGGTCAAATACCAATCTGGTTATCGTTTAGTAATG



Table 62: Comparative Sequences relating to SAG0690

GAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGTTT  
 TAAGCCAGGGGTGAGTTTTCATTTTACTTATCAAGATATCATCAATCATC  
 CTGATTCTATTTTGGATGGTTATCATCCTGCTAAAATTAAAAATCAGCTT  
 TCTTTAGCAGAACATTAGTTGCATGTGTATCCCAAAACATTATCAAGA  
 AGATTATCAAAGCCTTGTGCCAATGACTTGAACACAGGGTTTATTATT  
 TAGATTACTGTAACGAAACACTTTATGAGTGGAAATCAAAAAGTTTATGAT  
 TTTCTTTGTCATTTGGAAAATAAA

## SEQ ID NO. 6206

## STRAIN M732

TTGCTGGATTATCCTCGAATTAAGGCGTT  
 TGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATAAAA  
 GAAAACTGAGATACAATGTGACGATAAACATCTCCTCGCAAAAATTTGTT  
 CATTTTAAATAACAATAGTTTACITTTCCCTATATCCCAATATAG  
 AGAAGCGGCAGCTACTTTAATGAGGATGGTATTAGTTAACTTCTGATT  
 TTTAAGCCATACATGTACGATTGAACTGCAAACTAATTTTAAAGAA  
 GGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACT  
 GGTAAAAGATAAGAGGAATGCTGCTGGAGACCTTAAAGATTACTTTGACT  
 ATGTGATGTTGAACCTGGTCAAAATACCAATTCTGGTTATCGTTTAGTAATG  
 GAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGTTT  
 TAAGCCAGGGGTGAGTTTTCATTTTACTTATCAAGATATCATCAATCATC  
 CTGATTCTATTTTGGATGGTTATCATCCTGCTAAAATTAAAAATCAGCTT  
 TCTTTAGCAGAACATTAGTTGCATGTGTATCCCAAAACATTATCAAGA  
 AGATTATCAAAGCCTTGTGCCAATGACTTGAACACAGGGTTTATTATT  
 TAGATTACTGTAACGAAACACTTTATGAGTGGAAATCAAAAAGTTTATGAT  
 TTTCTTTGTCATTTGGAAAATAAA

## SEQ ID NO. 6207

## STRAIN COH1

## TTGCTGGAT

TATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAGC  
 TTACGAGAAACAATATAAAAGAAAACTGAGATACAATGTGACGATAAAC  
 ATCTCCTCGCAAAAATTTGTTTCAITTTTAAATAACAATAGTTTACTTTT  
 CCTATATTTCCCAATATAGAGAAGCGGCAGCTACTTTAATGAGGATGG  
 TATTAGTTTAACTTCTGATTTTTAAAGCCATACATGTACGATTGAAACTG  
 CAAACTAATTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTTT  
 AATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGAGA  
 CCTTAAAGATTACTTTGACTATGTGATGTTGAACCTGGTCAAAATACCAAT  
 CTGGTTATCGTTTAGTAATGGAAGATTGTTAGGCAAAGCACCATCTGAA  
 CAGGAGTTAACAGTAGGTTTAAAGCCAGGGGTGAGTTTTCATTTTACTTA  
 TCAAGATATCATCAATCATCTCTGATTCTATTTTGGATGGTTATCATCCTG  
 CTAAAATTAATAATCAGCTTCTTTAGCAGAACATTAGTTGCATGTGTT  
 ATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCAATGACTT  
 GAAACACAGGGTTTATTATTAGATTACTGTAAACGAAACACTTTATGAGT  
 GGAATCAAAAAGTTTATGATTTCCTTTGGCAITTTGGAAAATAAA

## SEQ ID NO. 6208

## STRAIN M781

## TTGCTGGA

TTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAG  
 CTTACGAGAAACAATATAAAAGAAAACTGAGATACAATGTGACGATAAA  
 CATCTCCTCGCAAAAATTTGTTTCAITTTTAAATAACAATAGTTTACTTT  
 TCCTATATTTCCCAATATAGAGAAGCGGCAGCTACTTTAATGAGGATG  
 GTATTAGTTTAACTTCTGATTTTTAAAGCCATACATGTACGATTGAACT  
 GCAAACTAATTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTTT  
 TAATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGAG  
 ACCCTAAAGATTACTTTGACTATGTGATGTTGAACCTGGTCAAAATACCAAT  
 TCTGGTTATCGTTTAGTAATGGAAGATTGTTAGGCAAAGCACCATCTGA  
 ACAGGAGTTAAACAGTAGGTTTAAAGCCAGGGGTGAGTTTTCATTTTACTT  
 ATCAAGATATCATCAATCATCTCTGATTCTATTTTGGATGGTTATCATCCT  
 GCTAAAATTAATAATCAGCTTCTTTAGCAGAACATTAGTTGCATGTGT  
 TATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCAATGACT  
 TGAACACAGGGTTTATTATTAGATTACTGTAAACGAAACACTTTATGAGT  
 TGGAAATCAAAAAGTTTATGATTTCCTTTGTCATTTGGAAAATAAA

## SEQ ID NO. 6209

## STRAIN CJB110

## TTGCTGGATTATCCTCGAATTAAGGC

GTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATA  
 AAAGAAAAATTTAGATACAATGTGACGATAAACATCTCCTCACAATAAT  
 GTTCATTTTAAATAACAATAGTTTACTTTTCCCTATATTTCCCAATA  
 TAGAGAAGCGGCAGCTACTTTAATGAGGATGGTATTAGTTTAACTTCTG  
 ATTTTAAAGCCATACATGTACGATTGAACTGCAAACTAATTTTAAAG  
 GAAGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGT  
 ACTGTAATGATAAGAGGAATGCTGCTGGAGACCTTAAAGATTACTTTG  
 ACTATGTGATGTTGAACCTGGTCAAAATACCAATCTGGTTATCGTTTAGTA  
 ATGGAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGC  
 TTTTAAAGCCAGGGGTGAGCTTTTCAITTTAATTTATCAAGATATCATCAATC  
 ATCCTGATTCTATTTTGGATGGTTATCATCCTGCTAAAATTAATAATCA  
 CTTTCTTTAGCAGAACATTAGTTGCATGTGTATCCCAAAACATTATCA  
 AGAAGATTATCAAAGCCTTGTGCCAATGACTTGAACACAGAGTTTATT  
 ATTTAGATTACTGTAACGAAACACTTTATGAGTGGAAATCAAAAAGTTTAT  
 GATTTCTTTGTCATTTGGAAAATAAA

Table 62: Comparative Sequences relating to SAG0690

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SEQ ID NO. 6210
STRAIN 1169NT
AATTAAGCGCTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGA
AACAAATATAAAAGAAAGAACTGAGATACAATGTGACGATAAACATCTCCTC
GCAAAAATTGTTTCAATTTTTTAAATACAAATAGTTTACTTTTCCCTATAT
TCCCAAATATAGAGAAGCGGCGAGCTACITTTAATGAGGATGCTATTAGTT
TAACCTTCTGATTTTTTAAGCCATACATGTACGATTGAAAGCTGCAAACTA
ATTTTTAAAGAAGGTAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCC
TGCTGAAGTACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCCATAAG
ATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATTCTGTTAT
CGTTTAGTAATGGAAAGATTGTTAGGCAAGCACCATCTGAACAGGAGTT
AACAGTAGGTTTAAAGCCAGGGGTCAGCTTTCATTTTACTTATCAAGATA
TCATCAATCATCCTGATTCTATTTTGTATGGTTATCATCCTGCTAAAT
AAAAATCAGCTTCTTTAGCAGAACATTAGTTGCGTGTGTATCCCAA
ACATTATCAAGAAGATTATCAAAATCTTGTGCCCAATGACTTGAAACACA
GAGTTTATTTATGATTACTGTAACGAAACACTTTATGAGTGGAAATCAA
AAAGTTTATGATTTTCTTTGTCATTTGGAATAA

SEQ ID NO. 6211
STRAIN JM9130013
ATAGGAGCTTTTCATAGCTTACGAGAAACAATATAAAAGAAAAATTGAGAT
ACAATGTGACGATAAACATCTCCTCACAATAATTGTTCAATTTTTTAAAT
ACAATAGTTTTACTTTTCCCTATATTTCCCAAATATAGAGAAGCGGCGAGCT
ACTTTTAATGAGGATGGTATTAGTTTAACTTCTGATTTTTTAAGCCATAC
ATGTACGATTGAAAGTGAACAACTAAATTTTTAAAGAAGGTAAATCTTAT
CAGCAGTTAAAGCCCTTAAATAAGCCTGCTGAAGTACTGGTAAATGATAAG
AGGAATGCTGCTGGAGACCCATAAGATTACTTTGACTATGTGATGTTGAA
CTGGTCAAATACCAATTTCTGGTTATCGTTTAGTAATGGAAAGATTGTTAG
GCAAAGCACCATCTGAACAGGAGTTAAACAGTAGCTTTAAGCCAGGGGTC
AGCTTTCATTTTAAATATCAAGATATCATCAATCATCCTGATTCTATTTT
TGATGGTTATCATCCTGCTAAATTAATAATCAACTTCTTTAGCAGAAC
ATTTAGTTGCAATGTGTTATCCCAAACATTATCAAGAAGATTATCAAGC
CTTGTGCTAATGACTTGAACACAGAGTTTATTATTTAGATTACTGTAA
CGAAACACTTTATGAGTGAATCAAAAAGTTTATGATTTTCTTTGTCATT
TGGAATAA

PRETTY of: /biotmp/msa185284.2(*) May 13, 2003 07:08 ..

      1                                     50
msa185284.2{271_090} ~~~~~~
msa185284.2{271_H36B} ~~~~~~
msa185284.2{271_JM9130013} ~~~~~~
msa185284.2{271_A909} ~~~~~~
msa185284.2{271_CJB110} ~~~~~~
msa185284.2{271_18RS21} ~~~~~~
msa185284.2{271_2603} atgattttaa aaatttgtcg tgcagcatat agtttacaat ggggaggtgt
msa185284.2{271_M732} ~~~~~~
msa185284.2{271_M781} ~~~~~~
msa185284.2{271_COH1} ~~~~~~
msa185284.2{271_1169NT} ~~~~~~
Consensus *****

      51                                     100
msa185284.2{271_090} ~~~~~~tggt attatcctct aattaaggcg tttgaattgg
msa185284.2{271_H36B} ~~~~~~ttaaaggcg tttgaattgg
msa185284.2{271_JM9130013} ~~~~~~
msa185284.2{271_A909} ~~~~~~TTGctgg attatcctcg aattaaggcg tttgaattgg
msa185284.2{271_CJB110} ~~~~~~TTGctgg attatcctcg aattaaggcg tttgaattgg
msa185284.2{271_18RS21} ~~~~~~TTGctgg attatcctcg aattaaggcg tttgaattgg
msa185284.2{271_2603} ttaccaatta gctTTGctgg attatcctcg aattaaggcg tttgaattgg
msa185284.2{271_M732} ~~~~~~TTGctgg attatcctcg aattaaggcg tttgaattgg
msa185284.2{271_M781} ~~~~~~TTGctgg attatcctcg aattaaggcg tttgaattgg
msa185284.2{271_COH1} ~~~~~~TTGctgg attatcctcg aattaaggcg tttgaattgg
msa185284.2{271_1169NT} ~~~~~~aattaaggcg tttgaattgg
Consensus *****

      101                                    150
msa185284.2{271_090} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_H36B} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_JM9130013} -----ATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_A909} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_CJB110} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_18RS21} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_2603} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_M732} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_M781} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_COH1} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
msa185284.2{271_1169NT} aaaggATAGG AGCTTTCATA GCTTACGAGA AACAAATATAA AAGAAAAAaT
Consensus -----*****

      151                                    200
msa185284.2{271_090} GAGATACAAT GTGACGATAA ACATCTCCTC aCAAAAATTG TTCATTTTTT

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Table 62: Comparative Sequences relating to SAG0690

msa185284.2{271_H36B}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_JM9130013}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_A909}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_CJB110}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_18RS21}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_2603}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_M732}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_M781}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_COH1}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_1169NT}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
Consensus	*****	*****	*****	-*****	*****
msa185284.2{271_090}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_H36B}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_JM9130013}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_A909}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_CJB110}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_18RS21}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_2603}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_M732}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_M781}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_COH1}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_1169NT}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_H36B}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_JM9130013}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_A909}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_CJB110}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_18RS21}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_2603}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_M732}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_M781}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_COH1}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
msa185284.2{271_1169NT}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACCTCTGA	TTTTTTAAGC
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_H36B}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_JM9130013}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_A909}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_CJB110}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_18RS21}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_2603}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_M732}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_M781}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_COH1}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_1169NT}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_H36B}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_JM9130013}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_A909}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_CJB110}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_18RS21}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_2603}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_M732}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_M781}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_COH1}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_1169NT}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_H36B}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_JM9130013}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_A909}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_CJB110}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_18RS21}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_2603}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_M732}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_M781}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_COH1}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_1169NT}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
Consensus	*****	*****	*****	*****	*****

Table 62: Comparative Sequences relating to SAG0690

msa185284.2{271_090}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_H36B}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_JM9130013}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_A909}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_CJB110}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_18RS21}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_2603}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_M732}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_M781}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_COH1}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
msa185284.2{271_1169NT}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAAGATT
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_H36B}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_JM9130013}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_A909}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_CJB110}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_18RS21}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_2603}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_M732}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_M781}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_COH1}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_1169NT}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_H36B}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_JM9130013}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_A909}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_CJB110}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_18RS21}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_2603}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_M732}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_M781}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_COH1}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_1169NT}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_H36B}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_JM9130013}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_A909}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_CJB110}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_18RS21}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_2603}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_M732}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_M781}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_COH1}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_1169NT}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_H36B}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_JM9130013}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_A909}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_CJB110}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_18RS21}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_2603}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_M732}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_M781}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_COH1}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_1169NT}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_H36B}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_JM9130013}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_A909}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_CJB110}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_18RS21}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_2603}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_M732}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_M781}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_COH1}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_1169NT}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
Consensus	*****	*****	*****	*****	*****

Table 62: Comparative Sequences relating to SAG0690

	751	800
msa185284.2{271_090}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_H36B}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_JM9130013}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_A909}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_CJB110}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_18RS21}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_2603}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_M732}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_M781}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_COH1}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_1169NT}	TGTAACGAAA CACTTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
Consensus	*****	*****

	801	816
msa185284.2{271_090}	tCATTTGGAA AATAAA	
msa185284.2{271_H36B}	tCATTTGGAA AATAAA	
msa185284.2{271_JM9130013}	tCATTTGGAA AATAAA	
msa185284.2{271_A909}	tCATTTGGAA AATAAA	
msa185284.2{271_CJB110}	tCATTTGGAA AATAAA	
msa185284.2{271_18RS21}	tCATTTGGAA AATAAA	
msa185284.2{271_2603}	tCATTTGGAA AATAAA	
msa185284.2{271_M732}	nCATTTGGAA AATAAA	
msa185284.2{271_M781}	tCATTTGGAA AATAAA	
msa185284.2{271_COH1}	gCATTTGGAA AATAAA	
msa185284.2{271_1169NT}	tCATTTGGAA AATAAA	
Consensus	*****	*****

## SEQ ID NO. 6212

## STRAIN 2603 frame: 1

MILKICRAAYSLQWGVYQLALLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHL  
AKIVHFLKYNSTFPYIPKYREAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSA  
VKAENKPAEVLVKDKRNAAGDPKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVG  
FKPGVSPHFYQDI INHPDSIFDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPND  
LKHRYVYLDYCNETLYEWNQKVYDFLCHLENK

## SEQ ID NO. 6213

## STRAIN A909 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKIEIQCDDKHLTKIVHFLKYNSTFPYIPKYR  
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD  
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSPHFYQDI INHPDSI  
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRYVYLDYCNETLYEWNQK  
VYDFLCHLENK

## SEQ ID NO. 6214

## STRAIN H36B frame: 3

KAFELERIGAFIAYEKQYKRKIEIQCDDKHLTKIVHFLKYNSTFPYIPKYREAAATFN  
EDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPKDYFDY  
VMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSPHFYQDI INHPDSIFDGYHPA  
KIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRYVYLDYCNETLYEWNQKVYDFLCH  
LENK

## SEQ ID NO. 6215

## STRAIN 18RS21 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLAKIVHFLKYNSTFPYIPKYR  
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD  
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSPHFYQDI INHPDSI  
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRYVYLDYCNETLYEWNQK  
VYDFLCHLENK

## SEQ ID NO. 6216

## STRAIN M732 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLAKIVHFLKYNSTFPYIPKYR  
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD  
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSPHFYQDI INHPDSI  
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRYVYLDYCNETLYEWNQK  
VYDFLCHLENK

## SEQ ID NO. 6217

## STRAIN COH1 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLAKIVHFLKYNSTFPYIPKYR  
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVKDKRNAAGD  
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSPHFYQDI INHPDSI  
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRYVYLDYCNETLYEWNQK  
VYDFLCHLENK

## SEQ ID NO. 6218

## STRAIN M781 frame: 1

Table 62: Comparative Sequences relating to SAG0690

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQDDKHLLAKIVHFLKYNSTFFPYIPKYR  
 EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD  
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFYQDIINHPDSI  
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQK  
 VYDFLCHLENK

SEQ ID NO. 6219

STRAIN CJB110 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKIEIQDDKHLLTKIVHFLKYNSTFFPYIPKYR  
 EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD  
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSI  
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQK  
 VYDFLCHLENK

SEQ ID NO. 6220

STRAIN 1169NT frame: 2

IKAFELERIGAFIAYEKQYKRKTEIQDDKHLLAKIVHFLKYNSTFFPYIPKYREAAATF  
 NEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPKDYFD  
 YVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFYQDIINHPDSIFDGYHP  
 AKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQKVYDFLC  
 HLENK

SEQ ID NO. 6221

STRAIN JM9130013 frame: 1

IGAFIAYEKQYKRKIEIQDDKHLLTKIVHFLKYNSTFFPYIPKYREAAATFNEDGISLT  
 SDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPKDYFDYVMLNWSN  
 TNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSIFDGYHPAKIKNQLS  
 LAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQKVYDFLCHLENK

SEQ ID NO. 6222

STRAIN 090 frame: 3

DYPLIKAFELERIGAFIAYEKQYKRKIEIQDDKHLLTKIVHFLKYNSTFFPYIPKYREA  
 AATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGDPK  
 DYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSIFD  
 GYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQKVY  
 DFLCHLENK

PRETTY of: /biotmp/msa185358.2{\*} May 13, 2003 07:11 ..

	1		50
msa185358.2{271_090}	-----	---dyplika	felerIGAFI
msa185358.2{271_JM9130013}	-----	-----	IGAFI
msa185358.2{271_H36B}	-----	-----	ka
msa185358.2{271_A909}	-----	~LLdyprika	felerIGAFI
msa185358.2{271_CJB110}	-----	~LLdyprika	felerIGAFI
msa185358.2{271_1169NT}	-----	-----	ika
msa185358.2{271_18RS21}	-----	~LLdyprika	felerIGAFI
msa185358.2{271_2603}	-----	~LLdyprika	felerIGAFI
msa185358.2{271_M732}	-----	~LLdyprika	felerIGAFI
msa185358.2{271_M781}	-----	~LLdyprika	felerIGAFI
msa185358.2{271_COH1}	-----	~LLdyprika	felerIGAFI
Consensus	*****	*****	*****
	51		100
msa185358.2{271_090}	EIQDDKHLL	tkIVHFLKYN	SFTFPYIPKY
msa185358.2{271_JM9130013}	EIQDDKHLL	tkIVHFLKYN	SFTFPYIPKY
msa185358.2{271_H36B}	EIQDDKHLL	tkIVHFLKYN	SFTFPYIPKY
msa185358.2{271_A909}	EIQDDKHLL	tkIVHFLKYN	SFTFPYIPKY
msa185358.2{271_CJB110}	EIQDDKHLL	tkIVHFLKYN	SFTFPYIPKY
msa185358.2{271_1169NT}	EIQDDKHLL	akIVHFLKYN	SFTFPYIPKY
msa185358.2{271_18RS21}	EIQDDKHLL	akIVHFLKYN	SFTFPYIPKY
msa185358.2{271_2603}	EIQDDKHLL	akIVHFLKYN	SFTFPYIPKY
msa185358.2{271_M732}	EIQDDKHLL	akIVHFLKYN	SFTFPYIPKY
msa185358.2{271_M781}	EIQDDKHLL	akIVHFLKYN	SFTFPYIPKY
msa185358.2{271_COH1}	EIQDDKHLL	akIVHFLKYN	SFTFPYIPKY
Consensus	*****	*****	*****
	101		150
msa185358.2{271_090}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_JM9130013}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_H36B}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_A909}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_CJB110}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_1169NT}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_18RS21}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_2603}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_M732}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_M781}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV
msa185358.2{271_COH1}	HTCTIETAKL	IFKEGKILSA	VKAFNKPAEV

Table 62: Comparative Sequences relating to SAG0690

Consensus	*****	*****	*****	**-*****	*****
	151				200
msa185358.2{271_090}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF <sub>n</sub>	YQDIINHPDS
msa185358.2{271_JM9130013}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF <sub>n</sub>	YQDIINHPDS
msa185358.2{271_H36B}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF <sub>n</sub>	YQDIINHPDS
msa185358.2{271_A909}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF <sub>n</sub>	YQDIINHPDS
msa185358.2{271_CJB110}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF <sub>n</sub>	YQDIINHPDS
msa185358.2{271_1169NT}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF <sub>t</sub>	YQDIINHPDS
msa185358.2{271_18RS21}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF <sub>t</sub>	YQDIINHPDS
msa185358.2{271_2603}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF <sub>t</sub>	YQDIINHPDS
msa185358.2{271_M732}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF <sub>t</sub>	YQDIINHPDS
msa185358.2{271_M781}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF <sub>t</sub>	YQDIINHPDS
msa185358.2{271_COH1}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF <sub>t</sub>	YQDIINHPDS
Consensus	*****	*****	*****-	*****-	*****
	201				250
msa185358.2{271_090}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_JM9130013}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_H36B}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_A909}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_CJB110}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_1169NT}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQnLVPND	LKHRVYYLDY
msa185358.2{271_18RS21}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_2603}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_M732}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_M781}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_COH1}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
Consensus	*****	*****	*****	*****	*****
	251				272
msa185358.2{271_090}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_JM9130013}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_H36B}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_A909}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_CJB110}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_1169NT}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_18RS21}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_2603}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_M732}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_M781}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_COH1}	CNETLYEWNQ	KVYDFLCHLE	NK		
Consensus	*****	*****	*****		

Table 63: Comparative Sequences relating to SAG1912

## SEQ ID NO. 6301

## STRAIN 2603

ATGAAAAGTCGAAAAAAGATAAATTGGTATTGAGGTTAACAACAACACTATTGGTTTTT  
GGTTTGGGTGGGGTTTGGTTTTATAATTATAAAAAATGATAATGTCCGAACCGACAGTCACT  
AGTGCAATCGGATCAAACGACGACTTTTATTCAAACGATTCTCCAACAGCTATTGAAATT  
TCTAAGACCTATGATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCC  
AGTGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAA  
TATAAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAAGGCAATATGACT  
CAAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTCACTATATGATTATGCT  
GAGTTAGTATCTAGTCAAAGTATGCATCTGTTTGGAAATCAAATACCTCTTCTTATAAG  
GATGCTACTGACGCTCTAACAGGCTCTTATGCGACAGATACTGCTTATGCTAGTAAATTA  
AACCAAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

## SEQ ID NO. 6302

## STRAIN 090

GGGGTTTGGTTTTTATAATTATAA  
AAATGATAATGTCCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA  
CTTTTATTCAAACGATTCTCCAACAGCTATTGAAATTCTAAGACCTAT  
GATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAG  
TGGACAATCAGATTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA  
AAGGAGAATATAAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGAT  
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA  
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGT  
ATGCATCTGTTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCA  
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTA  
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

## SEQ ID NO. 6303

## STRAIN A909

GGGGTTTGGTTTTTATAATTATAA  
AAATGATAATGTCCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA  
CTTTTATTCAAACGATTCTCCAACAGCTATTGAAATTCTAAGACCTAT  
GATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAG  
TGGACAATCAGATTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA  
AAGGAGAATATAAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGAT  
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA  
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGT  
ATGCATCTGCTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCA  
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTA  
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

## SEQ ID NO. 6304

## STRAIN H36B

GGGGTTTGGTTTTTATAATTATAAAAAATGATA  
ATGTCCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATT  
CAAACGATTCTCCAACAGCTATTGAAATTCTAAGACCTATGATTGTGA  
TGGCTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAGTGGACAAT  
CAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAA  
TATAAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAAGG  
CAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTG  
CTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGTATGCTACT  
GCTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGACGCTCTAAC  
AGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAAATTA  
TTGAAACCTACAGTCTAGATGCTTATGATAAA

## SEQ ID NO. 6305

## STRAIN 18RS21

GGGGTTTGGTTTTTATAATTATAAAAAATGATAATG  
TCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAA  
ACGATTCTCCAACAGCTATTGAAATTCTAAGACCTATGATTGTATGC  
GTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAGTGGACAATCAG  
ATTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAAATAT  
AAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAAGGCAA  
TATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTT  
CACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGTATGCTACTGTT  
TGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGACGCTCTAACAGG  
TCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAAATTAATG  
AAACCTACAGTCTAGATGCTTATGATAAA

## SEQ ID NO. 6306

## STRAIN M732

GGGGTTTGGTTTTTATAATTATAA  
AAATGATAATGTCCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA  
CTTTTATTCAAACGATTCTCCAACAGCTATTGAAATTCTAAGACCTAT  
GATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAG  
TGGACAATCAGATTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA  
AAGGAGAATATAAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGAT  
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA  
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGT  
ATGCATCTGTTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCA  
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTA  
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA



Table 63: Comparative Sequences relating to SAG1912

## SEQ ID NO. 6307

## STRAIN COH1

GGGGTTTGGTTTATAATTATAA  
 AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA  
 CTTTTATTCAAACGATTCTCCAACAGCTATTGAAATTTCTAAGACCTAT  
 GATTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGAATCATCCAG  
 TGGACAAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA  
 AAGGAGAATATAAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGAT  
 GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA  
 TTATCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGT  
 ATGCATCTGTTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCA  
 GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTA  
 CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

## SEQ ID NO. 6308

## STRAIN M781

GGGGTTTGGTTTATAATTATAAAATGA  
 TAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTA  
 TTCAAACGATTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTGG  
 TATGCGTCAGTCTTATTAGCACAAAGCTATTTTGAATCATCCAGTGGACA  
 ATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAG  
 AATATAAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAA  
 GGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTC  
 TGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCTAT  
 CTGTTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTA  
 ACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAAT  
 TATTGAAACCTACAGTCTAGATGCTTATGATAAA

## SEQ ID NO. 6309

## STRAIN CJB110

GGGGTTTGGTTTATAATTATAAAATGATAATGT  
 CGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAA  
 CGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTGTATGCG  
 TCAGTCTTATTAGCACAAAGCTATTTTGAATCATCCAGTGGACAATCAGA  
 TTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAATATA  
 AAGGTAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAAGGCAAT  
 ATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTC  
 ACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCTATGCTTT  
 GGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGGT  
 CTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAATATTGA  
 AACCTACAGTCTAGATGCTTATGATAAA

## SEQ ID NO. 6310

## STRAIN 1169NT

GGGGTTTGGTTTATAATTATAAAATGATAATGT  
 CGAACGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAA  
 CGATTTCCCCAACAGCTATTGAAATTTCTAAGACCTATGATTGTATGCG  
 TCAGTCTTATTAGCACAAAGCTATTTTGAATCATCCAGTGGACAATCAGA  
 TTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAATATA  
 AAGGTAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAAGGCAAT  
 ATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTC  
 ACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCTATGCTTT  
 GGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGGT  
 CTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAATATTGA  
 AACCTACAGTCTAGATGCTTATGATAAA

## SEQ ID NO. 6311

## STRAIN JM9130013

TTTGGTTTATAATTATAAAATGATAATGTCGAACCGACAGTCACTAGT  
 GCATCGGATCAAACGACGACTTTTATTCAAACGATTTCCCCAACAGCTAT  
 TGAATTTCTAAGACCTATGATTGTATGCGTCAGTCTTATTAGCACAAAG  
 CTATTTTGAATCATCCAGTGGACAATCAGATTTGTCTAAGGCTCCTAAT  
 TATAACCTCTTTGGCATCAAAGGAGAATATAAAGGTAATCTGTTCAAAT  
 GCCTACTTTAGAAGATGATGGGAAAGGTAATATGACCCAAATCCAAGCTC  
 CTTTTCGCGCCTATCCAAATTATTCTGCTTCACTATATGATTATGCTGAG  
 TTAGTATCTAGTCAAAAGTATGCTATGTTTGGAAATCAAATACCTCTTC  
 TTATAAGGATGCTACTGCAGCTCTAACAGGTCTTTATGCGACAGATACTG  
 CTTATGCTAGTAAATTAACCAAATATTGAAACTACAGTCTAGATGCT  
 TATGATAAA

PRETTY of: /biotmp/msa243324.2{\*} February 11, 2003 05:11 ..

	1				50
msa243324.2{275_A909}	-----	-----	-----	-----	-----
msa243324.2{275_H36B}	-----	-----	-----	-----	-----
msa243324.2{275_090}	-----	-----	-----	-----	-----
msa243324.2{275_18RS21}	-----	-----	-----	-----	-----
msa243324.2{275_2603}	atgaaaaagtc	gaaaaaaaaga	taaatgggta	ttgagggttaa	caacaacact
msa243324.2{275_CJB110}	-----	-----	-----	-----	-----
msa243324.2{275_COH1}	-----	-----	-----	-----	-----
msa243324.2{275_M732}	-----	-----	-----	-----	-----

Table 63: Comparative Sequences relating to SAG1912

msa243324.2{275_M781}	-----	-----	-----	-----	-----
msa243324.2{275_1169NT}	-----	-----	-----	-----	-----
msa243324.2{275_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
msa243324.2{275_A909}	-----	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_H36B}	-----	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_090}	-----	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_18RS21}	-----	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_2603}	attggttttt	gggtttgggtg	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_CJB110}	-----	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_COH1}	-----	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_M732}	-----	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_M781}	-----	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_1169NT}	-----	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_JM9130013}	-----	-----	---TTTGGTT	TTATAATTAT	AAAAATGATA
Consensus	*****	*****	-----	*****	*****
msa243324.2{275_A909}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_H36B}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_090}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_18RS21}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_2603}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_CJB110}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_COH1}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_M732}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_M781}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_1169NT}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_JM9130013}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
Consensus	*****	*****	*****	*****	*****
msa243324.2{275_A909}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_H36B}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_090}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_18RS21}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_2603}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_CJB110}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_COH1}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_M732}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_M781}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_1169NT}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_JM9130013}	CAAACGATTT	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
Consensus	*****	*-*****	*****	*****	*****
msa243324.2{275_A909}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_H36B}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_090}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_18RS21}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_2603}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_CJB110}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_COH1}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_M732}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_M781}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_1169NT}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_JM9130013}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
Consensus	*****	*****	*****	*****	*****
msa243324.2{275_A909}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_H36B}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_090}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_18RS21}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_2603}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_CJB110}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_COH1}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_M732}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_M781}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_1169NT}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_JM9130013}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
Consensus	*****	*****	*****	*****	*****
msa243324.2{275_A909}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_H36B}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_090}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_18RS21}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_2603}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_CJB110}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_COH1}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG

Table 63: Comparative Sequences relating to SAG1912

msa243324.2{275_M732}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_M781}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_1169NT}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_JM9130013}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
Consensus	*****	*****_**	*****	*****	*****
351					
msa243324.2{275_A909}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_H36B}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_090}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_18RS21}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_2603}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_CJB110}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_COH1}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_M732}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_M781}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_1169NT}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_JM9130013}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
Consensus	*****	*****	*****	*****	*****
401					
msa243324.2{275_A909}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_H36B}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_090}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_18RS21}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_2603}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_CJB110}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_COH1}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_M732}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_M781}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_1169NT}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_JM9130013}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
Consensus	*****	*****	*****	*****	*****
451					
msa243324.2{275_A909}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_H36B}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_090}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_18RS21}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_2603}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_CJB110}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_COH1}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_M732}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_M781}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_1169NT}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_JM9130013}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
Consensus	**_*****	*****_**	*****	*****	*****
501					
msa243324.2{275_A909}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_H36B}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_090}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_18RS21}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_2603}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_CJB110}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_COH1}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_M732}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_M781}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_1169NT}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_JM9130013}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
Consensus	*****	*****	*****	*****	*****
551					
msa243324.2{275_A909}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_H36B}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_090}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_18RS21}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_2603}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_CJB110}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_COH1}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_M732}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_M781}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_1169NT}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
msa243324.2{275_JM9130013}	TTGAAAcCTA	CAGTCTAGAT	GCCTATGATA	AA	
Consensus	*****_***	*****	*****	*****	*****
582					

SEQ ID NO. 6312

STRAIN 2603 frame: 1

MKSRKDKLVRLRLTTTLLVFLGGVWFYNYKNDNVEPTVTSASDQTTTFIQTFISPTAIEI  
 SKTYDLIASVLLAQAILSSSGQSDLSKAPNYNLFQIKGEYKGSVQMPTLEDDGKGNMT  
 QIQAPFRAYPNYSASLYDYAELVSSQKYASVWKSNTSSYKDATAALTLGLYATDTAYASKL  
 NQIETYSLDAYDK

Table 63: Comparative Sequences relating to SAG1912

SEQ ID NO. 6313  
STRAIN 090 frame: 1  
GVWFFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ  
SDLSKAPNYNLFGIKGEYKGKSVQMPLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV  
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6314  
STRAIN A909 frame: 1  
GVWFFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ  
SDLSKAPNYNLFGIKGEYKGKSVQMPLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV  
SSQKYASAWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6315  
STRAIN H36B frame: 1  
GVWFFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ  
SDLSKAPNYNLFGIKGEYKGKSVQMPLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV  
SSQKYASAWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6316  
STRAIN 18RS21 frame: 1  
GVWFFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ  
SDLSKAPNYNLFGIKGEYKGKSVQMPLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV  
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6317  
STRAIN M732 frame: 1  
GVWFFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ  
SDLSKAPNYNLFGIKGEYKGKSVQMPLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV  
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6318  
STRAIN M781 frame: 1  
GVWFFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ  
SDLSKAPNYNLFGIKGEYKGKSVQMPLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV  
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6319  
STRAIN CJB110 frame: 1  
GVWFFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ  
SDLSKAPNYNLFGIKGEYKGKSVQMPLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV  
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6320  
STRAIN 1169NT frame: 1  
GVWFFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ  
SDLSKAPNYNLFGIKGEYKGKSVQMPLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV  
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6321  
STRAIN JM9130013 frame: 3  
WFYNYKNDNVEPTVTSASDQTTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQSD  
LSKAPNYNLFGIKGEYKGKSVQMPLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELVSS  
QKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIENYSLDAYDK

PRETTY of: /biotmp/msa243476.2{\*} February 11, 2003 05:17 ..

	1					50
msa243476.2{275_090}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTTFI	
msa243476.2{275_18RS21}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTTFI	
msa243476.2{275_2603}	mksrkkdklv	lrltttllvf	glggvWFFYNY	KNDNVEpTVT	SASDQTTTTFI	
msa243476.2{275_CJB110}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTTFI	
msa243476.2{275_M732}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTTFI	
msa243476.2{275_M781}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTTFI	
msa243476.2{275_A909}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTTFI	
msa243476.2{275_H36B}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTTFI	
msa243476.2{275_JM9130013}	-----	-----	-----WFYNY	KNDNVEpTVT	SASDQTTTTFI	
msa243476.2{275_1169NT}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTTFI	
Consensus	*****	*****	***--*****	*****	*****	*****

  

	51					100
msa243476.2{275_090}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE	
msa243476.2{275_18RS21}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE	
msa243476.2{275_2603}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE	
msa243476.2{275_CJB110}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE	
msa243476.2{275_M732}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE	
msa243476.2{275_M781}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE	
msa243476.2{275_A909}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE	
msa243476.2{275_H36B}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE	
msa243476.2{275_JM9130013}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE	
msa243476.2{275_1169NT}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE	
Consensus	*****	*****	*****	*****	*****	*****

Table 63: Comparative Sequences relating to SAG1912

	101				150
msa243476.2{275_090}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_18RS21}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_2603}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_CJB110}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_M732}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_M781}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_A909}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_H36B}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_JM9130013}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_1169NT}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
Consensus	*****	*****	*****	*****	*****
	151				194
msa243476.2{275_090}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_18RS21}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_2603}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_CJB110}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_M732}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_M781}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_A909}	awKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_H36B}	awKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_JM9130013}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_1169NT}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
Consensus	-*****	*****	*****	*****	****

Table 64: Comparative Sequences relating to SAG 0827

## SEQ ID NO. 6401

## STRAIN 2603

ATGAACAAGTCTAAGAAAATCGAAAATTATCAATTATTATTACTACAAGCGCAAGCTCTA  
TTCTCAGATGAAACAAATGCTCTTGCCAACTTATCAAATGCTTCAGCTATGCTAAATGCT  
ATGCTTCCAAATCTGTATTTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAAATCTT  
GGCCCTTTCCAGGGTGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGT  
GAATCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATGCTAACTAT  
ATCTCCTGTGATTTCAAAGCTATGAGTGAAATCGTAGTACCTATGTTTAAAAATGGCAAA  
CTTCTAGGAGTTCTAGATTAGATTCTTCTTTAGTAGCAGATTATGATGAGATTGATCAA  
GAATACTTAGAAAAATTTGTAGGTATTCTAGTAGAACATACGATTGGAATTTGGATATG  
TTTGGAGTTGAAAAG

## SEQ ID NO. 6402

## STRAIN 090

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA  
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTAC  
AGGCTTTTATTTATTTGATGGAAAGGAGTTAATTCTTGCCCTTTCCAGG  
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGAA  
TCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC  
TAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCTA  
TGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTAGATTCTTCTTTA  
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG  
TATTCTAGTAGAACATACGATTGGAATTTGGATA

## SEQ ID NO. 6403

## STRAIN A909

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAA  
CTTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTAT  
TTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGCCCTTTTC  
CAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGG  
TGAATCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGC  
ATGCTAATATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTA  
CTATGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTAGATTCTTCT  
TTTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTG  
TAGGTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTT  
GAAAAG

## SEQ ID NO. 6404

## STRAIN H36B

CTCTATTCTCAGATGAAACAAATGCTCTTGCC  
CAACTTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGT  
TATTTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGCCCTT  
TTCCAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGT  
TGGTGAATCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAA  
AGCATGCTAATATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTA  
GTACCTATGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTAGATTCT  
TTCTTTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAAT  
TTGTAGGTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAG  
TTGAAAAG

## SEQ ID NO. 6405

## STRAIN 18RS21

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT  
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTA  
CAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGCCCTTTCCAG  
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA  
ATCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATG  
CTAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCT  
ATGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTAGATTCTTCTTT  
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG  
GTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAA  
AAG

## SEQ ID NO. 6406

## STRAIN M732

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT  
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTA  
CAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCTTGCCCTTTTCAG  
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA  
ATCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATG  
CTAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCC  
ATGTTTAAAAATGGCAAACTTCTAGGAGTTCTAGATTAGATTCTTCTTT  
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG  
GTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAA  
AAG

## SEQ ID NO. 6407

## STRAIN COH1

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT  
TTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTT  
TACAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCTTGCCCTTTTC  
AGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGT

Table 64: Comparative Sequences relating to SAG 0827

GAATCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCA  
TGCTAACTATATCTCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTAC  
CCATGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCCTCT  
TTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGT  
AGGTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTGGAGTTG  
AAAAG

SEQ ID NO. 6408

STRAIN M781

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT  
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCGTATTTA  
CAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCCTGGCCCTTTCCAG  
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA  
ATCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATG  
CTAACTATATCTCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCC  
ATGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCCTCTT  
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG  
GTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAA  
AAG

SEQ ID NO. 6409

STRAIN CJB110

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA  
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCGTATTTC  
AGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCCTGGCCCTTTCCAGG  
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA  
TCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC  
TAACCTATATCTCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCTA  
TGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCCTCTTA  
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG  
TATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAA  
AG

SEQ ID NO. 6410

STRAIN 1169NT

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA  
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCGTATTTC  
AGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCCTGGCCCTTTCCAGG  
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA  
TCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC  
TAACCTATATCTCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCCA  
TGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCCTCTTA  
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG  
TATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAA  
AG

SEQ ID NO. 6411

STRAIN JM9130013

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA  
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATTCGTATTTC  
AGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCCTGGCCCTTTCCAGG  
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA  
TCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATGC  
TAACCTATATCTCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCTA  
TGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCCTCTTA  
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG  
TATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAA  
AG

PRETTY of: /biotmp/msa236796.2{\*} February 11, 2003 02:42 ..

	1				50
msa236796.2{282_COH1}	-----	-----	-----	-----	-----
msa236796.2{282_M732}	-----	-----	-----	-----	-----
msa236796.2{282_M781}	-----	-----	-----	-----	-----
msa236796.2{282_090}	-----	-----	-----	-----	-----
msa236796.2{282_CJB110}	-----	-----	-----	-----	-----
msa236796.2{282_18RS21}	-----	-----	-----	-----	-----
msa236796.2{282_2603}	atgaacaagt	ctaagaaaat	cgaaaattat	caattattat	tactacaagc
msa236796.2{282_A909}	-----	-----	-----	-----	-----
msa236796.2{282_H36B}	-----	-----	-----	-----	-----
msa236796.2{282_JM9130013}	-----	-----	-----	-----	-----
msa236796.2{282_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****

  

	51				100
msa236796.2{282_COH1}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_M732}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_M781}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_090}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_CJB110}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_18RS21}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_2603}	gcaagCTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG

Table 64: Comparative Sequences relating to SAG 0827

msa236796.2{282_A909}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG		
msa236796.2{282_H36B}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG		
msa236796.2{282_JM9130013}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG		
msa236796.2{282_1169NT}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG		
Consensus	*****	*****	*****	*****	*****		
msa236796.2{282_COH1}	101	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT	150
msa236796.2{282_M732}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_M781}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_090}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_CJB110}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_18RS21}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_2603}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_A909}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_H36B}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_JM9130013}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_1169NT}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
Consensus	*****	*****	*****	*****	*****		
msa236796.2{282_COH1}	151	TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT	200
msa236796.2{282_M732}	TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
msa236796.2{282_M781}	TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
msa236796.2{282_090}	TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
msa236796.2{282_CJB110}	TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
msa236796.2{282_18RS21}	TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
msa236796.2{282_2603}	TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
msa236796.2{282_A909}	TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
msa236796.2{282_H36B}	TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
msa236796.2{282_JM9130013}	TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
msa236796.2{282_1169NT}	TATTTATTTG	ATGGAgAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
Consensus	*****	*****-_*	*****	*****-_*	*****		
msa236796.2{282_COH1}	201	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC	250
msa236796.2{282_M732}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_M781}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_090}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_CJB110}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_18RS21}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_2603}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_A909}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_H36B}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_JM9130013}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_1169NT}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
Consensus	*****	*****	*****	*****	*****		
msa236796.2{282_COH1}	251	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT	300
msa236796.2{282_M732}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_M781}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_090}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_CJB110}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_18RS21}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_2603}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_A909}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_H36B}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_JM9130013}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_1169NT}	AAACTGCTAA	GACGCTGATc	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
Consensus	*****	*****	*****	*****	*****		
msa236796.2{282_COH1}	301	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA	350
msa236796.2{282_M732}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_M781}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_090}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_CJB110}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_18RS21}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_2603}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_A909}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_H36B}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_JM9130013}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_1169NT}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
Consensus	*****	*****	*****	*****	*****	*-*****	
msa236796.2{282_COH1}	351	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG	400
msa236796.2{282_M732}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG		
msa236796.2{282_M781}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG		
msa236796.2{282_090}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG		
msa236796.2{282_CJB110}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG		
msa236796.2{282_18RS21}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG		



Table 64: Comparative Sequences relating to SAG 0827

msa236796.2{282_2603}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_A909}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_H36B}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_JM9130013}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_1169NT}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
Consensus	*****	*****	*****	*****	*****
401					
msa236796.2{282_COH1}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_M732}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_M781}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_090}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_CJB110}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_18RS21}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_2603}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_A909}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_H36B}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_JM9130013}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_1169NT}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
Consensus	*****	*****	*****	*****	*****
451					
msa236796.2{282_COH1}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_M732}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_M781}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_090}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_CJB110}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_18RS21}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_2603}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_A909}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_H36B}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_JM9130013}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_1169NT}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
Consensus	*****	*****	*****	*****	*****
495					
msa236796.2{282_COH1}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_M732}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_M781}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_090}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_CJB110}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_18RS21}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_2603}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_A909}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_H36B}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_JM9130013}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_1169NT}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
Consensus	*****	*****	*****	*****	*****

## SEQ ID NO. 6412

STRAIN 2603 frame: 1

MNKSCKIENYQLLLQAQALFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELIL  
GPFQGGVSCVHITLKGKVCGESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGK  
LLGVLDLSSSLVADYDEIDQEYLEKFVGILVEHTIWNLDMPGVEK

## SEQ ID NO. 6413

STRAIN 090 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC  
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID  
QEYLEKFVGILVEHTIWNLD

## SEQ ID NO. 6414

STRAIN A909 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC  
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID  
QEYLEKFVGILVEHTIWNLDMPGVEK

## SEQ ID NO. 6415

STRAIN H36B frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC  
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID  
QEYLEKFVGILVEHTIWNLDMPGVEK

## SEQ ID NO. 6416

STRAIN 18RS21 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC  
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID  
QEYLEKFVGILVEHTIWNLDMPGVEK

## SEQ ID NO. 6417

STRAIN M732 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC  
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID  
QEYLEKFVGILVEHTIWNLDMPGVEK

## SEQ ID NO. 6418

STRAIN COH1 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC  
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID  
QEYLEKFVGILVEHTIWNLDMPGVEK

## SEQ ID NO. 6419

STRAIN M781 frame: 3

LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC  
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID

Table 64: Comparative Sequences relating to SAG 0827

QEYLEKFVGIIVHEHTIWNLD MFGEK

SEQ ID NO. 6420

STRAIN M781 frame: 3

LFSDETNALANLSNASAMLNAMLPSVFTGFYLFDFGEEILILGPFQGGVSCVHITLGKGVG  
 GESAQTAKTLIVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSLVADYDEID  
 QEYLEKFVGIIVHEHTIWNLD MFGEK

SEQ ID NO. 6421

STRAIN CJB110 frame: 3

LFSDETNALANLSNASAMLNAMLPSVFTGFYLFDFGKEELILGPFQGGVSCVHITLGKGVG  
 GESAQTAKTLIVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSLVADYDEID  
 QEYLEKFVGIIVHEHTIWNLD MFGEK

SEQ ID NO. 6422

STRAIN 1169NT frame: 3

LFSDETNALANLSNASAMLNAMLPSVFTGFYLFDFGEEILILGPFQGGVSCVHITLGKGVG  
 GESAQTAKTLIVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSLVADYDEID  
 QEYLEKFVGIIVHEHTIWNLD MFGEK

SEQ ID NO. 6423

STRAIN JM9130013 frame: 3

LFSDETNALANLSNASAMLNAMLPSVFTGFYLFDFGEEILILGPFQGGVSCVHITLGKGVG  
 GESAQTAKTLIVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSLVADYDEID  
 QEYLEKFVGIIVHEHTIWNLD MFGEK

PRETTY of: /biotmp/msa237960.2{\*} February 11, 2003 02:46 ..

	1		50
msa237960.2{282_1169NT}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_18RS21}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_2603}	mnkskkieny qlllllqaqaL	FSDETNALAN	LSNASAMLNA
msa237960.2{282_A909}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_COH1}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_H36B}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_JM9130013}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_M732}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_M781}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_090}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_CJB110}	-----L	FSDETNALAN	LSNASAMLNA
Consensus	*****	*****	*****
	51		100
msa237960.2{282_1169NT}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_18RS21}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_2603}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_A909}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_COH1}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_H36B}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_JM9130013}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_M732}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_M781}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_090}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_CJB110}	YLFDFGELIL	GPFQGGVSCV	HITLGKGVCG
Consensus	*****	*****	*****
	101		150
msa237960.2{282_1169NT}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_18RS21}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_2603}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_A909}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_COH1}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_H36B}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_JM9130013}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_M732}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_M781}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_090}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_CJB110}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
Consensus	*****	*****	*****
	151		165
msa237960.2{282_1169NT}	VEHTIWNLDm	fgvek	
msa237960.2{282_18RS21}	VEHTIWNLDm	fgvek	
msa237960.2{282_2603}	VEHTIWNLDm	fgvek	
msa237960.2{282_A909}	VEHTIWNLDm	fgvek	
msa237960.2{282_COH1}	VEHTIWNLDm	fgvek	
msa237960.2{282_H36B}	VEHTIWNLDm	fgvek	
msa237960.2{282_JM9130013}	VEHTIWNLDm	fgvek	
msa237960.2{282_M732}	VEHTIWNLDm	fgvek	
msa237960.2{282_M781}	VEHTIWNLDm	fgvek	
msa237960.2{282_090}	VEHTIWNLDm	fgvek	
msa237960.2{282_CJB110}	VEHTIWNLDm	fgvek	
Consensus	*****	-----	

Table 65: Comparative Sequences relating to SAG0231

## SEQ ID NO. 6501

## STRAIN 2603

ATGAAAAAGAGTACCCAAATAATACTACTAATAGTTGCA  
 TTATTCTACTCTGTTTTAGCGGAGGATTTTATATGAAAGAACCAAGAAAGAAAGAA  
 CTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATTGAAAAATTCCTATGAG  
 AATATAGAAGAAATAAAATCACACATCCTGTTTCAACTGAAATTCCTGGAGATTGGCAT  
 TGTACTGTAAAGATTTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAAT  
 TTGGAATCGAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTTTTGAT  
 TCAAGAAATTGGTAAACAAAAAAACTATAAAAAATTATTTTTTCAGATGGTCAGGAGAAG  
 ATACAA

## SEQ ID NO. 6502

## STRAIN 090

GGAGGATTTTATATGAAAGAACA  
 ACAAGAAAGAAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAG  
 TCAAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATC  
 CATCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGAT  
 TTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGG  
 AATCGAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTT  
 TTTGATTCAAGAAATTGGTAAACAAAAAACTATAAAAAATTATTTTTTC  
 AGATGGTCAGGAGAAGATaCAA

## SEQ ID NO. 6503

## STRAIN A909

GGAGGATTTTATATGAAAGAACAACA  
 AGAAAGAAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAA  
 AGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATC  
 CTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTCA  
 TTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATC  
 GAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTTTTG  
 ATTCAGAAATTGGTAAACAAAAAACTATAAAAAATTATTTTTTCAGAT  
 GGTCAGGAGAAGATaCAA

## SEQ ID NO. 6504

## STRAIN H36B

GGAGGATTTTATATGAAAGAACA  
 ACAAGAAAGAAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAG  
 TCAAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATC  
 CATCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGAT  
 TTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGG  
 AATCGAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTT  
 TTTGATTCAAGAAATTGGTAAACAAAAAACTATAAAAAATTATTTTTTC  
 AGATGGTCAGGAGAAGATaCAA

## SEQ ID NO. 6505

## STRAIN 18RS21

GGAGGATTTTATATGAAAGAACAAC  
 AAAGAAAGAAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCT  
 AAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATC  
 TCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATT  
 CATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAA  
 TCGAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTTT  
 TGATTCAAGAAATTGGTAAACAAAAAACTATAAAAAATTATTTTTTCAG  
 ATGGTCAGGAGAAGATaCAA

## SEQ ID NO. 6506

## STRAIN M781

GGAGGATTTTATATGAAAGAACAACAAGAAAA  
 GAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATT  
 GAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATCCTGTTT  
 CAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCATTTAAT  
 GATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATCGAAAAA  
 AAATTATAGCGGAAATTTAATGAAAAAAATATGAATTTTTTTGATTCAAG  
 GAATTGGTAAACAAAAAACTATAAAAAATTATTTTTTCAGATGGTCAG  
 GAGAAGATACAA

## SEQ ID NO. 6507

## STRAIN CJB110

GGAGGATTTTATATGAAAGAACAACAAGAAAGAA  
 CTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATTGAAAAA  
 TTCCTATGAGAATATAGAAGAAATAAAATCACACATCCTGTTTCAACTG  
 AAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCATTTAATGATAAA  
 AATCTATTGTTTATAATATTACACATAATTTGGAATCGAAAAAAATTA  
 TAGCGGAAATTTAATGAAAAAAATATGAATTTTTTTGATTCAAGAAATTG  
 GTAAAACAAAAAACTATAAAAAATTATTTTTTCAGATGGTCAGGAGAAG  
 ATACAA

## SEQ ID NO. 6508

## STRAIN 1169NT

GGAGGATTTTATATGAAAGAACAACAAG  
 AAAAGAAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAG  
 CATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATCCT

Table 65: Comparative Sequences relating to SAG0231

GTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTTCATT  
 TAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATCGA  
 AAAAAAATTATAGTGGAAAATTTAATGAAAAAATATGAATTTTTTGGAT  
 TCAAGAAATGGTAAACAAAAAACTATAAAAAATTATTTTTTCAGATGG  
 TCAGGAGAAGATACAA

SEQ ID NO. 6509

STRAIN JM9130013

GGAGGATTTTATATGAAAGAACAAC

AAAGAAAAGAAAGAACTAAACCGGAATCGAGAATATGAAGTTAGTCTAGTC

AAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAATCACACA

TCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTT

CATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAA

TCGAAAAAATTTATAGCGGAAAATTTAATGAAAAAATATGAATTTTTT

TGATTCAAGAAATGGTAAACAAAAAACTATAAAAAATTATTTTTTCAG

AtGGtCAGGAGAAGATACAA

PRETTY of: /biotmp/msa75400.2{\*} March 10, 2003 09:56 ..

	1				50
msa75400.2{286_090}	-----	-----	-----	-----	-----
msa75400.2{286_CJB110}	-----	-----	-----	-----	-----
msa75400.2{286_18RS21}	-----	-----	-----	-----	-----
msa75400.2{286_2603}	atgaaaaaga	gtacccaaat	aataactacta	atagttgcat	tattcatact
msa75400.2{286_A909}	-----	-----	-----	-----	-----
msa75400.2{286_H36B}	-----	-----	-----	-----	-----
msa75400.2{286_JM9130013}	-----	-----	-----	-----	-----
msa75400.2{286_M781}	-----	-----	-----	-----	-----
msa75400.2{286_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa75400.2{286_090}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_CJB110}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_18RS21}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_2603}	tggtttttagc	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_A909}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_H36B}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_JM9130013}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_M781}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_1169NT}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
Consensus	*****	*****	*****	*****	*****
	101				150
msa75400.2{286_090}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_CJB110}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_18RS21}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_2603}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_A909}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_H36B}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_JM9130013}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_M781}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_1169NT}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
Consensus	*****	*****	*****	*****	*****
	151				200
msa75400.2{286_090}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_CJB110}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_18RS21}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_2603}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_A909}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_H36B}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_JM9130013}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_M781}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_1169NT}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
Consensus	*****	*****	*****	*****	*****
	201				250
msa75400.2{286_090}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_CJB110}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_18RS21}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_2603}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_A909}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_H36B}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_JM9130013}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_M781}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_1169NT}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
Consensus	*****	*****	*****	*****	*****
	251				300
msa75400.2{286_090}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_CJB110}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_18RS21}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT

Table 65: Comparative Sequences relating to SAG0231

```

msa75400.2{286_2603} AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
msa75400.2{286_A909} AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
msa75400.2{286_H36B} AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
msa75400.2{286_JM9130013} AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
msa75400.2{286_M781} AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
msa75400.2{286_1169NT} AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
Consensus *****

301 350
msa75400.2{286_090} AGcGGAAAT TTAATGAAAA AAATATGAAT TTTTGTGATT CAAGAATTGG
msa75400.2{286_CJB110} AGcGGAAAT TTAATGAAAA AAATATGAAT TTTTGTGATT CAAGAATTGG
msa75400.2{286_18RS21} AGcGGAAAT TTAATGAAAA AAATATGAAT TTTTGTGATT CAAGAATTGG
msa75400.2{286_2603} AGcGGAAAT TTAATGAAAA AAATATGAAT TTTTGTGATT CAAGAATTGG
msa75400.2{286_A909} AGcGGAAAT TTAATGAAAA AAATATGAAT TTTTGTGATT CAAGAATTGG
msa75400.2{286_H36B} AGcGGAAAT TTAATGAAAA AAATATGAAT TTTTGTGATT CAAGAATTGG
msa75400.2{286_JM9130013} AGcGGAAAT TTAATGAAAA AAATATGAAT TTTTGTGATT CAAGAATTGG
msa75400.2{286_M781} AGcGGAAAT TTAATGAAAA AAATATGAAT TTTTGTGATT CAAGAATTGG
msa75400.2{286_1169NT} AGcGGAAAT TTAATGAAAA AAATATGAAT TTTTGTGATT CAAGAATTGG
Consensus **-----* *****

351 400
msa75400.2{286_090} TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
msa75400.2{286_CJB110} TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
msa75400.2{286_18RS21} TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
msa75400.2{286_2603} TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
msa75400.2{286_A909} TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
msa75400.2{286_H36B} TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
msa75400.2{286_JM9130013} TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
msa75400.2{286_M781} TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
msa75400.2{286_1169NT} TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
Consensus *****

401
msa75400.2{286_090} TACAA
msa75400.2{286_CJB110} TACAA
msa75400.2{286_18RS21} TACAA
msa75400.2{286_2603} TACAA
msa75400.2{286_A909} TACAA
msa75400.2{286_H36B} TACAA
msa75400.2{286_JM9130013} TACAA
msa75400.2{286_M781} TACAA
msa75400.2{286_1169NT} TACAA
Consensus *****

SEQ ID NO. 6510
STRAIN 2603 frame: 1
MKKSTQIILLIVLFILVFSGGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKI
THPVSTEIPGDWHCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTK
KTIKIIIFSDGQEKIQ

SEQ ID NO. 6511
STRAIN 090
GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGD
WHCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQ
EKIQ

SEQ ID NO. 6512
STRAIN A909
GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWH
CTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQEK
IQ

SEQ ID NO. 6513
STRAIN H36B
GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGD
WHCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQ
EKIQ

SEQ ID NO. 6514
STRAIN 18RS21
GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDW
HCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQEK
KIQ

SEQ ID NO. 6515
STRAIN CJB110
GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVK
ISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQEKIQ

SEQ ID NO. 6516
STRAIN JM9130013
GGFYMKQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDW

```

Table 65: Comparative Sequences relating to SAG0231

HCTVKISFNDKKSIVYNITHNLESKKNYSGKFNEKNMNFDSRIGTKTKTIKIIFSDGQE  
KIQ

SEQ ID NO. 6517

STRAIN 1169NT frame: 1

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVKISF  
NDKKSIVYNITHNLESKKNYSGKFNEKNMNFDSRIGTKTKTIKIIFSDGQEKIQ

SEQ ID NO. 6518

STRAIN M781 frame: 1

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVKISF  
NDKKSIVYNITHNLESKKNYSGKFNEKNMNFDSRIGTKTKTIKIIFSDGQEKIQ

PRETTY of: /biotmp/msa75376.2{\*} March 10, 2003 10:01 ..

	1				50
msa75376.2{286_090}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN	
msa75376.2{286_1169NT}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN	
msa75376.2{286_18RS21}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN	
msa75376.2{286_2603}	mkkstqiill	ivalfilvfs	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN
msa75376.2{286_A909}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN	
msa75376.2{286_CJB110}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN	
msa75376.2{286_H36B}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN	
msa75376.2{286_JM9130013}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN	
msa75376.2{286_M781}	-----	GGFYMKEQQR	KEELKRNREY	EVSLVKALKN	
Consensus	*****	*****	*****	*****	*****

  

	51				100
msa75376.2{286_090}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI	THNLESKKNY
msa75376.2{286_1169NT}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI	THNLESKKNY
msa75376.2{286_18RS21}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI	THNLESKKNY
msa75376.2{286_2603}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI	THNLESKKNY
msa75376.2{286_A909}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI	THNLESKKNY
msa75376.2{286_CJB110}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI	THNLESKKNY
msa75376.2{286_H36B}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI	THNLESKKNY
msa75376.2{286_JM9130013}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI	THNLESKKNY
msa75376.2{286_M781}	SYENIEEIKI	THPVSTEIPG	DWHCTVKISF	NDKKSIVYNI	THNLESKKNY
Consensus	*****	*****	*****	*****	*****

  

	101				135
msa75376.2{286_090}	SGnFNEKNMN	FFDSRIGGTK	TKIKIIFSDG	QEKIQ	
msa75376.2{286_1169NT}	SGkFNEKNMN	FFDSRIGGTK	TKIKIIFSDG	QEKIQ	
msa75376.2{286_18RS21}	SGkFNEKNMN	FFDSRIGGTK	TKIKIIFSDG	QEKIQ	
msa75376.2{286_2603}	SGkFNEKNMN	FFDSRIGGTK	TKIKIIFSDG	QEKIQ	
msa75376.2{286_A909}	SGkFNEKNMN	FFDSRIGGTK	TKIKIIFSDG	QEKIQ	
msa75376.2{286_CJB110}	SGnFNEKNMN	FFDSRIGGTK	TKIKIIFSDG	QEKIQ	
msa75376.2{286_H36B}	SGkFNEKNMN	FFDSRIGGTK	TKIKIIFSDG	QEKIQ	
msa75376.2{286_JM9130013}	SGkFNEKNMN	FFDSRIGGTK	TKIKIIFSDG	QEKIQ	
msa75376.2{286_M781}	SGkFNEKNMN	FFDSRIGGTK	TKIKIIFSDG	QEKIQ	
Consensus	**~*****	*****	*****	*****	*****

Table 66: Comparative Sequences relating to SAG 0754

## SEQ ID NO. 6601

## STRAIN 2603

TTGACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAATGAAGGAGAGGGAAGTATG  
GAAATACGTATTGCAGGTGGTAGTGGTTTTTTAGGAAAGCAGATAATAAAGCAGCGCTT  
ACAAAAGGGCATAAAGTGGCTTACTTATCAAGACATGAAGGTAAAGGTGATATATTAAAG  
GATCCTAGATTAACTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAA  
GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATCAACTAGAT  
GAGCTTAACTTTAAAGCAACCCAAAAGCAGTAGCACTCTGTACAAAATCAAAATACCA  
AAGTTAGTTTATATTTAGCCCAACAGCGGCTATTAGCTTACATTAAAAGTAAAAGGAAG  
GCAGAGCAGATAATCAAAGCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATG  
TATGGTGAAGAGCGACCTCTCTCGATTTCAGCAAGCTGATATAAGTTATTTAGTCAT  
TTGCCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACCTAAGGTTGTAGTAGGGCA  
GAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAATCCTTTCTATTGAAGAA  
TTAAATAATAAA

## SEQ ID NO. 6602

## STRAIN 090

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAAT  
GAAGGAGAGGGAACCTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTT  
AGGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTT  
ACTTATCAAGACATGAAGGTAAAGGTGATATATTAAAGGATCCTAGATTAA  
ACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGA  
CAGAACCTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATC  
AACTAGATGAGCTTAACTTTAAAGCAACCCAAAAGCAGTAGCACTCTGT  
CACAAAATCAAATACCAAGTTAGTTTATATTTAGCCCAACAGCGGCTA  
TTAGCTTACATTAAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGCAA  
GCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAG  
CGACCTCTCTCGATTTCAGCAAGCTGATATAAGTTATTTAGTCATTT  
GCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACCTAAGGTTGTGA  
TAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAA  
ATCCTTTCTATTGAAGAATTAATAATAAA

## SEQ ID NO. 6603

## STRAIN A909

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAATG  
AAGGAGAGGGAACCTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTTA  
GGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTTAA  
CTTATCAAGACATGAAGGTAAAGGTGATATATTAAAGGATCCTAGATTAA  
CCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGAC  
AGAACCTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATCA  
ACTAGATGAGCTTAACTTTAAAGCAACCCAAAAGCAGTAGCACTCTGTCT  
ACAAAATCAAATACCAAGTTAGTTTATATTTAGCCCAACAGCGGCTAT  
TCAGCTTACATTAAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGCAAG  
CGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAGC  
GACCTCTCTCGATTTCAGCAAGCTGATATAAGTTATTTAGTCATTTG  
CCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACCTAAGGTTGTGAT  
AGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAA  
TCCTTTCTATTGAAGAATTAATAATAAA

## SEQ ID NO. 6604

## STRAIN H36B

TATAAAAATTTCTATACTAAATTTACAAAATGAAGGAGAGGGAAGTATGG  
AAATACGTATTGCAGGTGGTAGTGGTTTTTTAGGAAAGCAGATAATAAAA  
GCAGCGCTTACAAAAGGGCATAAAGTGGCTTACTTATCAAGACATGAAGG  
TAAAGGTGATATATTAAAGGATCCTAGATTAACTTACATTAGGGGAGATA  
TTACAGAAGCTGATAAGATTCAATTTAGAAGACAGAACCTTTTGATATATTA  
ATTGACTGTATTGGAGCGATTAAAGCCCAATCAACTAGATGAGCTTAACGT  
TAAAGCAACCCAAAAGCAGTAGCACTCTGTACAAAATCAAATACCAA  
AGTTAGTTTATATTTAGCCCAACAGCGGCTATTAGCTTACATTAAAAGT  
AAAAGGAAGGCAGAGCAGATAATCAAAGCAAGCGGTCTGGATTATCTTTT  
TGTAAGACCAGGTTTGATGTATGGTGAAGAGCGACCTCTCTCGATTTC  
AAGCCAAAGTGTATAAAGTTATTTAGTCATTTGCCCTTTCTTAGGTATTGTT  
GTACAAAAGGTCTTTCCAACCTAAGGTTGTAGTAGTGGCAGAAGCAATCGT  
TACTACGCTTAGGAAAAAACCAACCCAAAAATCCTTTCTATTGAAGAAT  
TAAATAATAAA

## SEQ ID NO. 6605

## STRAIN 18RS21

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAAT  
GAAGGAGAGGGAACCTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTT  
AGGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTT  
ACTTATCAAGACATGAAGGTAAAGGTGATATATTAAAGGATCCTAGATTAA  
ACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGA  
CAGAACCTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATC  
AACTAGATGAGCTTAACTTTAAAGCAACCCAAAAGCAGTAGCACTCTGT  
CACAAAATCAAATACCAAGTTAGTTTATATTTAGCCCAACAGCGGCTA  
TTAGCTTACATTAAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGCAA  
GCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAG  
CGACCTCTCTCGATTTCAGCAAGCTGATATAAGTTATTTAGTCATTT  
GCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACCTAAGGTTGTGA  
TAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAA  
ATCCTTTCTATTGAAGAATTAATAATAAA

Table 66: Comparative Sequences relating to SAG 0754

SEQ ID NO. 6606

STRAIN M732

CAAAATGAAGGAGAGGGAACCTATGgAAATACTGATTGCAGGTGGTAGTGG  
 TTTCTAGGGAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGG  
 TGGCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCCT  
 AGATTAACTTACATTAAAGGAGATATTACAGAAGCTGATAAGATTCATTT  
 AGaACATAGAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGC  
 CCAATCACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCA  
 CTCTGTCACAAAAATCAAATACCAAAGTTAGTTTACATTTAGCCCAATAG  
 CGGCTATTAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCA  
 AAGCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGT  
 GAAGAGCGACCTCTCTCGATTTCAGCAAGGTGATATAAAATTAATTAG  
 TCATTGCGCTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACTAAGG  
 TTGTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAACCAACT  
 CAAAAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6607

STRAIN COH1

ACAAGGCATATAAAAATTTCTATACTAAATTTAC  
 AAAATGAAGGAGAGGGAACCTATGGAATACTGATTGCAGGTGGTAGTGGT  
 TTTCTAGGGAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGGT  
 GGCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCCTA  
 GATTAACTTACATTAAAGGAGATATTACAGAAGCTGATAAGATTCATTTA  
 GAACATAGAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCC  
 CAATCACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCAC  
 TCTGTCACAAAAATCAAATACCAAAGTTAGTTTACATTTAGCCCAATAGC  
 GGCTATTAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCAA  
 AGCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTG  
 AAGAGCGACCTCTCTCGATTTCAGCAAGGTGATATAAAATTAATTAGT  
 CATTTGCGCTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACTAAGGT  
 TGTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAACCAACTC  
 AAAAAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6608

STRAIN M781

ACAAGGCATATAAAAATTTCTATACTAAATTTaCA  
 AAATGAAGGAGAGGGAACCTATGGAATACTGATTGCAGGTGGTAGTGGTT  
 TTCTAGGGAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGGTG  
 GCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCCTAG  
 ATTAACCTTACATTAAAGGAGATATTACAGAAGCTGATAAGATTCATTTAG  
 AACATAGAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCC  
 AATCACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACT  
 CTGTCACAAAAATCAAATACCAAAGTTAGTTTACATTTAGCCCAATAGCG  
 GCTATTAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCAA  
 GCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGA  
 AGAGCGACCTCTCTCGATTTCAGCAAGGTGATATAAAATTAATTAGTCA  
 ATTTGCGCTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACTAAGGTT  
 GTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAACCAACTCA  
 AAAAAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6609

STRAIN 1169NT

ACAAGGCATATAAAAATTTCTATACTAAATTTACAAA  
 ATGAAGGAGAGGGAACCTATGGAATACTGATTGCAGGTGGTAGTGGTTT  
 TTAGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGTTGGC  
 TTACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGAT  
 TAACCTACATTAAAGGAGATATTACAGAAGCTGATAAGATTCATTTAGAA  
 GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCAA  
 TCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCT  
 GTCACAAAATCAAATACCAAAGTTAGTTTACATTTAGCCCAACAGCGGC  
 TATTAGCTTACATTAGAAGTAAAGGAAGGCAGAGCAGATAATCAAAGC  
 AAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAG  
 AGCGACCTCTCTCGATTTCAGCAAGGTGATATAAAATTAATTAGTCAT  
 TTGCCCTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGT  
 GATAGTGGCAGAAGCAATCGTTACTACGCTTAGGACAAAACCAACTCAA  
 AAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6610

STRAIN CJB110

ACAAGGCATATAAAAATTTCTATACTAAATTTACAAA  
 ATGAAGGAGAGGGAACCTATGGAATACTGATTGCAGGTGGTAGTGGTTT  
 TTAGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGTTGGC  
 TTACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGAT  
 TAACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCATTTAGAA  
 GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCAA  
 TCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCT  
 GTCACAAAATCAAATACCAAAGTTAGTTTATATTTAGCCCAACAGCGGC  
 TATTAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGC  
 AAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAG  
 AGCGACCTCTCTCGATTTCAGCAAGGTGATATAAAATTAATTAGTCAT  
 TTGCCCTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGT  
 GATAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAACCAACTCAA  
 AAATCCTTTCTATTGAAGAATTAAATAATAAA



Table 66: Comparative Sequences relating to SAG 0754

SEQ ID NO. 6611

STRAIN JM9130013

ACAAGGCATATAAAATTCTTACTAAATTACAAAATG  
 AAGGAGAGGGAATATGGAAATCTGATTGCAGGTGGTAGTGGTTTTTTA  
 GGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTTA  
 CTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTAA  
 CcTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGAC  
 AGAACITTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAATCA  
 ACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCTGTG  
 ACAAAAATCAAATACCAAGTTAGTTTATATTTCAGCCAACACGGGCTAT  
 TCAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGCAAG  
 CGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAGC  
 GACCTCTCTCGATTTTCCAAGCCAAGTGTATAAAGTTATTTAGTCAATTG  
 CCTTTCTTAgGTATTGTGTACAAAAGGCTTTCCAACCTAAGGTTGTGAT  
 AGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAAA  
 TCCTTTCTATTGAAGAATTAATAATAAA

PRETTY of: /biotmp/msal37119.2{\*} April 10, 2003 03:30 ..

	1				50
msal37119.2{303_COH1}	---acaaggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_M732}	-----	-----	-----	-----CAAA	ATGAAGGAGA
msal37119.2{303_m781}	---acaaggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_090}	---acaaggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_18RS21}	---acaaggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_2603}	ttgacaaggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_A909}	---acaaggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_CJB110}	---acaaggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_H36B}	-----	-tataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_JM9130013}	---acaaggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_1169NT}	---acaaggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
Consensus	***-----	-----	-----	-----****	*****

	51				100
msal37119.2{303_COH1}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	cTAGGgAAGC
msal37119.2{303_M732}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	cTAGGgAAGC
msal37119.2{303_m781}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	cTAGGgAAGC
msal37119.2{303_090}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_18RS21}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_2603}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_A909}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_CJB110}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_H36B}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_JM9130013}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_1169NT}	GGGAACCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
Consensus	*****	*****	*****	*****	*****

	101				150
msal37119.2{303_COH1}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_M732}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_m781}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_090}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_18RS21}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_2603}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_A909}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_CJB110}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_H36B}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_JM9130013}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_1169NT}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
Consensus	*****	*****	*****	*****	*****

	151				200
msal37119.2{303_COH1}	AGgCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_M732}	AGgCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_m781}	AGgCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_090}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_18RS21}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_2603}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_A909}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_CJB110}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_H36B}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_JM9130013}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_1169NT}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
Consensus	***-----	-----	-----	-----	-----

	201				250
msal37119.2{303_COH1}	TAaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	cAtAGAAaTT
msal37119.2{303_M732}	TAaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	cAtAGAAaTT
msal37119.2{303_m781}	TAaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	cAtAGAAaTT
msal37119.2{303_090}	TAaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
msal37119.2{303_18RS21}	TAaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
msal37119.2{303_2603}	TAaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT

Table 66: Comparative Sequences relating to SAG 0754

msa137119.2{303_A909}	TagGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gACAGAAcTT	
msa137119.2{303_CJB110}	TagGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gACAGAAcTT	
msa137119.2{303_H36B}	TagGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gACAGAAcTT	
msa137119.2{303_JM9130013}	TagGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gACAGAAcTT	
msa137119.2{303_1169NT}	TaaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gACAGAAcTT	
Consensus	***-*****	*****	*****	*****	-*-*****	
msa137119.2{303_COH1}	251	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_M732}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT	
msa137119.2{303_m781}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT	
msa137119.2{303_090}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT	
msa137119.2{303_18RS21}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT	
msa137119.2{303_2603}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT	
msa137119.2{303_A909}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT	
msa137119.2{303_CJB110}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT	
msa137119.2{303_H36B}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT	
msa137119.2{303_JM9130013}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT	
msa137119.2{303_1169NT}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT	
Consensus	*****	*****	*****	*****	*****	
msa137119.2{303_COH1}	301	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_M732}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA	
msa137119.2{303_m781}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA	
msa137119.2{303_090}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA	
msa137119.2{303_18RS21}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA	
msa137119.2{303_2603}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA	
msa137119.2{303_A909}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA	
msa137119.2{303_CJB110}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA	
msa137119.2{303_H36B}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA	
msa137119.2{303_JM9130013}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA	
msa137119.2{303_1169NT}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA	
Consensus	*****	*****	*****	*****	*****	*****
msa137119.2{303_COH1}	351	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTTCAGCTT
msa137119.2{303_M732}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTTCAGCTT	
msa137119.2{303_m781}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTTCAGCTT	
msa137119.2{303_090}	TCAAATACCA	AAGTTAGTTT	AtATTTCAGC	CAAcAGCGGC	TATTTCAGCTT	
msa137119.2{303_18RS21}	TCAAATACCA	AAGTTAGTTT	AtATTTCAGC	CAAcAGCGGC	TATTTCAGCTT	
msa137119.2{303_2603}	TCAAATACCA	AAGTTAGTTT	AtATTTCAGC	CAAcAGCGGC	TATTTCAGCTT	
msa137119.2{303_A909}	TCAAATACCA	AAGTTAGTTT	AtATTTCAGC	CAAcAGCGGC	TATTTCAGCTT	
msa137119.2{303_CJB110}	TCAAATACCA	AAGTTAGTTT	AtATTTCAGC	CAAcAGCGGC	TATTTCAGCTT	
msa137119.2{303_H36B}	TCAAATACCA	AAGTTAGTTT	AtATTTCAGC	CAAcAGCGGC	TATTTCAGCTT	
msa137119.2{303_JM9130013}	TCAAATACCA	AAGTTAGTTT	AtATTTCAGC	CAAcAGCGGC	TATTTCAGCTT	
msa137119.2{303_1169NT}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAAcAGCGGC	TATTTCAGCTT	
Consensus	*****	*****	*-*****	***-*****	*****	*****
msa137119.2{303_COH1}	401	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_M732}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG	
msa137119.2{303_m781}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG	
msa137119.2{303_090}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG	
msa137119.2{303_18RS21}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG	
msa137119.2{303_2603}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG	
msa137119.2{303_A909}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG	
msa137119.2{303_CJB110}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG	
msa137119.2{303_H36B}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG	
msa137119.2{303_JM9130013}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG	
msa137119.2{303_1169NT}	ACATTaaAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG	
Consensus	*****-***	*****	*****	*****	*****	*****
msa137119.2{303_COH1}	451	GATTATCTTT	TTGTAAGACC	AGGTTTGTATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_M732}	GATTATCTTT	TTGTAAGACC	AGGTTTGTATG	TATGGTGAAG	AGCGACCTCT	
msa137119.2{303_m781}	GATTATCTTT	TTGTAAGACC	AGGTTTGTATG	TATGGTGAAG	AGCGACCTCT	
msa137119.2{303_090}	GATTATCTTT	TTGTAAGACC	AGGTTTGTATG	TATGGTGAAG	AGCGACCTCT	
msa137119.2{303_18RS21}	GATTATCTTT	TTGTAAGACC	AGGTTTGTATG	TATGGTGAAG	AGCGACCTCT	
msa137119.2{303_2603}	GATTATCTTT	TTGTAAGACC	AGGTTTGTATG	TATGGTGAAG	AGCGACCTCT	
msa137119.2{303_A909}	GATTATCTTT	TTGTAAGACC	AGGTTTGTATG	TATGGTGAAG	AGCGACCTCT	
msa137119.2{303_CJB110}	GATTATCTTT	TTGTAAGACC	AGGTTTGTATG	TATGGTGAAG	AGCGACCTCT	
msa137119.2{303_H36B}	GATTATCTTT	TTGTAAGACC	AGGTTTGTATG	TATGGTGAAG	AGCGACCTCT	
msa137119.2{303_JM9130013}	GATTATCTTT	TTGTAAGACC	AGGTTTGTATG	TATGGTGAAG	AGCGACCTCT	
msa137119.2{303_1169NT}	GATTATCTTT	TTGTAAGACC	AGGTTTGTATG	TATGGTGAAG	AGCGACCTCT	
Consensus	*****	*****	*****	*****	*****	*****
msa137119.2{303_COH1}	501	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_M732}	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TGCGCTTTCT	
msa137119.2{303_m781}	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TGCGCTTTCT	
msa137119.2{303_090}	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TGCGCTTTCT	
msa137119.2{303_18RS21}	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTTAGTCAT	TGCGCTTTCT	

Table 66: Comparative Sequences relating to SAG 0754

msa137119.2{303_2603}	CTCGATTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_A909}	CTCGATTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_CJB110}	CTCGATTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_H36B}	CTCGATTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_JM9130013}	CTCGATTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_1169NT}	CTCGATTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
Consensus	*****	*****	*****_**	*****	*****
551					
msa137119.2{303_COH1}	TAGGTATTGT	TGTACAAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_M732}	TAGGTATTGT	TGTACAAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_m781}	TAGGTATTGT	TGTACAAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_090}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_18RS21}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_2603}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_A909}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_CJB110}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_H36B}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_JM9130013}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_1169NT}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
Consensus	*****	*****_*	*****	*****	*****
601					
msa137119.2{303_COH1}	GAAGCAATCG	TTACTtCGCT	TAGGAaAAAA	CCAActCAAA	AAATCCTTTC
msa137119.2{303_M732}	GAAGCAATCG	TTACTtCGCT	TAGGAaAAAA	CCAActCAAA	AAATCCTTTC
msa137119.2{303_m781}	GAAGCAATCG	TTACTtCGCT	TAGGAaAAAA	CCAActCAAA	AAATCCTTTC
msa137119.2{303_090}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_18RS21}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_2603}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_A909}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_CJB110}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_H36B}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_JM9130013}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_1169NT}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
Consensus	*****	*****_****	*****_****	*****_****	*****
651					
msa137119.2{303_COH1}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_M732}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_m781}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_090}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_18RS21}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_2603}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_A909}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_CJB110}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_H36B}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_JM9130013}	TATTGAAGAA	TTAAATAATA	AA		
msa137119.2{303_1169NT}	TATTGAAGAA	TTAAATAATA	AA		
Consensus	*****	*****	**		
672					

## SEQ ID NO. 6612

## STRAIN 2603 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD  
 PRLTYIRGDIETADKIHLEDRFTDILIDCIGAIPNQLDELNVKATQKAVALKHNQIPK  
 LVYISANSYGSAIYKSKRKAQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSLH  
 PFLGIVQKVFPKVVIVABAIVITLRRKPTQKILSIEELNNK

## SEQ ID NO. 6613

## STRAIN 090 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD  
 PRLTYIRGDIETADKIHLEDRFTDILIDCIGAIPNQLDELNVKATQKAVALKHNQIPK  
 LVYISANSYGSAIYKSKRKAQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSLH  
 PFLGIVQKVFPKVVIVABAIVITLRRKPTQKILSIEELNNK

## SEQ ID NO. 6614

## STRAIN A909 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD  
 PRLTYIRGDIETADKIHLEDRFTDILIDCIGAIPNQLDELNVKATQKAVALKHNQIPK  
 LVYISANSYGSAIYKSKRKAQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSLH  
 PFLGIVQKVFPKVVIVABAIVITLRRKPTQKILSIEELNNK

## SEQ ID NO. 6615

## STRAIN H36B frame: 2

IKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKDPRL  
 TYIRGDIETADKIHLEDRFTDILIDCIGAIPNQLDELNVKATQKAVALKHNQIPKLVY  
 ISANSYGSAIYKSKRKAQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSLH  
 GIVVQKVFPKVVIVABAIVITLRRKPTQKILSIEELNNK

## SEQ ID NO. 6616

Table 66: Comparative Sequences relating to SAG 0754

## STRAIN 18RS21 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD  
 PRLTYIRGDI TEADKIHLEDRTFDILIDCIGAIPNQLDELNVKATQKAVALCHKNQIPK  
 LVYISANSYSAYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSL  
 PFLGIVVQVFPTKVIVAEIVTTLRKKPTQKILSIEELNNK

## SEQ ID NO. 6617

## STRAIN M732 frame: 1

QNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKDPRLTYIKGDIT  
 EADKIHLEHRNFDILIDCIGAIPNQLDELNVKATQKAVALCHKNQIPKLVYISANSYS  
 AYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSLPFLGIVVQVF  
 PTKVIVAEIVTSLRKKPTQKILSIEELNNK

## SEQ ID NO. 6618

## STRAIN COH1 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD  
 PRLTYIKGDIT EADKIHLEHRNFDILIDCIGAIPNQLDELNVKATQKAVALCHKNQIPK  
 LVYISANSYSAYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSL  
 PFLGIVVQVFPTKVIVAEIVTSLRKKPTQKILSIEELNNK

## SEQ ID NO. 6619

## STRAIN M781 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD  
 PRLTYIKGDIT EADKIHLEHRNFDILIDCIGAIPNQLDELNVKATQKAVALCHKNQIPK  
 LVYISANSYSAYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSL  
 PFLGIVVQVFPTKVIVAEIVTSLRKKPTQKILSIEELNNK

## SEQ ID NO. 6620

## STRAIN 1169NT frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKLAYLSRHEGKGDIFKD  
 PRLTYIKGDIT EADKIHLEDRTFDILIDCIGAIPNQLDELNVKATQKAVALCHKNQIPK  
 LVYISANSYSAYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSL  
 PFLGIVVQVFPTKVIVAEIVTTLRKKPTQKILSIEELNNK

## SEQ ID NO. 6621

## STRAIN CJB110 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD  
 PRLTYIRGDI TEADKIHLEDRTFDILIDCIGAIPNQLDELNVKATQKAVALCHKNQIPK  
 LVYISANSYSAYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSL  
 PFLGIVVQVFPTKVIVAEIVTTLRKKPTQKILSIEELNNK

## SEQ ID NO. 6622

## STRAIN JM9130013 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD  
 PRLTYIRGDI TEADKIHLEDRTFDILIDCIGAIPNQLDELNVKATQKAVALCHKNQIPK  
 LVYISANSYSAYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSL  
 PFLGIVVQVFPTKVIVAEIVTTLRKKPTQKILSIEELNNK

PRETTY of: /biotmp/msal37299.2{\*} April 10, 2003 03:37 ..

	1				50
msal37299.2{303_COH1}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_M732}	-----	-QNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_M781}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_090}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_18RS21}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_2603}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_A909}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_CJB110}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_JM9130013}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_H36B}	---ikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msal37299.2{303_1169NT}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKLAYLSR
Consensus	-----	*****	*****	*****	*****

  

	51				100
msal37299.2{303_COH1}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEh	RnFDILIDCI	GAIKPNQLDE
msal37299.2{303_M732}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEh	RnFDILIDCI	GAIKPNQLDE
msal37299.2{303_M781}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEh	RnFDILIDCI	GAIKPNQLDE
msal37299.2{303_090}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msal37299.2{303_18RS21}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msal37299.2{303_2603}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msal37299.2{303_A909}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msal37299.2{303_CJB110}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msal37299.2{303_JM9130013}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msal37299.2{303_H36B}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msal37299.2{303_1169NT}	HEGKGDIFKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
Consensus	*****	*****	*****	*****	*****

Table 66: Comparative Sequences relating to SAG 0754

	101		150		
msa137299.2{303_COH1}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_M732}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_M781}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_090}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_18RS21}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_2603}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_A909}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_CJB110}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_JM9130013}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_H36B}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
msa137299.2{303_1169NT}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy	SAYIkSKRKA	EQI IKASGLD
Consensus	*****	*****	*****	*****	*****
	151		200		
msa137299.2{303_COH1}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_M732}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_M781}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_090}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_18RS21}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_2603}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_A909}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_CJB110}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_JM9130013}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_H36B}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
msa137299.2{303_1169NT}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL	PFLGIVVQKV	FPTKVVIVAE
Consensus	*****	*****	*****	*****	*****
	201		223		
msa137299.2{303_COH1}	AIvTsLRkKP	TQKILSIEEL	NNK		
msa137299.2{303_M732}	AIvTsLRkKP	TQKILSIEEL	NNK		
msa137299.2{303_M781}	AIvTsLRkKP	TQKILSIEEL	NNK		
msa137299.2{303_090}	AIvTtLRkKP	TQKILSIEEL	NNK		
msa137299.2{303_18RS21}	AIvTtLRkKP	TQKILSIEEL	NNK		
msa137299.2{303_2603}	AIvTtLRkKP	TQKILSIEEL	NNK		
msa137299.2{303_A909}	AIvTtLRkKP	TQKILSIEEL	NNK		
msa137299.2{303_CJB110}	AIvTtLRkKP	TQKILSIEEL	NNK		
msa137299.2{303_JM9130013}	AIvTtLRkKP	TQKILSIEEL	NNK		
msa137299.2{303_H36B}	AIvTtLRkKP	TQKILSIEEL	NNK		
msa137299.2{303_1169NT}	AIvTtLRkKP	TQKILSIEEL	NNK		
Consensus	****-***	*****	***		

Table 67: Comparative Sequences relating to SAG0475

SEQ ID NO. 6701

STRAIN 090

CAATAACAACATTTGAAAAATAAAAAAGTTTGTAGTCCTTGGTTTAGCACGA  
 TCTGGAGAAGCCGCTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGAC  
 AGTTAATGATGGCAAACCATTTGATGAAAAATCCACAGCACAGTCTTTGT  
 TGGAAAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTA  
 GATGAGGATTTTGTACATGATTAAAAATCCAGGAATACCTTATAACAA  
 TCCTATGGTCAAAAAAGCATTAGAAAAACAAATCCCTGTTTGTACTGAAG  
 TGGAAATTAGCATACTTAGTTTCAGAAATCTCAGCTAATAGGTATTACAGGC  
 TCTAACGGGAAAAACGACACGACACGATGATGACAGAGTCTTAAATGC  
 TGGAGGTCAGAGAGGTTTGTAGCTGGGAATATCGGCTTTCCTGCTAGTG  
 AAGTTGTTTCAAGGCTGCGGATGATAAAGATATTCTAGTTATGGAATTATCA  
 AGTTTTTCAAGCTAATGGGAGTTAAGGAATTTCTGCTCATATTGCGATTAAT  
 TACTAATTTAATGCCAACTCAATTAGATTATCATGGGTCTTTTGAAGATT  
 ATGTTGCTGCAAAATGGAATATCCAAATCAAATGTCTTCATCTGATTTT  
 TTGGTACTTAATTTTAAATCAAGGTATTTCTAAAGAGTTAGCTAAACTAC  
 TAAAGCAACAATCGTTCCTTCTCTACTACGGAATAAGTTGATGGTGCTT  
 ACGTACAGACAAGCAACTTTTCTATAAAGGGGAGAAATATTATGTTAGTA  
 GATGACATTGGTGTCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAAC  
 TATTGCGGTTGCTAAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAA  
 CTTTAAGCAATTTTGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAAG  
 GTTCATGGTATTAGTTTCTATAACGACAGCAAGTCAACTAATATATTGGC  
 AACTCAAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTG  
 CAGGAGGTCCTGATCGCGGTAATGAGTTTGTGAATTGATACCAGATATC  
 ACTGGACTTAAACATATGGTTGTTTATAGGGGAATCGGCATCTCGAGTAAA  
 ACGTGCTGCACAAAAGCAGGAGTAACCTTATAGCGATGCTTTAGATGTTA  
 GAGATGCGGTACATAAAGCTTATGAGGTGGCACAAACAGGGCGATGTTATC  
 TTGCTAAGTCTGCAATGCATCATGGGACATGTATAAGAATTTGGAAGT  
 CCGTGGTGATGAATTCATTGATACCTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6702

STRAIN A909

CAATAACAACATTTGAAAAATAAAAAAGTTTGTAGTCCTTGGTTTAGCACGA  
 TCTGGAGAAGCTGCTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGAC  
 AGTTAATGATGGCAAACCATTTGATGAAAAATCCACAGCACAGTCTTTGT  
 TGGAAAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTA  
 GATGAGGATTTTGTACATGATTAAAAATCCAGGAATACCTTATAACAA  
 TCCTATGGTCAAAAAAGCATTAGAAAAACAAATCCCTGTTTGTACTGAAG  
 TGGAAATTAGCATACTTAGTTTCAGAAATCTCAGCTAATAGGTATTACAGGC  
 TCTAACGGGAAAAACGACACGACACGATGATGACAGAGTCTTAAATGC  
 TGGAGGTCAGAGAGGTTTGTAGCTGGGAATATCGGCTTTCCTGCTAGTG  
 AAGTTGTTTCAAGGCTGCGAATGATAAAGATACTCTAGTTATGGAATTATCA  
 AGTTTTTCAAGCTAATGGGAGTTAAGGAATTTCTGCTCATATTGCGATTAAT  
 TACTAATTTAATGCCAACTCAATTAGATTATCATGGGTCTTTTGAAGATT  
 ATGTTGCTGCAAAATGGAATATCCAAATCAAATGTCTTCATCTGATTTT  
 TTGGTACTTAATTTTAAATCAAGGTATTTCTAAAGAGTTAGCTAAACTAC  
 TAAAGCAACAATCGTTCCTTCTCTACTACGGAATAAGTTGATGGTGCTT  
 ACGTACAGACAAGCAACTTTTCTATAAAGGGGAGAAATATTATGTCAGTA  
 GATGACATTGGTGTCCAGGAAGCCATAACGTATAGAATGCTCTAGCAAC  
 TATTGCGGTTGCTAAACTGCGCTGGTATCAGTAATCAAGTTATTAGAGAAA  
 CTTTAAGCAATTTTGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAAG  
 GTTCATGGTATTAGTTTCTATAACGACAGCAAGTCAACTAATATATTGGC  
 AACTCAAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTG  
 CAGGAGGTCCTGATCGCGGTAATGAGTTTGTGAATTGATACCAGATATC  
 ACTGGACTTAAACATATGGTTGTTTATAGGGGAATCGGCATCTCGAGTAAA  
 ACGTGCTGCACAAAAGCAGGAGTAACCTTATAGCGATGCTTTAGATGTTA  
 GAGATGCGGTACATAAAGCTTATGAGGTGGCACAAACAGGGCGATGTTATC  
 TTGCTAAGTCTGCAATGCATCATGGGACATGTATAAGAATTTGGAAGT  
 CCGTGGTGATGAATTCATTGATACCTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6703

STRAIN H36B

GGACGAGTAATGAAAAAATAACAACATTTGAAAAAT  
 AAAAAAGTTTGTAGTCCTTGGTTTAGCACGATCTGGAGAAGCTGCTGCACG  
 TTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAACCAT  
 TTGATGAAAAATCCACAGCACAGTCTTTGTGGAAAGAGGGTATTAAAGTG  
 GTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTGTACAT  
 GATTAAAAATCCAGGAATACCTTATAACCAATCCTATGGTCAAAAAAGCAT  
 TAGAAAAACAAATCCCTGTTTGTAGTGAAGTGAATTAGCATACTTAGTT  
 TCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAAACGACAA  
 GACAACGATGATTGACAGAGTCTTAAATGCTGGAGGTGAGAGAGGTTTGT  
 TAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTCAAGGCTGCGAAT  
 GATAAAGATACTCTAGTTATGGAATATCAAGTTTTCAGCTAATGGGAGT  
 TRAGGAATTTCTGCTCATATTGACAGTAATTAATAATTAAATGCCAACTC  
 ATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAAATGGAAT  
 ATCCAAATCAAATGTCTTCATCTGATTTTGTGACTTAATTTTAAATCA  
 AGGTATTTCTAAAGAGTTAGCTAAACTACTAAAGCAACAATCGTTCCTT  
 TCTCTACTACGGAATAAGTTGATGGTGCTTACGTACAAGACAAGCAACTT  
 TTCTATAAAGGGGAGAAATATTATGTCAGTAGATGACATTGGTGTCCAGG  
 AAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAACTGG  
 CTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTTGGAGGT  
 GTTAAACACCGCTTCAATCACTCGGTAAGGTTTATGGTATTAGTTTCTA  
 TAACGACAGCAAG

Table 67: Comparative Sequences relating to SAG0475

SEQ ID NO. 6704

STRAIN 18RS21

GGACGAGTAATGAAAAACAATAACAACATTTG  
 AAAATAAAAAAGTTTGTAGTCCTTGGTTTAGCACGATCTGGAGAAGCTGCT  
 GCACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAA  
 ACCATTTGATGAAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTA  
 AAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTGT  
 TACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAA  
 AGCATTAGAAAAACAATCCCTGTTTGAAGTGAAGTTAGCATACT  
 TAGTTTCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAAACG  
 ACAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTCAGAGAGG  
 TTTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTGAGGCTG  
 CGAATGATAAAGATACTCTAGTTATGGAATTATCAAGTTTTCAGCTAATG  
 GGAGTTAAGGAATTCGTCTCATATTGACAGTAATTACTAATTTAATGCC  
 AACTCATTTAGATTATCATGGGCTCTTTGAAGATTATGTTGCTGCAAAAT  
 GGAATATCCAAAATCAAATGTCTTCATCTGATTTTGGTACTTAATTTT  
 AATCAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAATCGT  
 TCCTTTCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAAGC  
 AACTTTTCTATAAAGGGGAGAATATTATGTAGTAGATGACATTGGTGTC  
 CCAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAA  
 ACTGGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTTG  
 GAGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTATGTTATTAGT  
 TTCTATAACGACAGCAAGTCACTAATATATTGGCAACTCAAAAAGCATT  
 ATCTGGCTTTGATAATACTAAAGTTATCTAATTGACAGGAGGCTTGATC  
 GCGGTAATGAGTTTGTAGTAATTGATACAGATATCACTGGACTTAAACAT  
 ATGGTTGTTTGGGGGAATCGGCATCTCGAGTAAAACGCTGCTGCACAAAA  
 AGCAGGAGTAACCTTAGCGATGCTTTAGATGTTAGAGATGCGGTACATA  
 AAGCTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCCCTGCA  
 AATGCATCATGGGACATGTATAAGAATTTGGAAGTCCGTGGTGATGAATT  
 CATTGATACTTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6705

STRAIN M732

GGACGAGTAATGAAAAACAATAACAACATTTGAAA  
 ATAAAAAAGTTTGTAGTCCTTGGTTTAGCACGATCTGGAGAAGCCGCTGCA  
 CGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAACC  
 ATTTGATGAAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTAAAG  
 TGGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTGTATAC  
 ATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAAAGC  
 ATTAGAAAAACAATCCCTGTTTGAAGTGAAGTTAGCATACTTAG  
 TTTGAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAAACGACA  
 ACCGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTGAGAGAGGTTT  
 GTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTGAGGCTGCGG  
 aTGATAAAGATATTCTAGTTATGGAATTATCAAGTTTTCAGCTAATGGGA  
 GTTAAGGAATTTGCTCCTCATATTGACAGTAATTACTAATTTAATGCCAAC  
 TCACTTAGATTATCATGGGCTCTTTGAGAGTTATGTTGCTGCAAAATGGA  
 ATATCCAAAATCAAATGTCTTCATCTGATTTTGGTACTTAATTTAAT  
 CAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAaTCGTTCC  
 TTTCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAAGCAAC  
 TTTTCTATAAAGGGGAGAATATTATGTAGTAGATGACATTGGTGTCCTCA  
 GGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAACT  
 AGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTGGAG  
 GTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTATGTTATTAGTTTC  
 TATAACGACAGCAAGTCACTAATATATTGGCAACTCAAAAAGCATTATC  
 TGGCTTTGATAATACTAAAGTTATCCTAATTGACAGGAGGCTTGTATCGCG  
 GTAATGAGTTTGTAGTAATTGATACAGATATCACTGGACTTAAACATATG  
 GTTGTTTTAGGGGAATCGGCATCTCGAGTAAAACGCTGCTGCACAAAAAGC  
 AGGAGTAACCTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACATAAAG  
 CTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCCCTGCAAA  
 GCATCATGGGACATGTATAAGAATTTGGAAGTCCGTGGTGATGAATTAT  
 TGATACTTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6706

STRAIN COH1

GGACGAGTAATGAAAAACAATAACAACATTTGA  
 AAATAAAAAAGTTTGTAGTCCTTGGTTTAGCACGATCTGGAGAAGCCGCTG  
 CACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAA  
 CCATTTGATGAAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTAA  
 AGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTGT  
 ACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAA  
 GCATTAGAAAAACAATCCCTGTTTGAAGTGAAGTTAGCATACT  
 AGTTTCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAAACGA  
 CAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTGAGAGAGT  
 TTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTGAGGCTGC  
 GGAATGATAAAGATATTCTAGTTATGGAATTATCAAGTTTTCAGCTAATGG  
 GAGTTAAGGAATTTGCTCCTCATATTGACAGTAATTACTAATTTAATGCCA  
 ACTCATTTAGATTATCATGGGCTTTTGAAGATTATGTTGCTGCAAAATG  
 GAATATCCAAAATCAAATGTCTTCATCTGATTTTGGTACTTAATTTTA  
 ATCAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAaCAATCGTT  
 CCTTCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAAGCA  
 ACTTTTCTATAAAGGGGAGAATATTATGTAGTAGATGACATTGGTGTC  
 CAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAA

Table 67: Comparative Sequences relating to SAG0475

CTAGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTTGG  
AGGTGTTAAACACCGCTTGCAATCACTCGGTAAAGTTTCATGGTATTAGTT  
TCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCATTA  
TCTGGCTTTGATAATACTAAAGTTATCCTAATGCAGGAGGTCCTGATCG  
CGGTAATGAGTTTGATGAATTGATACCAGATATCACTGGACTTAAACATA  
TGGTTCTTTTAGGGGAATCGGCATCTCGAGTAAACGTGCTGCACAAAA  
GCAGGAGTAACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACATAA  
AGCTTATGAGGTGGCACAACAGGCGATGTTATCTTGCTAAGTCTTGCAA  
ATGCATCATGGGACATGTATAAGAATTTGAAAGTCCGTGGTGTGAATTC  
ATTGATACCTTCGAAA

SEQ ID NO. 6707

STRAIN M781

GGACGAGTAATGAAAACAATAACAACATT  
TGAAAATAAAAAAGTTTGTAGTCTTGGTTTAGCAGGATCTGGAGAAGCCG  
CTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGC  
AAACCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTAT  
TAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTTGTAGATGAGGATTTT  
GTTACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAA  
AAAGCATTAGAAAAACAATCCTGTTTGGACTGAAGTGAATTAGCATA  
CTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAA  
CGACACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTGAGAGA  
GGTTTGTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTACAGGC  
TGCGGATGATAAAGATATTTAGTTATGGAATTTATCAAGTTTTCAGCTAA  
TGGGAGTTAAGGAATTTCTGCTCATATTGCAGTAATTACTAATTTAATG  
CCAATCATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAA  
ATGGAAATATCCAAATCAAATGTCTTCATCTGATTTTTGGTACTTAATT  
TTAATCAAGGTATTTCTAAAGAGTTAGCTAAAACCTAAAGCAACAATC  
GTTCTTTTCTACTACGAAAAAGTTGATGGTGCCTACGTACAAGACAA  
GCAACTTTTCTATAAAGGGGAGAATATTTATGTAGTAGATGACATTGCTG  
TCCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTCGGGTGCT  
AAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAAATTTAAGCAATTT  
TGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTATGGTATTA  
GTTTCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCA  
TTATCTGGCTTTGATAATACTAAAGTTATCTAATTGCAGGAGGTCTTGA  
TCGCGGTAATGAGTTTGTAGTAATTGATACCAGATATCACTGGACTTAAAC  
ATATGGTTGTTTtagGGGAATCGGCATCTCGAGTAAACGTGCTGCACAA  
AAAGCAGGAGTAACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACA  
TAAAGCTTATGAGGTGGCACAACAGGCGATGTTATCTTGCTAAGTCTG  
CAAAATGCATCATGGACATGTATAAGAATTTGAAAGTCCGTGGTGTGAAT  
TTCATGATACTTTGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6708

STRAIN CJB110

GGACGAGTAATGAAAACAATAACAACATTTGA  
AAATAAAAAAGTTTGTAGTCTTGGTTTAGCAGGATCTGGAGAAGCCGCTG  
CACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAA  
CCATTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTAA  
AGTGGTTTGTGGTAGTCATCCTTTAGAATTTGTAGATGAGGATTTTGT  
ACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAA  
GCATTAGAAAAACAATCCTGTTTGGACTGAAGTGAATTAGCATACTT  
AGTTTCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAAACGA  
CAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTGAGAGAGGT  
TTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTAGGCTGC  
GGATGATAAAGATATTTAGTTATGGAATTTCAAGTTTTCAGCTAATGG  
GAGTTAAGGAATTTCTGCTCATATTGCAGTAATTACTAATTTAATGCCA  
ACTCATTTAGATTATCATGGGTCTTTTGAAGAATATGTTGCTGCAAAATG  
GAATATCCAAAATCAAATGTCTTCATCTGATTTTGGTACTTAATTTTIA  
ATCAAGGTATTTCTAAAGAGTTAGCTAAAACCTAAAGCAACAATCGTT  
CCTTTCTCTACTACGAAAAAGTTGATGGTCTTACGTACAAGACAAGCA  
ACTTTTCTATAAAGGGGAGAATATTATGTTAGTAGATGACATTGGTGTCC  
CAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTGTCTAAA  
CTAGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTGG  
AGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTATGGTATTAGTT  
TCTATATGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCATTA  
TCTGGCTTTGATAATACTAAAGTTATCCTAATTCAGGAGGTCTTGATCG  
CGGTAATGAGTTTGATGAATTGATACCAGATATCACTGGACTTAAACATA  
TGGTTGTTTtagGGGAATCGGCATCTCGAGTAAACGTGCTGCACAAAA  
GCAGGAGTAACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACATAA  
AGCTTATGAGGTGGCACAACAGGCGATGTTATCTTGCTAAGTCTTGCAA  
ATGCATCATGGGACATGTATAAGAATTTGAAAGTCCGTGGTGTGAATTC  
ATTGATACTTTGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6709

STRAIN 1169NT

CAATAACAACATTTGAAAATAAAAAAGTTTGTAGTCTTGGTTTAGCACGA  
TCTGGAGAAGCCGCTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGAC  
AGTTAATGATGGCAAAACATTTGATGAAAATCCAACAGCACAGTCTTTGT  
TGGAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTTGTTA  
GATGAGGATTTTGTACATGATTAAAAATCCAGGAATACCTTATAACAA  
TCCATATGGTCAAAAAGCATTAGAAAAACAATCCTGTTTGGACTGAAG  
TGAATTAGCATACTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGC  
TCTAACGGGAAAACGACAACGACAGATGATTGCAGAAGTCTTGAATGC



Table 67: Comparative Sequences relating to SAG0475

TGGAGGTGAGAGAGGTTTGTAGCTGGGAATATCGGCTTTCTGCTAGTG  
 AAGTTGTTTCAGGCTGCGGATGATAAGATACTAGTTATGGAATATCA  
 AGTTTTTCAGCTAATGGGAGTTAAGGAATTCGTCCTCATATGTCAGTAAT  
 TACTAATTTAATGCCAACTCATTAGATTATCATGGGCTTTTGAAGACT  
 ATGTGCTGCAAAATGGAATATCCAAATCAAATGCTTCTCATCTGATTTT  
 TTGGTACTTAATTTAATCAAGGTATTTCTAAAGAGTTAGCTAAACTAC  
 TAAAGCAACAATCGTTCCTTTCTCTACTACGGAAGGTTGATGGTGCTT  
 ACGTACAAGCAAGCAACTTTCTATAAGGGGAGAAATATTATGTCAGTA  
 GACGACATTTGGTGTCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAAC  
 TATTGCGGTTGCTAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAA  
 CTTTAAGCAATTTTGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAG  
 GTTCATGGTATTAGTTTCTATAACGACAGTAAGTCAACTAATATATTGGC  
 AACTCAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCTTAATTG  
 CAGGAGGTCTTGATCGCGGTAAATGAGTTTGTGAAITGATACCATATC  
 ACTGGACTTAAGCATATGGTTGTTTAGGGGAATCGGCATCTCGAGTAAA  
 ACGTGTGTCACAAAAGCAGGAGTAACCTTATAGCAATGCTTTAGATGTTA  
 GAGATGCGGTACATAAAGCTTATGAGGTGGCAACAGGGCGATGTTATC  
 TTGTTAGTCTCGCAATGCATCATGGGACATGTATAAGAAATTCGAAGT  
 CCGTGGTGATGAATTCATTGATACCTTCG

SEQ ID NO. 6710

STRAIN JM9130013

GGACGAGTAATGAAAACAATAACAACA

TTTGAAAATAAAAAAGTTTGTAGCTTGGTTTAGCAGCATCTGGAGAAGC  
 TGCTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATG  
 GCAAAACCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGT  
 ATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGCTAGATGAGGATTT  
 TTGTTACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCA  
 AAAAAGCATTAGAAAAACAATCCCTGTTTGTACTGAAGTGAATTAGCA  
 TACTTAGTTTCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAA  
 AAGCACAACGACAACGATGATTGCAAGTCTTAAATGCTGGAGGTGAGA  
 GAGGTTTGTAGCTGGGAATATCGGCTTTCTGCTAGTGAAGTTGTTGAG  
 GCTGCGAATGATAAAGATACTCTAGTTATGGAATTATCAAGTTTTCAGCT  
 AATGGGAGTTAAGGAATTTCTGCTCATATTGCAAGTAATTACTAATTTAA  
 TGCCAACTCATTTAGATTATCATGGGTCTTTGAAGATTATGTTGCTGCA  
 AAATGGAATATCCAAATCAAATGCTTCTCATCTGATTTTGGTACTTAA  
 TTTTAATCAAGGTATTCTAAAGAGTTAGCTAAACTACTAAAGCAACAA  
 TCGTTTCCTTTCTACTACGGAAGGTTGATGGTGTCTACGTACAAGAC  
 AAGCAACTTTCTATAAAGGGGAGAAATATTATGTCAGTAGATGACATTGG  
 TGTCCCAAGCAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTG  
 CTAAACTGGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAAT  
 TTTGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTCATGGTAT  
 TAGTTCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAG  
 CATTATCTGGCTTTGATAATACTAAAGTTATCTTAATGTCAGGAGGTCTT  
 GATCGCAGTAATGAGTTTGTAGAAITGATACCATATCACTGGACTTAA  
 ACATATGGTTGTTTATAGGGGAATCGGCATCTCGAGTAAACGTGCTGCAC  
 AAAAAGCAGGAGTAACCTTATAGCGATGCTTTAGATGTTAGAGATGCGGTA  
 CATAAAGCTTATGAGGTGGCAACAGGGCGATGTTATCTTGTCTAAGTCC  
 TGCAATGTCATCATGGGACATGTATAAGAAATTCGAAGTCCGTGGTGATG  
 AATTCATTGATACCTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6710

STRAIN 2603

ggacgagtaaatgaaaacaataacaacatttgaaaataaaaaagtttagt  
 ccttggttagcacgcatctggagaagctgctgcacgttggttagctaagt  
 taggagcaatagtgacagttaatgatggcaaacatttgatgaaaatcca  
 acagcacagtcttggtggaagagggtattaaagtggtttggttagtca  
 tccttagaattgtagatgaggatttttggtacatgattaaaaatccag  
 gaataccttataacaatcctatggtcaaaaagcattagaaaaacaatc  
 cctggtttgactgaagtgggaattagcatacttagttcagaatctcagct  
 aatagggtattacaggctctaacgggaaaaacgacaacgacacgatgattg  
 cagaagctttaaattgctggagggtcagagagggttggttagctgggaatatc  
 ggcttctcgtgtagtgaggttggtcagggtgcaaatgataaagatactct  
 agttatgggaattatcaagttttcagctaatgggagtttaaggaatttcgtc  
 ctcatattgacagtaattactaatttaattgccaactcatttagattatcat  
 gggctctttgaagattatggtgctgcaaaatgggaatccaaaatcaa  
 gtctctcatctgatttttggtacttaatttaatacaaggattttctaaag  
 agttagctaaaactactaaagcaacaatcgttctctctactacggaa  
 aaagttgatgggtgcttacgtacaagacaagcaactttctataaaggga  
 gaattatgctcagtagatgacattgggtgtcccaggaagccataacgtag  
 agaattgctctagcaactattgctgggtgctaaactgggtggtatcagta  
 caagttattagagaaactttaagcaattttggaggtgttaaacacccgctt  
 gcaatcactcggtaaggttcaggttatgattttctataacgacagcaagt  
 caactaatatattggcaactcaaaaagcatttatcggctttgataaact  
 aaagttatcctaatttgaggagggtcttgatcgcggttaagtagtttgatga  
 attgataccagatatactggacttaaacatatgggtgttttaggggaat  
 cggcatctcaggtaaaacgtgctgcacaaaagcaggagtaacttatagc  
 gatgcttttagatgttagagatgcggtacataaagcttatgaggtggcaca  
 acagggcgatggttatctgctaagtcctgcaaatgcatcatgggacatgt  
 ataagaatttcgaagtcctgggtgatgaattcattgatactttcgaaggt  
 ctttagggagag

Table 67: Comparative Sequences relating to SAG0475

## MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa30176.2{\*} April 29, 2002 02:09 ..

	1				50
msa30176.2{305_18RS21}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_2603}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_A909}	-----	-----CAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_H36B}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_JM9130013}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_COH1}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_M781}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305e_M732}	-----	-----CAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_090}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_CJB110}	-----	-----CAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_1169NT}	-----	-----CAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
Consensus	-----	-----CAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
	51				100
msa30176.2{305_18RS21}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_2603}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_A909}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_H36B}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_JM9130013}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_COH1}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_M781}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305e_M732}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_090}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_CJB110}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_1169NT}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
Consensus	*****	*****	*****	*****	*****
	101				150
msa30176.2{305_18RS21}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_2603}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_A909}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_H36B}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_JM9130013}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_COH1}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_M781}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305e_M732}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_090}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_CJB110}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_1169NT}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
Consensus	*****	*****	*****	*****	*****
	151				200
msa30176.2{305_18RS21}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_2603}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_A909}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_H36B}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_JM9130013}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_COH1}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_M781}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305e_M732}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_090}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_CJB110}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_1169NT}	ACAGCACAGT	CTTTGTTGGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
Consensus	*****	*****	*****	*****	*****
	201				250
msa30176.2{305_18RS21}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_2603}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_A909}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_H36B}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_JM9130013}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_COH1}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_M781}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305e_M732}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_090}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_CJB110}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_1169NT}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
Consensus	*****	*****	*****	*****	*****
	251				300
msa30176.2{305_18RS21}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_2603}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_A909}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_H36B}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_JM9130013}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_COH1}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_M781}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305e_M732}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_090}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305_CJB110}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCAITAGA	AAAACAAATC
msa30176.2{305_1169NT}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCAITAGA	AAAACAAATC
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	301				350
msa30176.2{305_2603}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_A909}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_H36B}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_JM9130013}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_COH1}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_M781}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305e_M732}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_090}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_CJB110}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_1169NT}	CCTGTTTTGA	CTGAAGTGGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	351				400
msa30176.2{305_2603}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_A909}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_H36B}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_JM9130013}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_COH1}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_M781}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305e_M732}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_090}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_CJB110}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_1169NT}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	401				450
msa30176.2{305_2603}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305_A909}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305_H36B}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305_JM9130013}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305_COH1}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305_M781}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305e_M732}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305_090}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305_CJB110}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
msa30176.2{305_1169NT}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTTAGC	TGGGAATATC
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	451				500
msa30176.2{305_2603}	GGCTTTCTCG	CTAGTGAAGT	TGTTTCAAGGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_A909}	GGCTTTCTCG	CTAGTGAAGT	TGTTTCAAGGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_H36B}	GGCTTTCTCG	CTAGTGAAGT	TGTTTCAAGGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_JM9130013}	GGCTTTCTCG	CTAGTGAAGT	TGTTTCAAGGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_COH1}	GGCTTTCTCG	CTAGTGAAGT	TGTTTCAAGGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_M781}	GGCTTTCTCG	CTAGTGAAGT	TGTTTCAAGGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305e_M732}	GGCTTTCTCG	CTAGTGAAGT	TGTTTCAAGGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_090}	GGCTTTCTCG	CTAGTGAAGT	TGTTTCAAGGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_CJB110}	GGCTTTCTCG	CTAGTGAAGT	TGTTTCAAGGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_1169NT}	GGCTTTCTCG	CTAGTGAAGT	TGTTTCAAGGCT	GCGaATGATA	AAGATAcTCT
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	501				550
msa30176.2{305_2603}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_A909}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_H36B}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_JM9130013}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_COH1}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_M781}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305e_M732}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_090}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_CJB110}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_1169NT}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	551				600
msa30176.2{305_2603}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305_A909}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305_H36B}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305_JM9130013}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305_COH1}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305_M781}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT
msa30176.2{305e_M732}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCAITT	AGATTATCAT

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305_090}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
msa30176.2{305_CJB110}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
msa30176.2{305_1169NT}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_2603}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_A909}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_H36B}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_JM9130013}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_COH1}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_M781}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305e_M732}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_090}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_CJB110}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_1169NT}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_2603}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_A909}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_H36B}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_JM9130013}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_COH1}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_M781}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305e_M732}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_090}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_CJB110}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_1169NT}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305_2603}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305_A909}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305_H36B}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305_JM9130013}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305_COH1}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305_M781}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305e_M732}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305_090}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305_CJB110}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
msa30176.2{305_1169NT}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCTTTTCTC	TACTACGGAA
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_2603}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_A909}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_H36B}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_JM9130013}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_COH1}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_M781}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305e_M732}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_090}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_CJB110}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_1169NT}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_2603}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_A909}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_H36B}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_JM9130013}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_COH1}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_M781}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305e_M732}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_090}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_CJB110}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_1169NT}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
Consensus	*****	*-*****	*****	*****	*****
msa30176.2{305_18RS21}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_2603}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_A909}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_H36B}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_JM9130013}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_COH1}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_M781}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305e_M732}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
msa30176.2{305_090}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
msa30176.2{305_CJB110}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
msa30176.2{305_1169NT}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
Consensus	*****	*****	*****	****_****	*****
msa30176.2{305_18RS21}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_2603}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_A909}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_H36B}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_JM9130013}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_COH1}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_M781}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305e_M732}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_090}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_CJB110}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_1169NT}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_2603}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_A909}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_H36B}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_JM9130013}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_COH1}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_M781}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305e_M732}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_090}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_CJB110}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_1169NT}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_2603}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_A909}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_H36B}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_JM9130013}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_COH1}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_M781}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305e_M732}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_090}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_CJB110}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_1169NT}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305_2603}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305_A909}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305_H36B}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305_JM9130013}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305_COH1}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305_M781}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305e_M732}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305_090}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305_CJB110}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
msa30176.2{305_1169NT}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaaatg	agtttgatga
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_2603}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_A909}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_H36B}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_JM9130013}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_COH1}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_M781}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305e_M732}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_090}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_CJB110}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_1169NT}	attgatacca	gatatactg	gacttaagca	tatggttggtt	ttaggggaat
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_2603}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_A909}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_H36B}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_JM9130013}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_COH1}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305_M781}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305e_M732}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_090}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_CJB110}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_1169NT}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_2603}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_A909}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_H36B}	-----	-----	-----	-----	-----
msa30176.2{305_JM9130013}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_COH1}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_M781}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305e_M732}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_090}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_CJB110}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
msa30176.2{305_1169NT}	aatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
msa30176.2{305_2603}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
msa30176.2{305_A909}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
msa30176.2{305_H36B}	-----	-----	-----	-----	-----
msa30176.2{305_JM9130013}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
msa30176.2{305_COH1}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
msa30176.2{305_M781}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
msa30176.2{305e_M732}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
msa30176.2{305_090}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
msa30176.2{305_CJB110}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
msa30176.2{305_1169NT}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaaagt
msa30176.2{305_2603}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaaagt
msa30176.2{305_A909}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaaagt
msa30176.2{305_H36B}	-----	-----	-----	-----	-----
msa30176.2{305_JM9130013}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaaagt
msa30176.2{305_COH1}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaaagt
msa30176.2{305_M781}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaaagt
msa30176.2{305e_M732}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaaagt
msa30176.2{305_090}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaaagt
msa30176.2{305_CJB110}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaaagt
msa30176.2{305_1169NT}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaaagt
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	cttagaggag	ag			
msa30176.2{305_2603}	cttagaggag	ag			
msa30176.2{305_A909}	cttagaggag	ag			
msa30176.2{305_H36B}	-----	-----			
msa30176.2{305_JM9130013}	cttagaggag	ag			
msa30176.2{305_COH1}	-----	-----			
msa30176.2{305_M781}	cttagaggag	ag			
msa30176.2{305e_M732}	cttagaggag	ag			
msa30176.2{305_090}	cttagaggag	ag			
msa30176.2{305_CJB110}	cttagaggag	ag			
msa30176.2{305_1169NT}	-----	-----			
Consensus	-----	-----			

SEQ ID NO. 6711

STRAIN 090 frame: 3

ITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGIKVVCGS  
HPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQIIGITGSNGK  
TTTTTMAIEVLNAGGQRLLAGNIGFPASEVVQAADKDIILVMESSFLMGVKEFRPHI  
AVITNLMPTHLDDYHGSFEDYVAAKWNINQMSSSDFLVNFNQGISKEKAKTTKATIVPF  
STTEKVDGAYVQDKQLFYKGENIMLVDDIGVPGSHNVENALATIAVAKLAGISNQVIRET  
LSNFGGVKHLRQSLGKVHGISFYNDKSTNIIATQKALSGFDNTKVILIAAGLDRGNEFD  
ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGDVILLSP  
ANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6712

STRAIN A909 frame: 3

ITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGIKVVCGS  
HPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQIIGITGSNGK  
TTTTTMAIEVLNAGGQRLLAGNIGFPASEVVQAADKDIILVMESSFLMGVKEFRPHI  
AVITNLMPTHLDDYHGSFEDYVAAKWNINQMSSSDFLVNFNQGISKEKAKTTKATIVPF  
STTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVXNALATIAVAKLAGISNQVIRET  
LSNFGGVKHLRQSLGKVHGISFYNDKSTNIIATQKALSGFDNTKVILIAAGLDRGNEFD

Table 67: Comparative Sequences relating to SAG0475

ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGDVILLSP  
ANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6713

STRAIN H36B frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEGI  
KVVC GSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQ LIGI  
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSS FQLMGVK  
EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVLNFNQGISKELAKTTK  
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISN  
QVIRETLSNFGGVKHLRQLSLGKVHGISFYNDSSKSTNIIATQKALSGFDNTKVIL IAGGLD  
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD

SEQ ID NO. 6714

STRAIN 18RS21 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEGI  
KVVC GSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQ LIGI  
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSS FQLMGVK  
EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVLNFNQGISKELAKTTK  
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISN  
QVIRETLSNFGGVKHLRQLSLGKVHGISFYNDSSKSTNIIATQKALSGFDNTKVIL IAGGLD  
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD  
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6715

STRAIN M732 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEGI  
KVVC GSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQ LIGI  
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSS FQLMGVK  
EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVLNFNQGISKELAKTTK  
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISN  
QVIRETLSNFGGVKHLRQLSLGKVHGISFYNDSSKSTNIIATQKALSGFDNTKVIL IAGGLD  
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD  
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6716

STRAIN COH1 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEGI  
KVVC GSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQ LIGI  
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSS FQLMGVK  
EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVLNFNQGISKELAKTTK  
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISN  
QVIRETLSNFGGVKHLRQLSLGKVHGISFYNDSSKSTNIIATQKALSGFDNTKVIL IAGGLD  
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD  
VILLSPANASWDMYKNFEVRGDEFIDTFE

SEQ ID NO. 6717

STRAIN M781 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEGI  
KVVC GSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQ LIGI  
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSS FQLMGVK  
EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVLNFNQGISKELAKTTK  
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISN  
QVIRETLSNFGGVKHLRQLSLGKVHGISFYNDSSKSTNIIATQKALSGFDNTKVIL IAGGLD  
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD  
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6718

STRAIN CJB110 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEGI  
KVVC GSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQ LIGI  
TGSNGKTTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSS FQLMGVK  
EFRPHIAVITNLMPTHLDDYHGSFEEYVAAKWNIONQMSSSDFLVLNFNQGISKELAKTTK  
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISN  
QVIRETLSNFGGVKHLRQLSLGKVHGISFYNDSSKSTNIIATQKALSGFDNTKVIL IAGGLD  
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD  
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6719

STRAIN 1169NT frame: 3

ITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEGIKVVC GS  
HPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQ LIGITGSNGK  
TTTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSS FQLMGVKEFRPHI  
AVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVLNFNQGISKELAKTTKATIVPF  
STTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATI AVAKLAGISNQVIRET  
LSNFGGVKHLRQLSLGKVHGISFYNDSSKSTNIIATQKALSGFDNTKVIL IAGGLDRGNEF  
ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSN ALDVRDAVHKAYEVAQQGDVILXSP  
ANASWDMYKNFEVRGDEFIDTF

Table 67: Comparative Sequences relating to SAG0475

SEQ ID NO. 6720

STRAIN JM9130013 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIIVTVNDGKPFDENPTAQSLLLEEGI  
 KVVCGSHPLELLEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQILIGI  
 TGSNGKTTTTMTIAEVLNAGGQRLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK  
 EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNINQMSSSDFLVLNFNQGISKELAKTTK  
 ATIVPFSTTEKVDGAYVDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN  
 QVIRETLSNFGGVKHLQSLGKVHGISFYNDKSTNIIATQKALSGFDNTKVILAGGLD  
 RSNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD  
 VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6721

STRAIN 2603 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIIVTVNDGKPFDENPTAQSLLLEEGI  
 KVVCGSHPLELLEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQILIGI  
 TGSNGKTTTTMTIAEVLNAGGQRLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK  
 EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNINQMSSSDFLVLNFNQGISKELAKTTK  
 ATIVPFSTTEKVDGAYVDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN  
 QVIRETLSNFGGVKHLQSLGKVHGISFYNDKSTNIIATQKALSGFDNTKVILAGGLD  
 RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD  
 VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

## MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa25243.2{\*} April 29, 2002 02:20 ..

	1		50
msa25243.2{305_18RS21}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_2603}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_JM9130013}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_COH1}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_M732}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_M781}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_1169NT}	-----ITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_A909}	-----ITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_CJB110}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_090}	-----ITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_H36B}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
Consensus	-----****	*****	*****
	51		100
msa25243.2{305_18RS21}	TAQSLLEEGI	KVVCGSHPLE	LLEDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_2603}	TAQSLLEEGI	KVVCGSHPLE	LLEDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_JM9130013}	TAQSLLEEGI	KVVCGSHPLE	LLEDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_COH1}	TAQSLLEEGI	KVVCGSHPLE	LLEDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_M732}	TAQSLLEEGI	KVVCGSHPLE	LLEDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_M781}	TAQSLLEEGI	KVVCGSHPLE	LLEDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_1169NT}	TAQSLLEEGI	KVVCGSHPLE	LLEDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_A909}	TAQSLLEEGI	KVVCGSHPLE	LLEDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_CJB110}	TAQSLLEEGI	KVVCGSHPLE	LLEDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_090}	TAQSLLEEGI	KVVCGSHPLE	LLEDEDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_H36B}	TAQSLLEEGI	KVVCGSHPLE	LLEDEDFCYMI KNPGIPYNNP MVKKALEKQI
Consensus	*****	*****	*****
	101		150
msa25243.2{305_18RS21}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_2603}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_JM9130013}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_COH1}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_M732}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_M781}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_1169NT}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_A909}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_CJB110}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_090}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_H36B}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
Consensus	*****	*****	*****
	151		200
msa25243.2{305_18RS21}	GFPASEVVQA	AnDKDtLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_2603}	GFPASEVVQA	AnDKDtLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_JM9130013}	GFPASEVVQA	AnDKDtLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_COH1}	GFPASEVVQA	AdDKDiLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_M732}	GFPASEVVQA	AdDKDiLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_M781}	GFPASEVVQA	AdDKDiLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_1169NT}	GFPASEVVQA	AdDKDtLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_A909}	GFPASEVVQA	AnDKDtLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_CJB110}	GFPASEVVQA	AdDKDiLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_090}	GFPASEVVQA	AdDKDiLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_H36B}	GFPASEVVQA	AnDKDtLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
Consensus	*****	*-***-*****	*****



Table 67: Comparative Sequences relating to SAG0475

		201					250
msa25243.2{305_18RS21}		GSFEdYVAAK	WNIQNMSSS	DFLVNLFNQG	ISKELAKTTK	ATIVPFSTTE	
msa25243.2{305_2603}		GSFEdYVAAK	WNIQNMSSS	DFLVNLFNQG	ISKELAKTTK	ATIVPFSTTE	
msa25243.2{305_JM9130013}		GSFEdYVAAK	WNIQNMSSS	DFLVNLFNQG	ISKELAKTTK	ATIVPFSTTE	
msa25243.2{305_COH1}		GSFEdYVAAK	WNIQNMSSS	DFLVNLFNQG	ISKELAKTTK	ATIVPFSTTE	
msa25243.2{305_M732}		GSFEdYVAAK	WNIQNMSSS	DFLVNLFNQG	ISKELAKTTK	ATIVPFSTTE	
msa25243.2{305_M781}		GSFEdYVAAK	WNIQNMSSS	DFLVNLFNQG	ISKELAKTTK	ATIVPFSTTE	
msa25243.2{305_1169NT}		GSFEdYVAAK	WNIQNMSSS	DFLVNLFNQG	ISKELAKTTK	ATIVPFSTTE	
msa25243.2{305_A909}		GSFEdYVAAK	WNIQNMSSS	DFLVNLFNQG	ISKELAKTTK	ATIVPFSTTE	
msa25243.2{305_CJB110}		GSFEdYVAAK	WNIQNMSSS	DFLVNLFNQG	ISKELAKTTK	ATIVPFSTTE	
msa25243.2{305_090}		GSFEdYVAAK	WNIQNMSSS	DFLVNLFNQG	ISKELAKTTK	ATIVPFSTTE	
msa25243.2{305_H36B}		GSFEdYVAAK	WNIQNMSSS	DFLVNLFNQG	ISKELAKTTK	ATIVPFSTTE	
Consensus		****-*****	*****	*****	*****	*****	
		251					300
msa25243.2{305_18RS21}		KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN	
msa25243.2{305_2603}		KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN	
msa25243.2{305_JM9130013}		KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN	
msa25243.2{305_COH1}		KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN	
msa25243.2{305_M732}		KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN	
msa25243.2{305_M781}		KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN	
msa25243.2{305_1169NT}		KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN	
msa25243.2{305_A909}		KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN	
msa25243.2{305_CJB110}		KVDGAYVQDK	QLFYKGENIM	lVDDIGVPGS	HNVeNALATI	AVAKLAGISN	
msa25243.2{305_090}		KVDGAYVQDK	QLFYKGENIM	lVDDIGVPGS	HNVeNALATI	AVAKLAGISN	
msa25243.2{305_H36B}		KVDGAYVQDK	QLFYKGENIM	sVDDIGVPGS	HNVeNALATI	AVAKLAGISN	
Consensus		*****	*****	-*****	*****	*****	
		301					350
msa25243.2{305_18RS21}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt	
msa25243.2{305_2603}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt	
msa25243.2{305_JM9130013}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt	
msa25243.2{305_COH1}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt	
msa25243.2{305_M732}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt	
msa25243.2{305_M781}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt	
msa25243.2{305_1169NT}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt	
msa25243.2{305_A909}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt	
msa25243.2{305_CJB110}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt	
msa25243.2{305_090}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt	
msa25243.2{305_H36B}		QVIRETLSNF	GGVKHRLQSL	GKVHGISFYN	DSKstnilat	qkalsgfdnt	
Consensus		*****	*****	*****	***-----	-----	
		351					400
msa25243.2{305_18RS21}		kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys	
msa25243.2{305_2603}		kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys	
msa25243.2{305_JM9130013}		kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys	
msa25243.2{305_COH1}		kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys	
msa25243.2{305_M732}		kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys	
msa25243.2{305_M781}		kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys	
msa25243.2{305_1169NT}		kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys	
msa25243.2{305_A909}		kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys	
msa25243.2{305_CJB110}		kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys	
msa25243.2{305_090}		kviliaggld	rgnefdelip	ditglkhmvv	lgesasrvkr	aaqkagvtys	
msa25243.2{305_H36B}		-----	-----	-----	-----	-----	
Consensus		-----	-----	-----	-----	-----	
		401					450
msa25243.2{305_18RS21}		daldvrdavh	kayevagggd	villspanas	wdmyknfevr	gdefidtfes	
msa25243.2{305_2603}		daldvrdavh	kayevagggd	villspanas	wdmyknfevr	gdefidtfes	
msa25243.2{305_JM9130013}		daldvrdavh	kayevagggd	villspanas	wdmyknfevr	gdefidtfes	
msa25243.2{305_COH1}		daldvrdavh	kayevagggd	villspanas	wdmyknfevr	gdefidtfes	
msa25243.2{305_M732}		daldvrdavh	kayevagggd	villspanas	wdmyknfevr	gdefidtfes	
msa25243.2{305_M781}		daldvrdavh	kayevagggd	villspanas	wdmyknfevr	gdefidtfes	
msa25243.2{305_1169NT}		naldvrdavh	kayevagggd	villxspanas	wdmyknfevr	gdefidtfes	
msa25243.2{305_A909}		daldvrdavh	kayevagggd	villspanas	wdmyknfevr	gdefidtfes	
msa25243.2{305_CJB110}		daldvrdavh	kayevagggd	villspanas	wdmyknfevr	gdefidtfes	
msa25243.2{305_090}		daldvrdavh	kayevagggd	villspanas	wdmyknfevr	gdefidtfes	
msa25243.2{305_H36B}		-----	-----	-----	-----	-----	
Consensus		-----	-----	-----	-----	-----	
		451					
msa25243.2{305_18RS21}		lrge					
msa25243.2{305_2603}		lrge					
msa25243.2{305_JM9130013}		lrge					
msa25243.2{305_COH1}		----					
msa25243.2{305_M732}		lrge					
msa25243.2{305_M781}		lrge					
msa25243.2{305_1169NT}		----					
msa25243.2{305_A909}		lrge					
msa25243.2{305_CJB110}		lrge					
msa25243.2{305_090}		lrge					
msa25243.2{305_H36B}		----					
Consensus		----					

Table 68: Comparative Sequences relating to SAG 0499

## SEQ ID NO. 6801

## STRAIN 2603

ATGGCTAAAGAGAGGGTAGATGTTCTTGCCTATAAACAGGGACTTTTGTATACACGAGAG  
CAAGCGAAACGTTGGTGTATGGCAGGAATGGTGTATTAACGTTATCAATGGAGAACGTTAT  
GATAAACCGAGGTGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTA  
AAATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTGAAATTTCA  
GTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTTACTGATGTTATG  
CTACAATCAGGAGCGCGTTTAGTTTACGCGAGTAGATGTAGGAACAAATCAATTAGTTTGG  
AAGTTACGTCAGGATCATCGTGTTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAA  
AAAGAAGATTTCAAGGAGGACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCT  
CTTAATTTGATTTTACCAGCTCTAAAAGAAATTTAGTGGATGGTGGACAAGTAGTGGCA  
TTAATTAACCAATTTGAAAGCAGGTGCTGAGCAAATTTGGTAAAATGTTATGTCAAA  
GACAAGTTGGTTTCATGAAAAGGTTTTCACAACAGTGACCAATTTACGAAAAGATTATGGA  
TATACGGTTAAACATCTTGATTTTTCGCCCATTCAGGTGGACATGGAAATATTGAGTTT  
TTAATGCATTTGCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAATACAGAT  
GTTATAGAAAAGCACATAAGGAATTTAAGAAAATGAAGAAGAG

## SEQ ID NO. 6802

## STRAIN 090

GCTAAAGAGAGGGTAGATGTTCTTGCCT  
ATAAACAGGGACTTTTGTATACACGAGAGCAAGCGAAACGTTGGTGTATG  
GCAGGAATGGTGATTAACTTATCAATGGAGAACGTTATGATAAACAGG  
TGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAA  
AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTT  
GAAATTTAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG  
TGGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG  
TAGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGTCAGGATCATCGT  
GTTGCTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAGAGATTT  
CAAGGAGGAGCTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTC  
TTAATTTGATTTTACCAGCTCTAAAAGAAATTTAGTGGATGGTGGACAA  
GTAGTGGCATTAAATTAACCAATTTGAAGCAGGTGCTGAGCAAATTTGG  
TAAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAA  
CAGTGACCAATTTACGAAAAGATTATGGATATACGGTTAAACATCTTGAT  
TTTTCGCCCATTCAGGTGGACATGGAATATTGAGTTTTTAATGCATTT  
GCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAATACAGATG  
TTATAGAAAAGCACATAAGGAATTTAAGAAAATGAAGAAGAG

## SEQ ID NO. 6803

## STRAIN A909

GCTAAAGAGAGGGTAGATGTTCTTGCCTA  
TAAACAGGGACTTTTGTATACACGAGAGCAAGCGAAACGTTGGTGTATGG  
CAGGAATGGTGATTAACTTATCAATGGAGAACGTTATGATAAACAGGT  
GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAAA  
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG  
AAATTTCAAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG  
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT  
AGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGTCAGGATCATCGTG  
TTGCTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAGAGATTTT  
AAGGAGGAGCTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTCT  
TAATTTGATTTTACCAGCTCTAAAAGAAATTTAGTGGATGGTGGACAAG  
TAGTGGCATTAAATTAACCAATTTGAAGCAGGTGCTGAGCAAATTTGGT  
AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAA  
AGTGACCAATTTACGAAAAGATTATGGATATACGGTTAAACATCTTGAT  
TTTTCGCCCATTCAGGTGGACATGGAATATTGAGTTTTTAATGCATTTG  
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAATACAGATGT  
TATAGAAAAGCACATAAGGAATTTAAGAAAATGAAGAAGAG

## SEQ ID NO. 6804

## STRAIN H36B

GCTAAAGAGAGGGTAGATGTTCTTGCCTATAAACAGG  
GACTTTTGTATACACGAGAGCAAGCGAAACGTTGGTGTATGGCAGGAATG  
GTGATTAACTTATCAATGGAGAACGTTATGATAAACAGGTGAAAAGGT  
TGCAAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAAAATATGTTA  
GTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTGAAATTTCA  
GTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTTAC  
TGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCGATAGATGTAG  
GAACAAATCAATTAGTTTGGAAAGTTACGTCAGGATCATCGTGTTCGTTCT  
ATGGAACAATATAATTTTAGGTATGCCCAAAAGAGATTTCAAGGAGGG  
ACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTCTTAATTTGA  
TTTACCAGCTCTAAAAGAAATTTAGTGGATGGTGGACAAGTAGTGGCA  
TTAATTAACCAATTTGAAGCAGGTGCTGAGCAAATTTGGTAAAAATGG  
TATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAACAGTGACCA  
ATTTACGAAAAGATTATGGATATACGGTTAAACATCTTGATTTTTCGCCC  
ATTCAGGTGGACATGGAATATTGAGTTTTTAATGCATTTGCAAAAGTG  
TCAGATCCACAAAATCTTGTGCTTGACCAATACAGATGTTATAGAAA  
AAGCACATAAGGAATTTAAGAAAATGAAGAAGAG

## SEQ ID NO. 6805

## STRAIN 18RS21

GCTAAAGAGAGGGTAGATGTTCTTGCCTA  
TAAACAGGGACTTTTGTATACACGAGAGCAAGCGAAACGTTGGTGTATGG  
CAGGAATGGTGATTAACTTATCAATGGAGAACGTTATGATAAACAGGT

Table 68: Comparative Sequences relating to SAG 0499

GAAAAGGTTGCAGACGATACTGAATTAAACTAAAAGGTGAAAACTAAA  
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTGTG  
 AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT  
 GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT  
 AGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGT CAGGATCATCGTG  
 TTCGTTCTATGGAACAAATATAATTTAGGTATGCCCAAAAGAAGATTTC  
 AAGGAGGACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTCT  
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG  
 TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCGTGAGCAAATGGT  
 AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTGGACAAC  
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT  
 TTTCCGCCATTCAAGGTGGACATGGAATATTGAGTTTAAATGCATTTG  
 CAAAAGTGTCAAGATCCACAAATCTTGTGCTTGACCAAAATACAAGATGT  
 TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

## SEQ ID NO. 6806

## STRAIN M732

GCTAAAGAGAGGGTAGATGTTCTTGCCTA

TAAACAGGGACTTTTGTATACAGAGAGCAAGCGAAACGTGGTGTATGG  
 CAGGACTGGTGATTAACTGTTATCAATGGAGAACGTTATGATAAACAGGC  
 GAAAAGGTTGCAGACGATACTGAATTAATACTAAAAGGTGAAAACTAAA  
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTGTG  
 AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT  
 GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT  
 AGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGT CAGGATCATCGTG  
 TTCGTTCTATGGAACAAATATAATTTAGGTATGCCCAAAAGAAGATTTC  
 AAGGAGGACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTCT  
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG  
 TAGTGGCATTAAATTAACCAACAATTTGAAGCAGGTCGTGAGCAAATGGT  
 AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTGGACAAC  
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT  
 TTTCCGCCGTTCAAGGTGGACATGGAATATTGAGTTTAAATGCATTTG  
 CAAAAGTGTCAAGATCCACAAATCTTGTGCTTGACCAAAATACAAGATGT  
 TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

## SEQ ID NO. 6807

## STRAIN COH1

GCTAAAGAGAGGGTAGATGTTCTTGCCT

ATAAACAGGGACTTTTGTATACAGAGAGCAAGCGAAACGTGGTGTATG  
 GCAGGACTGGTGATTAACTGTTATCAATGGAGAACGTTATGATAAACAGG  
 CGAAAAGGTTGCAGACGATACTGAATTAATACTAAAAGGTGAAAACTAA  
 AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTGT  
 GAAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG  
 TGGTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG  
 TAGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGT CAGGATCATCGT  
 GTTCGTTCTATGGAACAAATATAATTTAGGTATGCCCAAAAGAAGATTTC  
 CAAGGAGGACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTC  
 TTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAA  
 GTAGTGGCATTAAATTAACCAACAATTTGAAGCAGGTCGTGAGCAAATGG  
 TAAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTGGACAA  
 CAGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGAT  
 TTTTCGCCCGTTCAAGGTGGACATGGAATATTGAGTTTAAATGCATTT  
 GCAAAAGTGTCAAGATCCACAAATCTTGTGCTTGACCAAAATACAAGATG  
 TTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

## SEQ ID NO. 6808

## STRAIN M781

GCTAAAGAGAGGGTAGATGTTCTTGCCT

ATAAACAGGGACTTTTGTATACAGAGAGCAAGCGAAACGTGGTGTATG  
 GCAGGACTGGTGATTAACTGTTATCAATGGAGAACGTTATGATAAACAGG  
 CGAAAAGGTTGCAGACGATACTGAATTAATACTAAAAGGTGAAAACTAA  
 AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTGT  
 GAAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG  
 TGGTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG  
 TAGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGT CAGGATCATCGT  
 GTTCGTTCTATGGAACAAATATAATTTAGGTATGCCCAAAAGAAGATTTC  
 CAAGGAGGACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTC  
 TTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAA  
 GTAGTGGCATTAAATTAACCAACAATTTGAAGCAGGTCGTGAGCAAATGG  
 TAAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTGGACAA  
 CAGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGAT  
 TTTTCGCCCGTTCAAGGTGGACATGGAATATTGAGTTTAAATGCATTT  
 GCAAAAGTGTCAAGATCCACAAATCTTGTGCTTGACCAAAATACAAGATG  
 TTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

## SEQ ID NO. 6809

## STRAIN CJB110

GCTAAAGAGAGGGTAGATGTTCTTGCCTA

TAAACAGGGACTTTTGTATACAGAGAGCAAGCGAAACGTGGTGTATGG  
 CAGGAATGGTGATTAACTGTTATCAATGGAGAACGTTATGATAAACAGGT  
 GAAAAGGTTGCAGACGATACTGAATTAATACTAAAAGGTGAAAACTAAA  
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTGTG  
 AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT

Table 68: Comparative Sequences relating to SAG 0499

GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTAGTTTACGCAGT  
 AGATGTAGGAACAAATCAATTAGTTTGGAGTTACGTCAGGATCATCGTG  
 TTCGTTCTATGGAACAATATAATTTTAGGTATGCCAAAAAGAGATTTC  
 AAGGAGGGAGCTGCCTGAATTTGCATCGATAGATGTCATTATCTCTCT  
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG  
 TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCGTGAGCAAATTTGGT  
 AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAAC  
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT  
 TTTTCGCCCATTCAGGTTGACATGGAAATATTGAGTTTTAATGCATTTG  
 CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT  
 TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6810

STRAIN 1169NT

GCTAAAGAGAGGGTAGATGTTCTTGCCTA

TAAACAGGGACTTTTGTATACACGAGAGCAAGCAACGTTGGTGTATGG  
 CAGGACTGGTGATTACGTTATCAATGGAGAACGTTATGATAAACAGGC  
 GAAAAGGTTGCAGACGATCTGAATTAAGCTAAAAGGTTGAAAACTAAA  
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG  
 AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCTCTACGGGT  
 GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT  
 AGATGTAGGAACAAATCAATTAGTTTGGAGTTACGTCAGGATCATCGTG  
 TTCGTTCTATGGAACAATATAATTTTAGGTATGCCAAAAAGAGATTTC  
 AAGGAGGGAGCTGCCTGAATTTGCATCGATAGATGTCATTATCTCTCT  
 TAATTTGATTTTGCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG  
 TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCGTGAGCAAATTTGGT  
 AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAAC  
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT  
 TTTTCGCCCATTCAGGTTGACATGGAAATATTGAGTTTTAATGCATTTG  
 CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT  
 TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6811

STRAIN JM9130013

GCTAAAGAGAGGGTAGATGTTCTTGCCTA

TAAACAGGGACTTTTGTATACACGAGAGCAAGCAACGTTGGTGTATGG  
 CAGGAATGGTGATTAAACGTTATCAATGGAGAACGTTATGATAAACAGGT  
 GAAAAGGTTGCAGACGATCTGAATTAAGCTAAAAGGTTGAAAACTAAA  
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG  
 AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCTCTACGGGT  
 GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT  
 AGATGTAGGAACAAATCAATTAGTTTGGAGTTACGTCAGGATCATCGTG  
 TTCGTTCTATGGAACAATATAATTTTAGGTATGCCAAAAAGAGATTTC  
 AAGGAGGGAGCTGCCTGAATTTGCATCGATAGATGTCATTATCTCTCT  
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG  
 TAGTGGCATTAAATTAACCACAATTTGAAGCAGGTCGTGAGCAAATTTGGT  
 AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAAC  
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT  
 TTTTCGCCCATTCAGGTTGACATGGAAATATTGAGTTTTAATGCATTTG  
 CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT  
 TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

PRETTY of: /biotmp/msa236683.2{\*} May 14, 2003 02:57 ..

	1		50
msa236683.2{310_090}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_18R521}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_2603}	atgGCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_A909}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_CJB110}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_H36B}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_JM9130013}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_COH1}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_M732}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_M781}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_1169NT}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
Consensus	*****	*****	*****
	51		100
msa236683.2{310_090}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_18R521}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_2603}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_A909}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_CJB110}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_H36B}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_JM9130013}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_COH1}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_M732}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_M781}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_1169NT}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
Consensus	*****	*****	*****

Table 68: Comparative Sequences relating to SAG 0499

		101			150
msa236683.2{310_090}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_18RS21}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_2603}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_A909}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_CJB110}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_H36B}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_JM9130013}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_COH1}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GcGAAAAGGT	TGCAGACGAT
msa236683.2{310_M732}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GcGAAAAGGT	TGCAGACGAT
msa236683.2{310_M781}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GcGAAAAGGT	TGCAGACGAT
msa236683.2{310_1169NT}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GcGAAAAGGT	TGCAGACGAT
Consensus		*****	*****	*****	*****
		151			200
msa236683.2{310_090}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG
msa236683.2{310_18RS21}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG
msa236683.2{310_2603}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG
msa236683.2{310_A909}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG
msa236683.2{310_CJB110}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG
msa236683.2{310_H36B}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG
msa236683.2{310_JM9130013}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG
msa236683.2{310_COH1}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG
msa236683.2{310_M732}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG
msa236683.2{310_M781}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG
msa236683.2{310_1169NT}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTTA	GTAGAGGTGG
Consensus		*****	*****	*****	*****
		201			250
msa236683.2{310_090}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_18RS21}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_2603}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_A909}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_CJB110}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_H36B}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_JM9130013}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_COH1}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_M732}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_M781}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_1169NT}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
Consensus		*****	*****	*****	*****
		251			300
msa236683.2{310_090}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_18RS21}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_2603}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_A909}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_CJB110}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_H36B}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_JM9130013}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_COH1}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_M732}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_M781}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_1169NT}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
Consensus		*****	*****	*****	*****
		301			350
msa236683.2{310_090}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_18RS21}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_2603}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_A909}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_CJB110}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_H36B}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_JM9130013}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_COH1}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_M732}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_M781}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_1169NT}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
Consensus		*****	*****	*****	*****
		351			400
msa236683.2{310_090}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_18RS21}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_2603}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_A909}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_CJB110}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_H36B}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_JM9130013}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_COH1}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_M732}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_M781}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_1169NT}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
Consensus		*****	*****	*****	*****

Table 68: Comparative Sequences relating to SAG 0499

		401			450
msa236683.2{310_090}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_18RS21}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_2603}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_A909}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_CJB110}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_H36B}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_JM9130013}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_COH1}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_M732}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_M781}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_1169NT}	ATAATTTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
Consensus	*****	*****	*****	*****	*****
		451			500
msa236683.2{310_090}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_18RS21}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_2603}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_A909}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_CJB110}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_H36B}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_JM9130013}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_COH1}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_M732}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_M781}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_1169NT}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
Consensus	*****	*****	*****	*****	*****
		501			550
msa236683.2{310_090}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_18RS21}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_2603}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_A909}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_CJB110}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_H36B}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_JM9130013}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_COH1}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_M732}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_M781}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_1169NT}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
Consensus	*****	*****	*****	*****	*****
		551			600
msa236683.2{310_090}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_18RS21}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_2603}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_A909}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_CJB110}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_H36B}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_JM9130013}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_COH1}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_M732}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_M781}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_1169NT}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
Consensus	*****	*****	*****	*****	*****
		601			650
msa236683.2{310_090}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_18RS21}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_2603}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_A909}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_CJB110}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_H36B}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_JM9130013}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_COH1}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_M732}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_M781}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
msa236683.2{310_1169NT}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTCAACGAA
Consensus	*****	*****	*****	*****	*****
		651			700
msa236683.2{310_090}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_18RS21}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_2603}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_A909}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_CJB110}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_H36B}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_JM9130013}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_COH1}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_M732}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_M781}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_1169NT}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG

Table 68: Comparative Sequences relating to SAG 0499

Consensus	*****	*****	*****	*****	*****	*****
	701					750
msa236683.2{310_090}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_18RS21}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_2603}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_A909}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_CJB110}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_H36B}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_JM9130013}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_COH1}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_M732}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_M781}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_1169NT}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
Consensus	*****	*****	*****	*****	*****	*****
	751					800
msa236683.2{310_090}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_18RS21}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_2603}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_A909}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_CJB110}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_H36B}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_JM9130013}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_COH1}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_M732}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_M781}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_1169NT}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
Consensus	*****	*****	*****	*****	*****	*****
	801					825
msa236683.2{310_090}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_18RS21}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_2603}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_A909}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_CJB110}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_H36B}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_JM9130013}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_COH1}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_M732}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_M781}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_1169NT}	GGAATTTAAG	AAAAATGAAG	AAGAG			
Consensus	*****	*****	*****			
<b>SEQ ID NO. 6812</b>						
<b>STRAIN 2603 frame: 1</b>						
MAKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTTELKLKGEKLEK						
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK						
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL						
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL						
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEB						
<b>SEQ ID NO. 6813</b>						
<b>STRAIN 090 frame: 1</b>						
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTTELKLKGEKLEK						
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK						
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL						
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL						
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEB						
<b>SEQ ID NO. 6814</b>						
<b>STRAIN A909 frame: 1</b>						
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTTELKLKGEKLEK						
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK						
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL						
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL						
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEB						
<b>SEQ ID NO. 6815</b>						
<b>STRAIN 18RS21 frame: 1</b>						
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTTELKLKGEKLEK						
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK						
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL						
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL						
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEB						
<b>SEQ ID NO. 6816</b>						
<b>STRAIN M732 frame: 1</b>						
AKERVDVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTTELKLKGEKLEK						
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK						
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL						

Table 68: Comparative Sequences relating to SAG 0499

IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL  
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6817

STRAIN COH1 frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLG  
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK  
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL  
IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL  
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6818

STRAIN M781 frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLG  
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK  
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL  
IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL  
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6819

STRAIN CJB110 frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLG  
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK  
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL  
IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL  
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6820

STRAIN 1169NT frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLG  
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK  
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL  
IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL  
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6821

STRAIN JM9130013 frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLG  
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK  
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL  
IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL  
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6822

STRAIN H36B frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLG  
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK  
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL  
IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL  
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

PRETTY of: /biotmp/msa236800.2{\*} May 14, 2003 02:58 ..

	1		50
msa236800.2{310_090}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_18R21}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_2603}	mAKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_A909}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_CJB110}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_H36B}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_JM9130013}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_COH1}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGl VINVINGERY DKPGEKVADD
msa236800.2{310_M732}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGl VINVINGERY DKPGEKVADD
msa236800.2{310_M781}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGl VINVINGERY DKPGEKVADD
msa236800.2{310_1169NT}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGl VINVINGERY DKPGEKVADD
Consensus	*****	*****	*****

  

	51		100
msa236800.2{310_090}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_18R21}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_2603}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_A909}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_CJB110}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_H36B}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_JM9130013}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_COH1}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_M732}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_M781}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_1169NT}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
Consensus	*****	*****	*****

101

150



Table 68: Comparative Sequences relating to SAG 0499

msa236800.2{310_090}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_18RS21}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_2603}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_A909}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_CJB110}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_H36B}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_JM9130013}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_COH1}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_M732}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_M781}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_1169NT}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
Consensus	*****	*****	*****	*****	*****
151					
msa236800.2{310_090}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_18RS21}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_2603}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_A909}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_CJB110}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_H36B}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_JM9130013}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_COH1}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_M732}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_M781}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_1169NT}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
Consensus	*****	*****	*****	*****	*****
201					
msa236800.2{310_090}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_18RS21}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_2603}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_A909}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_CJB110}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_H36B}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_JM9130013}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_COH1}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	vQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_M732}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	vQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_M781}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	vQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_1169NT}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
Consensus	*****	*****	*****	*****	*****
251					
msa236800.2{310_090}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_18RS21}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_2603}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_A909}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_CJB110}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_H36B}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_JM9130013}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_COH1}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_M732}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_M781}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_1169NT}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
Consensus	*****	*****	*****		
275					

Table 69: Comparative Sequences relating to SAG0032

SEQ ID NO. 6901

STRAIN 2603

ATGAATAAAAAGGTACTATTGACATCGACAATGGCAGCTTCGCTATTATCAGTCGCAAGT  
 GTTCAAGCACAAAGAACAGATACGACGTGGACAGCAGTACTGTTTCAGAGGTAAGGCT  
 GATTGGTAAAGCAAGACAAATAATCATCATATACTGTGAAATATGGTGATACACTAAGC  
 GTTATTTTCAGAAGCAATGTCAATTGATATGAATGTCTTAGCAAAAATAAATAACATTGCA  
 GATATCAATCTTATTATCTCTGAGACAACACTGACAGTAACCTACGATCAGAAGAGTCAT  
 ACTGCCACTTCAATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCT  
 ACTGTGGATTTGAAAACCAATCAAGTTTCTGTGTCAGACCAAAAAGTTTCTCTCAATACA  
 ATTTTCGAAGGTATGACACCAGAAGCAGCAACACGATTGTTTCGCCAATGAAGACATAT  
 TCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTATTAGCACAAGAGCAAGCTGTTAGTCAA  
 GCAGCAGCTAATGAACAGGTATCACCAGCTCCTGTGAAGTCGATTACTTCAGAAAGTTCCA  
 GCAGCTAAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCA  
 CCAGCTTCTGTTGCCGTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCCGGTAAGAACT  
 GTAGCAGCCCCTAGAGTGGCAAGTGTAAAGTAGTCACTCCTAAAGTAGAACTGGTGCA  
 TCACCAGAGCATGTATCAGCTCCAGCAGTTCTGTGACTACGACTTCACCAGCTACAGAC  
 AGTAAGTTACAAGCGACTGAAGTTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCA  
 ACACCGGTAGCACAAACAGCTTCAACAACAAATGCAGTAGCTGCACATCTGAAAATGCA  
 GGGCTCCAACCTCATGTTGCGAGCTTATAAAGAAAAAGTAGCGTCAACTTTATGGAGTTAAT  
 GAATTCAGTACATACCTGCGGGAGATCCAGGTGATCATGGTAAAGGTTTAGCAGTTGAC  
 TTTATTTAGGTACTAATCAAGCACTTGGTAATAAAGTTGCACAGTACTTACACAAAAT  
 ATGCGAGCAAAATACAACTTTCATATGTTATCTGGCAACAAAAGTTTACTCAAATACAAAC  
 AGTATTTATGGAGCTGCTAATACCTTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCC  
 AACCCTATGACCAGCTTCAGTATCATTTAAACAAATAATATAAAAAAGGAAGCTATTTCG  
 GCTTCTTTTATATGCTTGAATAGACTTTCAGGTTCTTATATAATTTTATTA

SEQ ID NO. 6902

STRAIN 090

TGAGACAACACTGACAGTAACCTACGATCAGAAGAGTCATACTGCCACTT  
 CAATGAAAATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACACCAGCT  
 ACTGTGGATTTGAAAACCAATCAAGTTTCTGTGTCAGACCAAAAAGTTTC  
 TCTCAATACAATTTCCGAAGGTATGACACCAGAAGCAGCAACACAGATTG  
 TTTCCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAGAA  
 GTATTAGCACAAAGAGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGT  
 ATCAACAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAG  
 AGGAAGTTAAACCACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCA  
 CCAGCTTCTGTTGCCGTGAAACACCAGCTCCAGTAGCTAAAGTAGCACC  
 GGTAAGAACTGTAGCAGCCCTAGAGTGGCAAGTGTAAAGTAGTCACTC  
 CTAAAGTAGAAACTGGTGATCACCAGAGCATGTATCAGCTCCAGCAGTT  
 CCTGTGACTACGACTTCAACAGCTACAGACAGTAAGTTACAAGCGACTGA  
 AGTTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAG  
 CACAACAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCA  
 GGGCTCCAACCTCATGTTGCGAGCTTATAAAGAAAAAGTAGCGTCAACTTA  
 TGGAGTTAATGAATTCACTACATACCGTGCAGGTGATCCAGGTGATCATG  
 GTAAGGTTTAGCAGTCGACTTTATTGTAGGTAACCAAGCACTTGGT  
 AATGAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAAATAACATTTT  
 ATATGTTATCTGGCAACAAAAGTTTACTCAAATACAAATAGTATTATG  
 GACCTGCTAATACTTGAATGCAATGCCAGATCGTGGTGGCGTTACTGCC  
 AACCATTATGACCAGTGTTCAGTATCATTTAAACAAATAATATAAAAAAGG  
 AAGCTATTGGCTTCTTTTATATGCTTGAATAGACTTTCAGGTTCT  
 TATATAAATTTTATTA

SEQ ID NO. 6903

STRAIN A909

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAA  
 ATATGGTGATACACTAAGCGTTATTTTCAGAAGCAATGTCAATTGATATGA  
 ATGTCTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCT  
 GAGACAACACTGACAGTAACCTACGATCAGAAGAGTCATACTGCTACTTC  
 AATGAAAATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTA  
 CTGTGATTTGAAAACCAATCAAGTTTCTGTGTCAGACCAAAAAGTTTCT  
 CTCATACAAATTTCCGAAGGTATGACACCAGAAGCAGCAACACGATTTGT  
 TTCGCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAGAA  
 TATTAGCACAAAGGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTA  
 TCACAGCTCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGA  
 GGAAGTTAAACCACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCAC  
 CAGCTTCTGTTGCCGTGAAACACCAGCTCCAGTAGCTAAAGTAGCACC  
 GTAAGAACTGTAGCAGCCCTAGAGTGGCAAGTGTAAAGTAGTCACTCC  
 TAAAGTAGAACTGGTGATCACCAGAGCATGTATCAGCTCCAGCAGTTT  
 CTGTGACTACGACTTCAACAGCTACAGACAGTAAGTTACAAGCGACTGAA  
 GTTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGC  
 ACAACAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCA  
 GGGCTCCAACCTCATGTTGCGAGCTTATAAAGAAAAAGTAGCGTCAACTTA  
 GGAGTTAATGAATTCAGTACATACCGTGCAGGAGATCCAGGTGATCATGG  
 TAAAGGTTTAGCAGTTGACTTTATTGTAGGTAACCAAGCACTTGGTA  
 ATGAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAAATAACATTTCA  
 TATGTTATCTGGCAACAAAAGTTTACTCAAATACAAATAGTATTATG  
 ACCCTGCTAATACTTGAATGCAATGCCAGATCGTGGTGGCGTTACTGCC  
 ACCCATATGACCAGTTCAGTATCATTTAAACAAATAATATAAAAAAGGA  
 AGCTATTGGCTTCTTTTATATGCTTGAATAGACTTTCAGGTTCTT  
 ATATAAATTTTATTA

SEQ ID NO. 6904

STRAIN H36B

Table 69: Comparative Sequences relating to SAG0032

CTGATTGGTAAAGCAAGACAATAAATCATCATATAcTGTGAAATA  
 TGGTGATACAcTAAGCGTTATTTGAGAAGCAATGTCaATTGATATGAATG  
 TCTTAGCAAAAATTAAATACATTGCAGATATCAATCTTATTTATCCTGAG  
 ACAACaCTGaCAGTAaCTTACGATCAGAAGAGTCATACTGCTACTTCAAT  
 GAAAAATAGAAACACCAGCAACAATGCTGCTGGTCAAAACACAGCTACTG  
 TCGATTGGAAAACCAATCAAGTTTCGTGTGCAGACCAAAAAGTTCTCTC  
 AATACAATTTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTC  
 GCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTAT  
 TAGCACAAGGGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTATCA  
 CCAGCTCCTGTGAAGTCGATTACTTCAGAAGTCCAGCAGCTAAAGAGGA  
 AGTTAAACCAACTCAGACCTCAGTCAGTCAGTCAGTCAACAACAGTATCACCAG  
 CTTCTGTGCGCTGAAACACCAGCTCCAGTAGcTAAAGTAGCACCAGTA  
 AGAATCTGTAGCAGCCCTAGAGTGGCAAGTGTAAAGTAGTCACTCCTAA  
 AGTAGAAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCCTG  
 TGACTACGACTTCAACAGCTACAGACAGTAAGTTACAAGCGACTGAAGTT  
 AAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGCACA  
 ACCAGCTTCAACAACAATGCGAGTAGCTGCACATCCTGAAAAATGCAAGGC  
 TCCAACCTCATGTTGCAGCTTATAAGAAAAAGTAGCGTCAACTTATGGA  
 GTTAATGAATTCACTACATACCGTGCAGGAGATCCAGGTGATCATGGTAA  
 AGGTTTAGCAGTTGACTTTATTGTAGGTAAAAACCAAGCACTTGGTAAATG  
 AAGTTGCACAGTACTCTACACAAAATaTGGCAGCAAAATACATTTTATAT  
 GTTATCTGGCaaCAAAAAGTTTACTCAAAATACAAATAGTATTTATGGACC  
 TGCTAATACTTGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCC  
 ACTATGACCAGCTTCAGTATCATTTAACAATAATATAAAAAAGGAAGC  
 TATTGGCTTCTTTTATATGCCTTGCATAGACcTTCAAGGTTCTTATA  
 TAATTTTATTA

SEQ ID NO. 6905

STRAIN 18RS21

CTGATTGGTAAAGCAAGACAAT  
 AAATCATCATATACCTGTGAAATATGGTGATACAcTAAGcGTTATTTGAGA  
 AGCAATGTCAATTGATATGAATGCTCTTAGCAAAAaTAAATAACATTGCAG  
 ATATCAATCTTATTTATCCTGAGACAAcCTGaCAGTAACCTTACGATCAG  
 AAGAGTCATACTGCCaCTTCAATGAAATAGAAACACCAGCAaCAAAATGC  
 TGCTGGTCAaACAaCAGCTACTGTGGATTGAAAACCAATCAaGTTTCTG  
 TTGCAGACCAAAAAGTTTCTCTCAATACAATTTTCGGAAGGTATGACACCA  
 GAAGCAGCAACAACGATTGTTTTCGCCAATGAAGACaTATTCTTCTGCGCC  
 AGCTTTGAAaTCAAAAGAAGTATTAGCACAAAGAGCAAGCTGTTAGTCAAG  
 CAGCAGCTAATGAACAGGTATCACCAGCTCCTGTGAAGTCGATTACTTCA  
 GAAGTTCCAGCAGCTAAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAG  
 TCAGTCAACAACAGTATCACCAGCTTCTGTTGCGCTGAAACACCAGCTC  
 CAGTAGCTAAAGTAGCACCGGTAAAGAACTGTAGCAGCCCTAGAGTGGCA  
 AGTGTAAAGTAGTCACTCCTAAAGTAGAAACTGGTGCATCACCAGAGCA  
 TGTATCAGCTCCAGCAGTTCCTGTGACTACGACTTCACCAGCTACAGACA  
 GTAAGTTACAAGCGACTGAAGTTAAGAGCGTTCCGGTAGCACAAAAGCT  
 CCAACAGCAACACCGGTAGCACAAACCAGCTTCAACAACAATGCAGTAGC  
 TGCACATCCTGAAATGCAGGGCTCCAACCTCATGTTGCAGCTTATAAAG  
 AAAAAGTAGCGTCAACTTATGGAGTTAATGAATTCACTACATACCGTGGC  
 GGAGATCCAGGTGATCATGGTAAAGGTTTAGCAGTTGACTTTATTGTAGG  
 TACTAATCAAGCACTTGGTAATAAAGTTGCACAGTACTcTACACAAAATA  
 TGGCAGCAAAATAACATTTATATGTTATCTGGCAACAAAAGTTTACTCA  
 AATACAAACAGTATTTATGGACCTGCTAATCTTGAATGCAATGCCAGA  
 TCGTGGTGGCGTTACTGCCAACCACTATGACCAGCTTACGTATCATTTA  
 ACAATAATATAAAAAAGGAAGCTATTGGCTTCTTTTTATATGCCTTG  
 AATAGACTTTCAAGGTTCTTATATAATTTTATTA

SEQ ID NO. 6906

STRAIN COH1

CTGATT  
 GGTAAAGCAAGACAATAAATCATCATATACCTGTGAAATATGGTGATACAC  
 TAAGCGTTATTTGAGAAGCAATGTCAATTGATATGAATGTCTTAGCAAAA  
 ATTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAACTGAC  
 AGTAACCTTACGATCAGAAGAGTCATACTGCCACTTCAATGAAATAGAAA  
 CACCAGCAACAATGCTGCTGGTCAAAACAACAGcTACTGTCTGATTGAAA  
 ACCAATCAAGTTTTGTTGCAGACCAAAAAGTTTCTCTCAATACAATTC  
 GGAAGGTATGACACCAGaaGCAGCAACAACGATTGTTTTCGCCAATGAAGA  
 CaTATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTATTAGCACAAAGAG  
 CAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAGCTCCTGT  
 GAAGTCGATTACTTCAAGAGTCCAGCAGCTAAAGAGGAAGTTAAACCA  
 CTCAGACGTCAGTCAGTCAGTTAACAACAGTATCACCAGCTTCTGTTGCC  
 GCTGAAACACCAGCTCCAGTAGCTAAGTAGCACCGGTAAAGAACTGTAGC  
 AGCCCCTAGAGTGGCAAGTGcTAAAGTAGTCACTCCTAAAGTAGAACTG  
 GTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCCTGTGACTACGACT  
 TCACCAGCTACAGACAGTAAGTTACAAGCGACTGAAGTTAAGAGCGTTCC  
 GGTAGCACAAAAGCTCCAACAGCAACACCGGTAGCACAAACCAGCTTCAA  
 CAACAATGCAGTAGCTGCATCCTGAAATGCAGGGCTCCAACCTCAT  
 GTTGACGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTAATGAATT  
 CAGTACATACCGTGCAGGAGATCCAGGTGATCATGGTAAAGGTTTAGCAG  
 TTGACTTTATTGTAGGTAAAAACCAAGCACTTGGTAATGAAGTTGCACAG  
 TaCTCTACACAAAATATGGCAGCAAAATAACATTTATATGTTATCTGGCA  
 ACAAAAGTTTTATTCAAATACAATAGTATTTATGGACCTGCTAATACTT  
 GGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTATGACCAC  
 GTTCAGTATCATTTAACAATAATATAAAAAAGGAAGCTATTGGCTTCT

Table 69: Comparative Sequences relating to SAG0032

TTTTTTATATGCCTTGAATAGACTTTCAAGGTTCTTATATAATTTTTATT  
A

SEQ ID NO. 6907

STRAIN M732

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGT  
GATACAnTAAGCGTTATTTTCAGAAGCAATGTCAATTGATATGAATGTCTT  
AGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAA  
CACTGACAGTAACCTTACGATCAGAAGAGTCATCTGCCACTTCAATGAAA  
ATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTcGA  
TTTGAAAACCAATCAAGTTTGTGTTGCAGACCAAAAAGTTTCTCTCAATA  
CAATTTCCGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCA  
ATGAAGACATATTTCTTCTGCCCGAGCTTTGAAATCAAAGAAGTATTAGC  
ACAAGAGCAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAG  
CTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGAGGAAGTT  
AAACCAACTCAGACGTCAGTCAGTCAGTTAAACAACAGTATCACCAGCTTC  
TGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAA  
CTGTAGCAGCCCCCTAGAGTGGCAAGTGCTAAAGTAGTCACTCCTAAAGTA  
GAAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCTGTGAC  
TACGACTTCACCAGCTACAGACAGTAAGTTACAAGCGACTGAAGTTAAGA  
GCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCAGTAGCACAAACCA  
GCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCA  
ACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTA  
ATGAATTCAAGTACATACCGTGCGGAGATCCAGGTGATCATGGTAAAGGT  
TTAGCAGTTGACTTTAttgtaggtaaaaaaccAAGCACTTGGTAATGAAGT  
TGCACAGTACTcTACACAAAATATGGCAGCAAAATAACATTTATATGTGTA  
TCTGGCAACAAAAGTTTATTCAAATACAAATAGTATTATGGACCTGCT  
AATACCTTGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTA  
TGACCACGTTACGATATCATTTAAACAAATAATATAAAAAAGGAAGCTATT  
TGGCTTCTTTTTTATATGCCTTGAATAGACTTTCAAGGTTCTTATATAAT  
TTTTATTA

SEQ ID NO. 6908

STRAIN M781

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGT  
GATACACTAAGCGTTATTTTCAGAAGCAATGTCAATTGATATGAATGTCTT  
AGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAA  
CACTGACAGTAACCTTACGATCAGAAGAGTCATACTGCCACTTCAATGAAA  
ATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTcGA  
TTTGAAAACCAATCAAGTTTGTGTTGCAGACCAAAAAGTTTCTCTCAATA  
CAATTTCCGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCA  
ATGAAGACATATTTCTTCTGCCCGAGCTTTGAAATCAAAGAAGTATTAGC  
ACAAGAGCAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAG  
CTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGAGGAAGTT  
AAACCAACTCAGACGTCAGTCAGTCAGTTAAACAACAGTATCACCAGCTTC  
TGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAA  
CTGTAGCAGCCCCCTAGAGTGGCAAGTGCTAAAGTAGTCACTCCTAAAGTA  
GAAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCTGTGAC  
TACGACTTCACCAGCTACAGACAGTaaGTTACAAGCGACTGAAGTTAAGA  
GCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCAGTAGCACAAACCA  
GCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCA  
ACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTA  
ATGAATTCAAGTACATACCGTGCGGAGATCCAGGTGATCATGGTAAAGGT  
TTAGCAGTTGACTTTATTGTAGGTAAAAACCAAGCACTTGGTAATGAAGT  
TGCACAGTACTCTACACAAAATATGGCAGCAAAATAACATTTATATGTGTA  
TCTGGCAACAAAAGTTTATTCAAATACAAATAGTATTATGGACCTGCT  
AATACCTTGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTA  
TGACCACGTTACGATATCATTTAAACAAATAATATAAAAAAGGAAGCTATT  
TGGCTTCTTTTTTATATGCCTTGAATAGACTTTCAAGGTTCTTATATAAT  
TTTTATTA

SEQ ID NO. 6909

STRAIN CJB110

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAA  
TATGGTGATACACTAAGCGTTATTTTCAGAAGCAATGTCAATTGATATGAA  
TGCTTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCTG  
AGACAACACTGCAGTAACCTTACGATCAGAAGAGTCATACTGCCACTTCA  
ATGAAAATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTAC  
TGTGGATTTGAAAACCAATCAAGTTTcTGTGTCAGACCAAAAAGTTTCTC  
TCAATACAATTTCCGAAGGTATGACACCAGAAGCAGCAACAACGATTGTT  
TCGCCAATGAAGACATATTTCTTCTGCCCGAGCTTTGAAATCAAAGAAGT  
ATTAGCACAAGAGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTAT  
CAACAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGAG  
GAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCACC  
AGCTTCTGTGCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGG  
TAAGAACTGTAGCAGCCCCCTAGAGTGGCAAGTGTTAAAGTAGTCACTCCT  
AAAGTAGAAAATGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCC  
TGTGACTACGACTTCAACAGcTACAGACAGTaaGTTaCAAGCGACTGAAG  
TTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCAGTAGCA  
CAACAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGG  
GCTCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATG  
GAGTTAATGAATTCAGTACATaCCGTGCAAGGTGATCCAgGTGATCATGGT  
AAAGGTTTAGCAGTcGACTTTATTGTAGTAAAAACCAAGCACTTGGTAA

Table 69: Comparative Sequences relating to SAG0032

TGAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAATAACATTTTCAT  
 ATGTTTATCTGGCAACAAAAGTTTTACTCAAATACAAATAGTATTTATGGA  
 CCTGCTAATACCTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAA  
 CCATTATGACCATGTTACGATATCATTTAAACAAATAATATAAAAAAGGAA  
 GCTATTTGGCTTCTTTTATATGCCTTGAATAGACTTCAAGGTTCTTA  
 TATAATTTTTATTA

SEQ ID NO. 6910

STRAIN 1169NT

CTGATTTG

GTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGTGATACACT  
 AAGCGTTATTTTCAGAACCAATGTCAATTGATATGAATGTCTTAGCAAAAA  
 TTAATAACATTGCGATATCAATCTTATTTATCCTGAGACCAACTGACA  
 GTAACCTACGATCagAAGAGTCATCTGCCACTTCAATGAAAATAGAAAC  
 ACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTGGATTTGAAAA  
 CCAATCAAGTTTCTGTGTCAGACCAAAAAGTTTCTCTCAATCAATTTTCG  
 GAAGGTATGACACCAAGAGCagCAACAACGATTGTTTCGCCAATGAAGAC  
 ATATTTCTTCTGCGCCAGCTTTgAAATCAAAGAAGTATTAGCACAAGAGC  
 AAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTATCACCAGCTCCTGTG  
 AAGTCGATTACTTCAgAAGTTCCAgCAGCTAAAGAGGAAGTTAGACCAaC  
 TcAGACGTCAGTCAGTCAGTCAACAACAGTATCACCagCTTCTGTGCGCG  
 CTGAAACACCCAGCTCCAGTAGCTAAAGTAGCACCGGTAAAGAACTGTAGCA  
 GCCCCAGCCCTAGAGTGGCAAGTGTAAAGTAGTCACTCTTAAAGTAGA  
 AAcTGGTGATCACCAGAGCATGTACCAGCTCCAGCAGTTCTGTGACTA  
 cGACTTCAACAGCTACaGACaTaAGTTACAAGCGACTGAAGTTAAgAGC  
 GTCCGGTGGCAAAAAGCTTCAACAGCAACACCGGTaGCACAACCCAGC  
 TTcAACAAACAAATGCGATGcTGACATCTGAAAATGCAGGACTCCAAC  
 CTCATGTTGCGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTAAT  
 GAATTCAGTACATaCCGTGCGGGAGATCCAGGTGATCATGGTAAAGGTTT  
 AGCAGTTGACTTTATTTGTaGTAAAAACCAAGCACTTGGTAATGAAGTTG  
 CACAGTACTCTACACAAAATATGGCAGCAAATAACATTTTCATATGTTATC  
 TGGCAACAAAAGTTTACTCAAATACAAATAGTATTTATGGACCTGCTAA  
 TACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTATG  
 ACCAGGTTACGATCATTTAAACAAATAATATAAAAAAGGAAGCTATTTG  
 GCTTCTTTTATATGCCTTGAATAGACTTCAAGGCTCTTATATAATTT  
 TTATTA

SEQ ID NO. 6911

STRAIN JM9130013

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACT

GTGAAATATGGTGATACACTAAGCGTTATTTTCAGAAAGCAATGTCAATTGA  
 TATGAATGTCTTAGCAAAAAATAAATCAATTCAGATATCAATCTTATTT  
 ATCCTGAGACAACACTGACAGTAACCTACGATCAGAAGAGTCATACCTGCC  
 ACTTCAATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAAC  
 AGCTACTGTGGATTTGAAAAACCAATCAAGTTTCTGTTGTCAGACCAAAAAG  
 TTTCTCTCAATACAATTTGGAAGGTATGACACCAGAAGCAGCAACCAACG  
 ATTGTTTCCGCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAA  
 AGAAGTATTAGCACAGAGCAAGCTGTAGTCAAGCAGCAGCTAATGAAC  
 AGGTATCACCAGCTCCTGTGAAGTCGATTACTTCAAGAGTTCCAGCAGCT  
 AAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGT  
 ATCACCAGCTTCTGTTGCGCGTGAACACCAGCTCCAGTAGCTAAAGTAG  
 CACCGGTAAAGAACTGTAGCAGCCCTAgAGTGGCAAGTGTAAAGTAGTC  
 ACTCTAAAGTAGAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGC  
 AGTTCTGTGACTACGACTTCAACAGCTACAGaCAGTAAGTTACAAGCGA  
 cTGAAGTTAAGAGCGTTCCGGTAGCACAAAAGCTTCAACAGCAACACCG  
 GTAGCaCAACAGCTTCAACAACAAATGCAGTAGCTGCACATCTGAAAA  
 TGCAGGGCTCCAACCTCATGTTGCGCTTATAAAGAAAAAGTAGCGTCAA  
 CTTATGGAGTTAATGAATTCAGTACATACCGTGGGGAGATCCAGGTGAT  
 CATGGTAAAGGTTAGCAGTTGACTTTATTTGAGGTACTAATCAAGCACT  
 TGGTAATAAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAATAACA  
 TTTCTATATGTTATCTGGCAACAAAAGTTTACTCAAATACAAACAGTATT  
 TATGGACCTGCTAATACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTAC  
 TGCCAACCACTATGACCAGCTTCAAGTATCATTTAAACAAATAATATAAAA  
 AAGGAAGCTATTTGGCTTCTTTTATATGCCTTGAATAGACTTCAAGG  
 TTCTTATATAATTTTTATTA

PRETTY of: /biotmp/msa167919.2{\*} March 11, 2003 08:55 ..

	1	50
msa167919.2{322_COH1}	-----	-----
msa167919.2{322_M781}	-----	-----
msa167919.2{322_M732}	-----	-----
msa167919.2{322_18RS21}	-----	-----
msa167919.2{322_2603}	atgaataaaa aggtactatt gacatcgaca atggcagctt cgctattatc	
msa167919.2{322_JM9130013}	-----	-----
msa167919.2{322_090}	-----	-----
msa167919.2{322_CJB110}	-----	-----
msa167919.2{322_A909}	-----	-----
msa167919.2{322_H36B}	-----	-----
msa167919.2{322_1169NT}	-----	-----
Consensus	*****	*****

51

100

Table 69: Comparative Sequences relating to SAG0032

msa167919.2{322_COH1}	-----	-----	-----	-----	-----
msa167919.2{322_M781}	-----	-----	-----	-----	-----
msa167919.2{322_M732}	-----	-----	-----	-----	-----
msa167919.2{322_18RS21}	-----	-----	-----	-----	-----
msa167919.2{322_2603}	agtcgcaagt	gttcaagcac	aagaaacaga	tacgacgtgg	acagcacgta
msa167919.2{322_JM9130013}	-----	-----	-----	-----	-----
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	-----	-----	-----	-----	-----
msa167919.2{322_A909}	-----	-----	-----	-----	-----
msa167919.2{322_H36B}	-----	-----	-----	-----	-----
msa167919.2{322_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
msa167919.2{322_COH1}	-----	-----ct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_M781}	-----	-----ct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_M732}	-----	-----ct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_18RS21}	-----	-----ct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_2603}	ctgtttcaga	ggtaaaggct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_JM9130013}	-----	-----ct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	-----	-----ct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_A909}	-----	-----ct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_H36B}	-----	-----ct	gatttggtta	agcaagacaa	taaatcatca
msa167919.2{322_1169NT}	-----	-----ct	gatttggtta	agcaagacaa	taaatcatca
Consensus	*****	*****-	-----	-----	-----
msa167919.2{322_COH1}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_M781}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_M732}	tatactgtga	aatatgggtga	tacantaagc	gttatttcag	aagcaatgtc
msa167919.2{322_18RS21}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_2603}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_JM9130013}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_A909}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_H36B}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_1169NT}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
Consensus	-----	-----	-----	-----	-----
msa167919.2{322_COH1}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_M781}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_M732}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_18RS21}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_2603}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_JM9130013}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_A909}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_H36B}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_1169NT}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
Consensus	-----	-----	-----	-----	-----
msa167919.2{322_COH1}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_M781}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_M732}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_18RS21}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_2603}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_JM9130013}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_090}	-----	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_CJB110}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_A909}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_H36B}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_1169NT}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
Consensus	-----	*****	*****	*****	*****
msa167919.2{322_COH1}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_M781}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_M732}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_18RS21}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_2603}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_JM9130013}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_090}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_CJB110}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_A909}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_H36B}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_1169NT}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
Consensus	*****	*****	*****	*****	*****

Table 69: Comparative Sequences relating to SAG0032

	351		400
msa167919.2{322_COH1}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA TCAAGTTTtT GTTGCAGACC
msa167919.2{322_M781}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA TCAAGTTTtT GTTGCAGACC
msa167919.2{322_M732}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA TCAAGTTTtT GTTGCAGACC
msa167919.2{322_18RS21}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_2603}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_JM9130013}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_090}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_CJB110}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_A909}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_H36B}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_1169NT}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
Consensus	*****	*****	*****
	401		450
msa167919.2{322_COH1}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_M781}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_M732}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_18RS21}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_2603}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_JM9130013}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_090}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_CJB110}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_A909}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_H36B}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_1169NT}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
Consensus	*****	*****	*****
	451		500
msa167919.2{322_COH1}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_M781}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_M732}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_18RS21}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_2603}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_JM9130013}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_090}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_CJB110}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_A909}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_H36B}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_1169NT}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
Consensus	*****	*****	*****
	501		550
msa167919.2{322_COH1}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTTAGTCAA GtAGCAGCTA
msa167919.2{322_M781}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTTAGTCAA GtAGCAGCTA
msa167919.2{322_M732}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTTAGTCAA GtAGCAGCTA
msa167919.2{322_18RS21}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTTAGTCAA GcAGCAGCTA
msa167919.2{322_2603}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTTAGTCAA GcAGCAGCTA
msa167919.2{322_JM9130013}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTTAGTCAA GcAGCAGCTA
msa167919.2{322_090}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTTAGTCAA GcAGCAGCTA
msa167919.2{322_CJB110}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTTAGTCAA GcAGCAGCTA
msa167919.2{322_A909}	ATCAAAAGAA	GTATTAGCAC	AAGgGCAAGC TGTTAGTCAA GcAGCAGCTA
msa167919.2{322_H36B}	ATCAAAAGAA	GTATTAGCAC	AAGgGCAAGC TGTTAGTCAA GcAGCAGCTA
msa167919.2{322_1169NT}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTTAGTCAA GcAGCAGCTA
Consensus	*****	*****	*****
	551		600
msa167919.2{322_COH1}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_M781}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_M732}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_18RS21}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_2603}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_JM9130013}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_090}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_CJB110}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_A909}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_H36B}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_1169NT}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
Consensus	*****	*****	*****
	601		650
msa167919.2{322_COH1}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_M781}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_M732}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_18RS21}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_2603}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_JM9130013}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_090}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_CJB110}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_A909}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_H36B}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
msa167919.2{322_1169NT}	GCAGCTAAAG	AGGAAGTTAg	ACCAACTCAG ACGTCAGTCA GTCAGTcAAC
Consensus	*****	*****	*****

Table 69: Comparative Sequences relating to SAG0032

	651			700	
msa167919.2{322_COH1}	AACAGTATCA	CCAGCTTCTG	TTGCCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_M781}	AACAGTATCA	CCAGCTTCTG	TTGCCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_M732}	AACAGTATCA	CCAGCTTCTG	TTGCCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_18RS21}	AACAGTATCA	CCAGCTTCTG	TTGCCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_2603}	AACAGTATCA	CCAGCTTCTG	TTGCCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_JM9130013}	AACAGTATCA	CCAGCTTCTG	TTGCCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_090}	AACAGTATCA	CCAGCTTCTG	TTGCCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_CJB110}	AACAGTATCA	CCAGCTTCTG	TTGCCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_A909}	AACAGTATCA	CCAGCTTCTG	TTGCCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_H36B}	AACAGTATCA	CCAGCTTCTG	TTGCCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_1169NT}	AACAGTATCA	CCAGCTTCTG	TTGCCCGCTGA	AACACCAGCT	CCAGTAGCTA
Consensus	*****	*****	*****	*****	*****
	701			750	
msa167919.2{322_COH1}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_M781}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_M732}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_18RS21}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_2603}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_JM9130013}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_090}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_CJB110}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_A909}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_H36B}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_1169NT}	AAGTAGCACC	GGTAAGAACT	GTAGcagccc	CAGCCCCTAG	AGTGGCAAGT
Consensus	*****	*****	****----	*****	*****
	751			800	
msa167919.2{322_COH1}	GcTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_M781}	GcTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_M732}	GcTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_18RS21}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_2603}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_JM9130013}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_090}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_CJB110}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_A909}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_H36B}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_1169NT}	GcTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
Consensus	*-*****	*****	*****	*****	*****
	801			850	
msa167919.2{322_COH1}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_M781}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_M732}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_18RS21}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_2603}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_JM9130013}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_090}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_CJB110}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_A909}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_H36B}	AtcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_1169NT}	AccCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACaTA
Consensus	*-*****	*****	*****	****-*****	*****-***
	851			900	
msa167919.2{322_COH1}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_M781}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_M732}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_18RS21}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_2603}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_JM9130013}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_090}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_CJB110}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_A909}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_H36B}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_1169NT}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTgGCACA	AAAAGCTCCA
Consensus	*****	*****	*****	*****	*****
	901			950	
msa167919.2{322_COH1}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_M781}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_M732}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_18RS21}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_2603}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_JM9130013}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_090}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_CJB110}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_A909}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_H36B}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_1169NT}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC



Table 69: Comparative Sequences relating to SAG0032

Consensus	*****	*****	*****	*****	*****
	951				1000
msa167919.2{322_COH1}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_M781}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_M732}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_18RS21}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_2603}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_JM9130013}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_090}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_CJB110}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_A909}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_H36B}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_1169NT}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
Consensus	*****	*****-*-*	*****	*****	*****
	1001				1050
msa167919.2{322_COH1}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGga
msa167919.2{322_M781}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGga
msa167919.2{322_M732}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGga
msa167919.2{322_18RS21}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGga
msa167919.2{322_2603}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGga
msa167919.2{322_JM9130013}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGga
msa167919.2{322_090}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGgt
msa167919.2{322_CJB110}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGgt
msa167919.2{322_A909}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGga
msa167919.2{322_H36B}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGga
msa167919.2{322_1169NT}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGga
Consensus	*****	*****	*****	*****	*****-*-*
	1051				1100
msa167919.2{322_COH1}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_M781}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_M732}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_18RS21}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_2603}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_JM9130013}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_090}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_CJB110}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_A909}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_H36B}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_1169NT}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
Consensus	*****	*****	*****	*****	*****
	1101				1150
msa167919.2{322_COH1}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_M781}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_M732}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_18RS21}	tAAtCAAGCA	CTTGGTAATa	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_2603}	tAAtCAAGCA	CTTGGTAATa	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_JM9130013}	tAAtCAAGCA	CTTGGTAATa	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_090}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_CJB110}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_A909}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_H36B}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_1169NT}	aAAcCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
Consensus	-*-*****	*****	*****	*****	*****
	1151				1200
msa167919.2{322_COH1}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_M781}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_M732}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_18RS21}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_2603}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_JM9130013}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_090}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_CJB110}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_A909}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_H36B}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_1169NT}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
Consensus	*****	*****	*****	*****	*****
	1201				1250
msa167919.2{322_COH1}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_M781}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_M732}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_18RS21}	ACAAAcAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_2603}	ACAAAcAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_JM9130013}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_090}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_CJB110}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_A909}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_H36B}	ACAAAtAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG

Table 69: Comparative Sequences relating to SAG0032

msal67919.2{322_1169NT}	ACAAATAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
Consensus	*****	*****	*****	*****	*****
	1251				1300
msal67919.2{322_COH1}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_M781}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_M732}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_18RS21}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_2603}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_JM9130013}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_090}	TGGTGGCGTT	ACTGCCAACC	AtTATGACCA	tGTTcACGTA	TCATTTAACA
msal67919.2{322_CJB110}	TGGTGGCGTT	ACTGCCAACC	AtTATGACCA	tGTTcACGTA	TCATTTAACA
msal67919.2{322_A909}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_H36B}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_1169NT}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
Consensus	*****	*****	*-*****	-*****	*****
	1301				1350
msal67919.2{322_COH1}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_M781}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_M732}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_18RS21}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_2603}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_JM9130013}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_090}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_CJB110}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_A909}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_H36B}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_1169NT}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
Consensus	*****	*****	*****	*****	*****_**
	1351				1382
msal67919.2{322_COH1}	AGACTTTCAA	GGTTCCTTATA	TAATTTTTAT	TA	
msal67919.2{322_M781}	AGACTTTCAA	GGTTCCTTATA	TAATTTTTAT	TA	
msal67919.2{322_M732}	AGACTTTCAA	GGTTCCTTATA	TAATTTTTAT	TA	
msal67919.2{322_18RS21}	AGACTTTCAA	GGTTCCTTATA	TAATTTTTAT	TA	
msal67919.2{322_2603}	AGACTTTCAA	GGTTCCTTATA	TAATTTTTAT	TA	
msal67919.2{322_JM9130013}	AGACTTTCAA	GGTTCCTTATA	TAATTTTTAT	TA	
msal67919.2{322_090}	AGACTTTCAA	GGTTCCTTATA	TAATTTTTAT	TA	
msal67919.2{322_CJB110}	AGACTTTCAA	GGTTCCTTATA	TAATTTTTAT	TA	
msal67919.2{322_A909}	AGACTTTCAA	GGTTCCTTATA	TAATTTTTAT	TA	
msal67919.2{322_H36B}	AGACTTTCAA	GGTTCCTTATA	TAATTTTTAT	TA	
msal67919.2{322_1169NT}	AGACTTTCAA	GGTTCCTTATA	TAATTTTTAT	TA	
Consensus	*****	*****	*****	**	
<b>SEQ ID NO. 6912</b>					
<b>STRAIN 2603 frame: 1</b>					
MNKKVLLTSTMAASLLSVASVQAQETDITWTARTVSEVKADLVKQDNKSSYTVKYGDTLS					
VISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSHATSMKIEPATNAAGQTTA					
TVDLKTNQVSVADQKVSINLI SEGMPPEAATTIVSPMKTYSSAPALKSKEVLQAQVQAVS					
AAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVSPASVAEETPAPVAKVAPVRT					
VAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSPATDSKLQATEVKSVPVQAQKAPT					
TPVQAQASTTNAVAHAHPENAGLQPHVAAYKEKVASTYGVNEFSTYRAGDPGDHGKGLAVD					
FIVGTNQALGNKVAQYSTQNMAANNISYVIWQQKFYSNTNSIYGPANTWNAMPDRGGVTA					
NHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY					
<b>SEQ ID NO. 6913</b>					
<b>STRAIN 090 frame: 2</b>					
ETTLTVTYDQKSHATSMKIEPATNAAGQTPATVTLKTNQVSVADQKVSINLI SEGMP					
EAATTIVSPMKTYSSAPALKSKEVLQAQVQAVSQAANEQVSTAPVKSITSEVPAAKEEVK					
PTQTSVSQSTTVSPASVAEETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVS					
PAVPVTTTSTATDSKLQATEVKSVPVQAQKAPTATPVAQPASTTNAVAHAHPENAGLQPHVA					
AYKEKVASTYGVNEFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNIS					
YVIWQQKFYSNTNSIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYAL					
NRLSRFLYNFY					
<b>SEQ ID NO. 6914</b>					
<b>STRAIN A909 frame: 3</b>					
DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH					
TATSMKIEPATNAAGQTTATVTLKTNQVSVADQKVSINLI SEGMPPEAATTIVSPMKTY					
SSAPALKSKEVLQAQVQAVSQAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS					
PASVAEETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSTATD					
SKLQATEVKSVPVQAQKAPTATPVAQPASTTNAVAHAHPENARLQPHVAAYKEKVASTYGVN					
EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN					
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALHRLSRFLYNFY					
<b>SEQ ID NO. 6915</b>					
<b>STRAIN H36B frame: 3</b>					
DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH					
TATSMKIEPATNAAGQTTATVTLKTNQVSVADQKVSINLI SEGMPPEAATTIVSPMKTY					
SSAPALKSKEVLQAQVQAVSQAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS					
PASVAEETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSTATD					
SKLQATEVKSVPVQAQKAPTATPVAQPASTTNAVAHAHPENARLQPHVAAYKEKVASTYGVN					

Table 69: Comparative Sequences relating to SAG0032

EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN  
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

## SEQ ID NO. 6916

STRAIN 18RS21 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH  
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLTISEGMTPEAATTIVSPMKTY  
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS  
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSPATD  
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAHPENAGLQPHVAAYKEKVASTYGVN  
EFSTYRAGDPGDHKGGLAVDFIVGTNQLGKNVAQYSTQNMANNISYVIWQKQFYSNTN  
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

## SEQ ID NO. 6917

STRAIN M732 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH  
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLTISEGMTPEAATTIVSPMKTY  
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS  
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVT PKVETGASPEHVSAPAVPVTTTSPATD  
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAHPENAGLQPHVAAYKEKVASTYGVN  
EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN  
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

## SEQ ID NO. 6918

STRAIN COH1 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH  
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLTISEGMTPEAATTIVSPMKTY  
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS  
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVT PKVETGASPEHVSAPAVPVTTTSPATD  
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAHPENAGLQPHVAAYKEKVASTYGVN  
EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN  
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

## SEQ ID NO. 6919

STRAIN M781 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH  
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLTISEGMTPEAATTIVSPMKTY  
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS  
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVT PKVETGASPEHVSAPAVPVTTTSPATD  
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAHPENAGLQPHVAAYKEKVASTYGVN  
EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN  
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

## SEQ ID NO. 6920

STRAIN CJB110 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH  
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLTISEGMTPEAATTIVSPMKTY  
SSAPALKSKEVLAEQAVSQAAANEQVSTAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS  
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSTATD  
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAHPENAGLQPHVAAYKEKVASTYGVN  
EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN  
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

## SEQ ID NO. 6921

STRAIN 1169NT frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH  
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLTISEGMTPEAATTIVSPMKTY  
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS  
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVT PKVETGASPEHVPAPAVPVTTTSTA  
TDNKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAHPENAGLQPHVAAYKEKVASTYGVN  
VNEFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSN  
TNSIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

## SEQ ID NO. 6922

STRAIN JM9130013 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH  
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINLTISEGMTPEAATTIVSPMKTY  
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS  
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSPATD  
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAHPENAGLQPHVAAYKEKVASTYGVN  
EFSTYRAGDPGDHKGGLAVDFIVGTNQLGKNVAQYSTQNMANNISYVIWQKQFYSNTN  
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

PRETTY of: /biotmp/msa237049.2{\*} May 14, 2003 03:04 ..

	1	50
msa237049.2{322_COH1}	-----	dlvkqdnkss
msa237049.2{322_M781}	-----	dlvkqdnkss
msa237049.2{322_M732}	-----	dlvkqdnkss
msa237049.2{322_A909}	-----	dlvkqdnkss
msa237049.2{322_H36B}	-----	dlvkqdnkss
msa237049.2{322_090}	-----	-----

Table 69: Comparative Sequences relating to SAG0032

msa237049.2{322_CJB110}	-----	-----	-----	-----	dlvkqdnkss
msa237049.2{322_18RS21}	-----	-----	-----	-----	dlvkqdnkss
msa237049.2{322_2603}	mnkvvlltst	maasllsvas	vqagetdtw	tartvsevka	dlvkqdnkss
msa237049.2{322_JM9130013}	-----	-----	-----	-----	dlvkqdnkss
msa237049.2{322_1169NT}	-----	-----	-----	-----	dlvkqdnkss
Consensus	*****	*****	*****	*****	-----
msa237049.2{322_COH1}	51				100
msa237049.2{322_M781}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_M732}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_A909}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_H36B}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_090}	-----	-----	-----	-----	ETT LTVTYDQKSH
msa237049.2{322_CJB110}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_18RS21}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_2603}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_JM9130013}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_1169NT}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
Consensus	-----	-----	-----	-----	*****
msa237049.2{322_COH1}	101				150
msa237049.2{322_M781}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_M732}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_A909}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_H36B}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_090}	TATSMKIETP	ATNAAGQTpA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_CJB110}	TATSMKIETP	ATNAAGQTpA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_18RS21}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_2603}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_JM9130013}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_1169NT}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
Consensus	*****	*****	*****	*****	*****
msa237049.2{322_COH1}	151				200
msa237049.2{322_M781}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	VAANEQVSpA	PVKSIITSEVP
msa237049.2{322_M732}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	VAANEQVSpA	PVKSIITSEVP
msa237049.2{322_A909}	TTIVSPMKTY	SSAPALKSKE	VLAQgQAVSQ	AAANEQVSpA	PVKSIITSEVP
msa237049.2{322_H36B}	TTIVSPMKTY	SSAPALKSKE	VLAQgQAVSQ	AAANEQVSpA	PVKSIITSEVP
msa237049.2{322_090}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVStA	PVKSIITSEVP
msa237049.2{322_CJB110}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVStA	PVKSIITSEVP
msa237049.2{322_18RS21}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVSpA	PVKSIITSEVP
msa237049.2{322_2603}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVSpA	PVKSIITSEVP
msa237049.2{322_JM9130013}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVSpA	PVKSIITSEVP
msa237049.2{322_1169NT}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVSpA	PVKSIITSEVP
Consensus	*****	*****	*****	*****	*****
msa237049.2{322_COH1}	201				250
msa237049.2{322_M781}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_M732}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_A909}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_H36B}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_090}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_CJB110}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_18RS21}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_2603}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_JM9130013}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_1169NT}	AAKEEVrPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VaapAPRVAS
Consensus	*****	*****	*****	*****	*****
msa237049.2{322_COH1}	251				300
msa237049.2{322_M781}	aKVVTpKVET	GASPEHVsAP	AVPVTTTSpA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_M732}	aKVVTpKVET	GASPEHVsAP	AVPVTTTSpA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_A909}	aKVVTpKVET	GASPEHVsAP	AVPVTTTStA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_H36B}	aKVVTpKVET	GASPEHVsAP	AVPVTTTStA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_090}	aKVVTpKVET	GASPEHVsAP	AVPVTTTStA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_CJB110}	aKVVTpKVET	GASPEHVsAP	AVPVTTTStA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_18RS21}	aKVVTpKVET	GASPEHVsAP	AVPVTTTSpA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_2603}	aKVVTpKVET	GASPEHVsAP	AVPVTTTSpA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_JM9130013}	aKVVTpKVET	GASPEHVsAP	AVPVTTTSpA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_1169NT}	aKVVTpKVET	GASPEHVsAP	AVPVTTTStA	TdSKLQATEV	KSVpVAQKAP
Consensus	*****	*****	*****	*****	*****
msa237049.2{322_COH1}	301				350
msa237049.2{322_M781}	TATpVAQPAS	TTNAVAHPE	NagLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_M732}	TATpVAQPAS	TTNAVAHPE	NagLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_A909}	TATpVAQPAS	TTNAVAHPE	NarLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_H36B}	TATpVAQPAS	TTNAVAHPE	NarLQPHVAA	YKEKVASTYG	VNEFSTYRAG

Table 69: Comparative Sequences relating to SAG0032

msa237049.2{322_090}	TatPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_CJB110}	TatPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_18RS21}	TatPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_2603}	TatPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_JM9130013}	TatPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_1169NT}	TatPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
Consensus	***-*****	*****-***	***-*****	*****-***	*****-***
351 400					
msa237049.2{322_COH1}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_M781}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_M732}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_A909}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_H36B}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_090}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_CJB110}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_18RS21}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_2603}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_JM9130013}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_1169NT}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
Consensus	*****	*****-***	***-*****	*****-***	*****-***
401 450					
msa237049.2{322_COH1}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALn
msa237049.2{322_M781}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALn
msa237049.2{322_M732}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALn
msa237049.2{322_A909}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALh
msa237049.2{322_H36B}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALh
msa237049.2{322_090}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALn
msa237049.2{322_CJB110}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALn
msa237049.2{322_18RS21}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALn
msa237049.2{322_2603}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALn
msa237049.2{322_JM9130013}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALn
msa237049.2{322_1169NT}	TNSIYGPANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFYALn
Consensus	*****	*****	*****	*****	*****-***
451 460					
msa237049.2{322_COH1}	RLSRFLYNFY				
msa237049.2{322_M781}	RLSRFLYNFY				
msa237049.2{322_M732}	RLSRFLYNFY				
msa237049.2{322_A909}	RLSRFLYNFY				
msa237049.2{322_H36B}	RLSRFLYNFY				
msa237049.2{322_090}	RLSRFLYNFY				
msa237049.2{322_CJB110}	RLSRFLYNFY				
msa237049.2{322_18RS21}	RLSRFLYNFY				
msa237049.2{322_2603}	RLSRFLYNFY				
msa237049.2{322_JM9130013}	RLSRFLYNFY				
msa237049.2{322_1169NT}	RLSRFLYNFY				
Consensus	*****				

Table 70: Comparative Sequences relating to SAG 1280

SEQ ID. NO. 7001

STRAIN 2603

ATGGGAGGGAAAATGAATCAAGAAGTCTTACTACAAATGATGAGAGCCACTATTCTC  
 GTGATAGAGCCTTGCTTGAGGCATTTTATATATACCAAGCAGAGCATTTTGATGAGGAGT  
 GGGATAGTCTTATTATCATGATTTATGACCAATAGGCAAGAAATAAATAAGTCTGTTCAAG  
 TACTTCACTTTGAGACAGATGTTTCAAGCTTTTGTCCAGGCTAGTCTTATGATAGTCTC  
 ATGATCTATTGACCTATACACAAGTTTTCGGCCAAAGTGGTCTTCAAAAACCTAGATAAAC  
 TATCGCCGTCTGAAAAAACTTGGTGTAGAAAGTGGCCTTGTTCAATCTGGCCACTCGTT  
 TTCAATTATTGGATTCCCAATGGACACTACCAAAACCATATCGCCGGATTCACTCTTACAAA  
 AGAGTAGGGGAGCTAATTTGGTCAATGTGTATCGTGTGGCTAATAATTAGCGGATCGTA  
 TTAGTTCGAGATATTGAACAGTTTCTCTTAACCTACGAGCCTGAGCTTGAAACTAGAGCTG  
 ATGAAACTGTTCTAGAAAAATGAAGAACTGTTGATGAGCACAAAACAGTGTTCATCAAG  
 CAATATCTTTTCGAGAAGAGGGCTCTCTGGTTATTGTCTAGTTTGGATGTAGATTGTCTC  
 AACTAGATGTTCAAAATAGGAAAAACAGTCACTCTGCCAGCTTATGAAGAGTTATCCTTAC  
 GACGTAATTTGAGATTCTAACATATTTTGACCAATTCGAAATGAACGTTCCAAAGTCC  
 CAAGTTTGTAGCAGAGGTGATTTTGACACAGAGATGGAAATGACACCACTCTTGTAGTGGC  
 AGGAAATTACTTACTTATCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAACGAACCTGA  
 CTACAGTTCGAAGAAAGGAATTAGAAAAAATTGGACAAGCCATTAGGATAGAAAACTAAG  
 AAAAATTGACTCAGCTAGGGAATTGATTTATCTCAGTTTGACCCAGACCGAGTCTGTTATT  
 TATTGGATGACAGAGGTGTTTTCGTTTAAAAAATGCAGACCTTGCTTTACTAGGTGGTT  
 ATCCCAAGCCTCGGTAACTCACTAGCCCTTGCGACAGAACTACTCCAAATGGGACTAA  
 GTCATGAAAAAGTTTGAATTTTCTTGGTAGCCAGCTTCCATTGAAGAGCTGCGACAAAG  
 TTGCCTACGCCCTTTTATACCAAGAACTCAGCAGAGAAGTGGGAGCAATTGAAAAAG  
 ATAAAGGTAACTCAGCCAGATTTAACTCTCAGAGATTGGAAGCAAGCTAGAGAAAGCTG  
 AGGGAAGAGAGTAGTTGATGAAGAAATTCGCGGAAAATCCACTGGTTTCAAGAGATTGG  
 ACCTTATCTCTCTGGGGTCACTGGTTTCTTATAAGGGACAGGACTTTGAGGTCACTGCGG  
 TCAGCGATGCTCGAATTGAACGGTTTGAATTCGGAATTGAGTTAGTCAATGACTTTTTCGGATA  
 TCATTGAACAAAATCCAGTTCTTTATGTGAGGACCTGGGAAGAGTCACTCAGGCACTTC  
 ATCAGCCAAAGGCAGAACCAAAAACAGAGTTAGAAGAAGCGGACCAAGAAATTAAACCTAT  
 TCTCAATTCTGGAAGAGGAGCCAGTTTCAAGATTGGAAGTATGGAACCAAGATGATTGAG  
 AAAATGGTCATAACCATGATCTTGAAGAAAACAGATAATCAAATTCCTGAAGAGGAAG  
 TCGTCGAAACAAATTCAGAGATTCCAGTAACGGACTTTTATTTCGAGAAGATTGACGG  
 ACTTTTATCTAAGACTGCTAGAGATAAGGTTGAGACAAACATTGTGGCCATTCTGTTGG  
 TAAAAAATCTAGAAAGTAGAGCACCGCAATGCTTACCAAGTGAACAGAACTCCTTGCCA  
 AGTATGTAGGCTGGGGTGGACTAGCCCAATGAATTTTGTATGACTATAATCCAAATTTT  
 CTAAGGAACGAGAAGAACTGAAGAGCCTAGTCACAGATAAAGAGTATTCGGATATGAAAC  
 AGTCTCTCCCTGACAGCCTATTACACAGACCCATCCCTGATCCGTCAGATGTGGGATAAGT  
 TGGAAAGAGATTGGCTTTACAGGTGGCAAAATCCTAGATCCTTCCATGGGAACAGGGAAAT  
 TCTTTGCGGCTATGCCAAAACACTTAAGAGAAAAGAGTGAAGTTGATGGCGTAGAGTTAG  
 ATACTATTACAGAGCTATTGCCCCAACCTTCAATCCCAATAGTCATATTGAAATTAAGG  
 GATTGTGAGACGGTGGCTTTTAAACGACAATAGTTTGTATTGGTGATTTCAAATGTGCCCT  
 TTGCCAATATACGAATTGGCGATAATAGGTACGATAGGCCCTTACATGATTCTAGTACTCT  
 TTGTCAAAAAGTCACTTGATTTGCTTTCATGATGGTGGACAAAGTAGCGATTATCTCTTCCA  
 CAGGAATCTATGGATAAGCGAACAGAAAACATCTTACAAGATATTCGTGAGACAACTGAAT  
 TTCTTGGTGGGGTTCGACTGCTGCTTAAAGGCCATTGACGGAACGAGTGTCA  
 CAACGGATATGTTATCTTCCAGAAACACTTAGACAAGGGATATGTGGCAGACGATTAG  
 CCTTTTCAGGTTCCATTGCTATGACAAGGATAGTGCATTTGGCTCAATCCTTATTTTG  
 ATGGAGAATAACAATAGCCAGGTGCTAGGAACCTACGAGGTGAGGAATTTAAACGGAGGAA  
 CACTTTCTGTTAAGGGGACTAGTGATGACTTGATTGCAAGTGTGAAACAGCTCTAAATC  
 ACGTTAAGGCCCAAGAGAGATTGATAGAAATGAGGTCACTTAACCCAGATGTGTTGA  
 CCAAAACAGTCAATGATACCTCCATTCCAGCTGAATGAGGGAAAACTAGGTCAGTACA  
 GTTTTGGTTATCAGGGGTCTACAGTTTACTATCGAGATAACAAAGGCATTTCGAGTCGGAA  
 CCAAGACGGAAGAAATCAGTTACTATGTCTGATGAAGAGGGCAACTTCAAGCATGGGACA  
 CCAACATTCTCAAAAGCAGATTGATCGCTTAAATGCCCTAGAAAGTACTGATAACACTG  
 CTCTGGATGTCTATGTGACCGATGATGCAGCCAAACGTGGTCAAGTTAAGGGGTATTATA  
 AAAAGACAGTTTCTATGAAGCTCCATTGCTTATAAAGAAAGTGGCAGGTATCAAAAGGAA  
 TGGTCGATATTGCGAATGCCATCAAGAAAGTATTGCCATTCAACGCTATTATGACTATG  
 ATAAGGAGACCTTTAACCACTTGTAGGCAACTCAATCGTACCTATGATAGCTTTGTCA  
 AACACTATGGGTATTGAATAGTGTGTGAACCGCAATCTTTTGTATAGTGATGATAAGT  
 ATTCGCTTCTGTAGTTTGAAGATGAAAGTCTGGATCCAAGTGAAGAGTCTGTTATCT  
 ATACTAAATCCCTTGCTTTGAGAAGGCTCTAGTGCCTGCTGAAAAAGAGGTTAAAAAGG  
 TGCATACCTGCCCTTATGCTTAAATTCGAGCTTGGCTGACGGACGAGGTGTGATTTCG  
 CTTATATGATGCTCTATCTACAGGTGAATCGCAGATGACCTTGATTGAGGAGTTAGGCG  
 ACCTCATTATGCTGATCCTGAGAAGTATTGAATGGAGAATTGACCTATGTTTCTCGCC  
 AAGACTTCTTTTCAGGGGATGTCGTCACTAAGTTAGAAGTGGTAGATCTATTGCTCAAAC  
 AAGACAATCAGGACTTAACTGGTCACTTATGCGGGACTTCTAGAAGCTATCAAAACGAG  
 CCCGATATCTTTTGGCAGACATTGATTATCGAATCGGTTACGCTGGATTCTCTGGCTG  
 TTTATGAAAAATTTGCCCAAGAAACCTTTATGGGGAAGCCTATGAAGTGTGAGACCAAG  
 AAGTAGCGACAGTCTGAGAAGTCAAGTCCATGACGGGGTATCACTTACCAATCTAAGT  
 TTGCCCTACACCTATTCCAACGCAACGGATAGGAGTTTAGGTGCTCCTGCTTACGCTATG  
 ATAGTGTGCAAAAATCTTTGAAAATCTCCTGAATTCCAATCAACCAACCATCACAAAAAC  
 AAGTTGTGCAAGGGGATAAGAAAAAGATGTGACGGATGTAGAGAAAAACACGGTCTGCTG  
 GTGCCAAGGAACACACCTTACAAGAACTCTTTCAAGGTTTGTAGCAAGTATCCAGAAG  
 TCCAACAAATGATTGAAGACACCTATAATAGGCTCTACAATCGTACGGTATCAAAAGTCT  
 ATGATGTAGTCAATTAACCAATTGATGGAAGTCTCAGAAATATCTCTTACGCTCTCACC  
 AAAAGAAATGCCATTCAACGAATTGTGAGGAAAAACGTGCTCTACTAGCTCATGAAGTTG  
 GTTCAGGTAAACACTTACCATGCTTGGGGCAGGATTCAAACTGAAAGAACTCGGAATGG  
 TACATAAACCACTTTATGTGGTGGCTGCTAGTCTGACTGCTCAGTTGGTCAAGAAATCA  
 TGAATTTTTCCTTCAACGAAGTCTATGTGACTACTAAGAAAGACTTTGCCAAAGCCA  
 AACGCAAGCAGTTTGTGCTCCGTATTATTACAGGGGACTATGATGCCATTGTGATTGGGG  
 ATTCACAAATTTGAGAAGATACCGATGAGTCTGAAAAACAGGTCACTTATCAATGACA  
 AACCTTGAGCAACTCCGAGAAATCAAGCTAGGAAGTGACAGTGAATTACACGGTGAAGAAG  
 CGGAACGTTGATTGAAGGATTAGAACCAGGTTGGAAGAACTCCAAAACTAGAGCGAG